

Weibo Xie

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

7,836
citations

66250

44
h-index

64407

83
g-index

91
all docs

91
docs citations

91
times ranked

9222
citing authors

#	ARTICLE	IF	CITATIONS
1	CancerMIRNome: an interactive analysis and visualization database for miRNome profiles of human cancer. <i>Nucleic Acids Research</i> , 2022, 50, D1139-D1146.	6.5	49
2	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. <i>Nature Communications</i> , 2022, 13, 820.	5.8	4
3	Multi-omics analysis dissects the genetic architecture of seed coat content in <i>Brassica napus</i> . <i>Genome Biology</i> , 2022, 23, 86.	3.8	23
4	Fixation of hybrid sterility genes and favorable alleles of key yield-related genes with dominance contribute to the high yield of the Yongyou series of intersubspecific hybrid rice. <i>Journal of Genetics and Genomics</i> , 2022, 49, 448-457.	1.7	2
5	Identification of Expression QTL by QTLtools in a Rice Recombinant Inbred Line Population. <i>Bio-protocol</i> , 2022, , .	0.2	0
6	Boosting predictabilities of agronomic traits in rice using bivariate genomic selection. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	6
7	Genome- and transcriptome-wide association studies provide insights into the genetic basis of natural variation of seed oil content in <i>Brassica napus</i> . <i>Molecular Plant</i> , 2021, 14, 470-487.	3.9	107
8	Genome-wide association study of flowering time reveals complex genetic heterogeneity and epistatic interactions in rice. <i>Gene</i> , 2021, 770, 145353.	1.0	6
9	PlantDeepSEA, a deep learning-based web service to predict the regulatory effects of genomic variants in plants. <i>Nucleic Acids Research</i> , 2021, 49, W523-W529.	6.5	20
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	Bract suppression regulated by the miR156/529-SPLs-NL1-PLA1 module is required for the transition from vegetative to reproductive branching in rice. <i>Molecular Plant</i> , 2021, 14, 1168-1184.	3.9	35
12	The Bnapus50K array: a quick and versatile genotyping tool for <i>Brassica napus</i> genomic breeding and research. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	11
13	An inferred functional impact map of genetic variants in rice. <i>Molecular Plant</i> , 2021, 14, 1584-1599.	3.9	48
14	Analysis of trait heritability in functionally partitioned rice genomes. <i>Heredity</i> , 2020, 124, 485-498.	1.2	7
15	Features of sRNA biogenesis in rice revealed by genetic dissection of sRNA expression level. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3207-3216.	1.9	2
16	ATAC-seq with unique molecular identifiers improves quantification and footprinting. <i>Communications Biology</i> , 2020, 3, 675.	2.0	21
17	A laminâ€like protein OsNMCP1 regulates drought resistance and root growth through chromatin accessibility modulation by interacting with a chromatin remodeller OsSWI3C in rice. <i>New Phytologist</i> , 2020, 227, 65-83.	3.5	20
18	Genomeâ€wide association analyses reveal the genetic basis of combining ability in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 2211-2222.	4.1	26

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19	Identification of optimal prediction models using multi-omic data for selecting hybrid rice. <i>Heredity</i> , 2019, 123, 395-406.	1.2	43
20	A directed learning strategy integrating multiple omic data improves genomic prediction. <i>Plant Biotechnology Journal</i> , 2019, 17, 2011-2020.	4.1	29
21	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	1.2	59
22	Rice Information GateWay: A Comprehensive Bioinformatics Platform for Indica Rice Genomes. <i>Molecular Plant</i> , 2018, 11, 505-507.	3.9	33
23	The E3 Ubiquitin Ligase HAF1 Modulates Circadian Accumulation of EARLY FLOWERING3 to Control Heading Date in Rice under Long-Day Conditions. <i>Plant Cell</i> , 2018, 30, 2352-2367.	3.1	28
24	Genome-Wide Association Studies Reveal the Genetic Basis of Ionomic Variation in Rice. <i>Plant Cell</i> , 2018, 30, 2720-2740.	3.1	164
25	Natural selection of a GSK3 determines rice mesocotyl domestication by coordinating strigolactone and brassinosteroid signaling. <i>Nature Communications</i> , 2018, 9, 2523.	5.8	60
26	Genome-wide association studies reveal that members of bHLH subfamily 16 share a conserved function in regulating flag leaf angle in rice (<i>Oryza sativa</i>). <i>PLoS Genetics</i> , 2018, 14, e1007323.	1.5	52
27	Genome-wide Association Analyses Reveal the Genetic Basis of Stigma Exsertion in Rice. <i>Molecular Plant</i> , 2017, 10, 634-644.	3.9	66
28	Genetic Architecture of Natural Variation in Rice Nonphotochemical Quenching Capacity Revealed by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2017, 8, 1773.	1.7	33
29	Genome-Wide Association Analysis Reveals Different Genetic Control in Panicle Architecture Between <i>Indica</i> and <i>Japonica</i> Rice. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0115.	1.6	57
30	Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. <i>Scientific Reports</i> , 2016, 6, 18936.	1.6	68
31	Origination and Establishment of a Trigenic Reproductive Isolation System in Rice. <i>Molecular Plant</i> , 2016, 9, 1542-1545.	3.9	18
32	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
33	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
34	Genomewide association analysis for awn length linked to the seed shattering gene qSH1 in rice. <i>Journal of Genetics</i> , 2016, 95, 639-646.	0.4	10
35	A Novel Tiller Angle Gene, TAC3, together with TAC1 and D2 Largely Determine the Natural Variation of Tiller Angle in Rice Cultivars. <i>PLoS Genetics</i> , 2016, 12, e1006412.	1.5	106
36	Genome-wide Association Study (GWAS) of mesocotyl elongation based on re-sequencing approach in rice. <i>BMC Plant Biology</i> , 2015, 15, 218.	1.6	116

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37	RiceVarMap: a comprehensive database of rice genomic variations. <i>Nucleic Acids Research</i> , 2015, 43, D1018-D1022.	6.5	219
38	Three CCT domain-containing genes were identified to regulate heading date by candidate gene-based association mapping and transformation in rice. <i>Scientific Reports</i> , 2015, 5, 7663.	1.6	61
39	Transcriptome-based analysis of mitogen-activated protein kinase cascades in the rice response to <i>Xanthomonas oryzae</i> infection. <i>Rice</i> , 2015, 8, 4.	1.7	36
40	Genetic Architecture of Natural Variation in Rice Chlorophyll Content Revealed by a Genome-Wide Association Study. <i>Molecular Plant</i> , 2015, 8, 946-957.	3.9	106
41	Loss of function of OsMADS3 via the insertion of a novel retrotransposon leads to recessive male sterility in rice (<i>Oryza sativa</i>). <i>Plant Science</i> , 2015, 238, 188-197.	1.7	14
42	Exploring the rice dispensable genome using a metagenome-like assembly strategy. <i>Genome Biology</i> , 2015, 16, 187.	3.8	90
43	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5411-9.	3.3	165
44	Genetic basis of sRNA quantitative variation analyzed using an experimental population derived from an elite rice hybrid. <i>ELife</i> , 2015, 4, e04250.	2.8	12
45	Identification of quantitative trait loci for phosphorus use efficiency traits in rice using a high density SNP map. <i>BMC Genetics</i> , 2014, 15, 155.	2.7	26
46	Natural Variation in the Sequence of SNAC1 and Its Expression Level Polymorphism in Rice Germplasms under Drought Stress. <i>Journal of Genetics and Genomics</i> , 2014, 41, 609-612.	1.7	14
47	A whole-genome SNP array (RICE6K) for genomic breeding in rice. <i>Plant Biotechnology Journal</i> , 2014, 12, 28-37.	4.1	163
48	Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice. <i>Nature Communications</i> , 2014, 5, 5087.	5.8	490
49	OsAAP6 functions as an important regulator of grain protein content and nutritional quality in rice. <i>Nature Communications</i> , 2014, 5, 4847.	5.8	214
50	Chalk5 encodes a vacuolar H ⁺ -translocating pyrophosphatase influencing grain chalkiness in rice. <i>Nature Genetics</i> , 2014, 46, 398-404.	9.4	281
51	An expression quantitative trait loci-guided co-expression analysis for constructing regulatory network using a rice recombinant inbred line population. <i>Journal of Experimental Botany</i> , 2014, 65, 1069-1079.	2.4	74
52	A High-Density SNP Genotyping Array for Rice Biology and Molecular Breeding. <i>Molecular Plant</i> , 2014, 7, 541-553.	3.9	251
53	Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism. <i>Nature Genetics</i> , 2014, 46, 714-721.	9.4	560
54	QTL Scanning for Rice Yield Using a Whole Genome SNP Array. <i>Journal of Genetics and Genomics</i> , 2013, 40, 629-638.	1.7	21

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55	Comparative Analysis of Differentially Expressed Genes in Rice Under Nitrogen and Phosphorus Starvation Stress Conditions. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 160-173.	1.0	45
56	Natural variation in Ghd7.1 plays an important role in grain yield and adaptation in rice. <i>Cell Research</i> , 2013, 23, 969-971.	5.7	222
57	Genetic composition of yield heterosis in an elite rice hybrid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15847-15852.	3.3	214
58	RNA-Directed DNA Methylation Is Involved in Regulating Photoperiod-Sensitive Male Sterility in Rice. <i>Molecular Plant</i> , 2012, 5, 1210-1216.	3.9	127
59	Rice functional genomics research: Progress and implications for crop genetic improvement. <i>Biotechnology Advances</i> , 2012, 30, 1059-1070.	6.0	100
60	Transcriptome response to nitrogen starvation in rice. <i>Journal of Biosciences</i> , 2012, 37, 731-747.	0.5	124
61	The Rice B-Box Zinc Finger Gene Family: Genomic Identification, Characterization, Expression Profiling and Diurnal Analysis. <i>PLoS ONE</i> , 2012, 7, e48242.	1.1	120
62	Transcriptome response to phosphorus starvation in rice. <i>Acta Physiologiae Plantarum</i> , 2012, 34, 327-341.	1.0	26
63	Reasons for lower transformation efficiency in indica rice using <i>Agrobacterium tumefaciens</i> -mediated transformation: lessons from transformation assays and genome-wide expression profiling. <i>Plant Molecular Biology</i> , 2012, 78, 1-18.	2.0	45
64	Comprehensive Sequence and Whole-Life-Cycle Expression Profile Analysis of the Phosphate Transporter Gene Family in Rice. <i>Molecular Plant</i> , 2011, 4, 1105-1122.	3.9	134
65	Dynamic programming procedure for searching optimal models to estimate substitution rates based on the maximum-likelihood method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7860-7865.	3.3	15
66	Gains in QTL Detection Using an Ultra-High Density SNP Map Based on Population Sequencing Relative to Traditional RFLP/SSR Markers. <i>PLoS ONE</i> , 2011, 6, e17595.	1.1	228
67	Genomic survey, characterization and expression profile analysis of the peptide transporter family in rice (<i>Oryza sativa</i> L.). <i>BMC Plant Biology</i> , 2010, 10, 92.	1.6	46
68	A dynamic gene expression atlas covering the entire life cycle of rice. <i>Plant Journal</i> , 2010, 61, 752-766.	2.8	326
69	A global analysis of QTLs for expression variations in rice shoots at the early seedling stage. <i>Plant Journal</i> , 2010, 63, 1063-1074.	2.8	69
70	Parent-independent genotyping for constructing an ultrahigh-density linkage map based on population sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10578-10583.	3.3	299
71	Exploring transcriptional signalling mediated by OsWRKY13, a potential regulator of multiple physiological processes in rice. <i>BMC Plant Biology</i> , 2009, 9, 74.	1.6	68
72	Expression profile of calcium-dependent protein kinase (CDPKs) genes during the whole lifespan and under phytohormone treatment conditions in rice (<i>Oryza sativa</i> L. ssp. indica). <i>Plant Molecular Biology</i> , 2009, 70, 311-325.	2.0	63

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73	Comprehensive sequence and expression profile analysis of Hsp20 gene family in rice. <i>Plant Molecular Biology</i> , 2009, 70, 341-357.	2.0	95
74	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
75	Molecular analyses of the rice glutamate dehydrogenase gene family and their response to nitrogen and phosphorous deprivation. <i>Plant Cell Reports</i> , 2009, 28, 1115-1126.	2.8	47
76	Multiple gene loci affecting genetic background-controlled disease resistance conferred by R gene Xa3/Xa26 in rice. <i>Theoretical and Applied Genetics</i> , 2009, 120, 127-138.	1.8	25
77	Aspartic proteases gene family in rice: Gene structure and expression, predicted protein features and phylogenetic relation. <i>Gene</i> , 2009, 442, 108-118.	1.0	63
78	Sequence and expression analysis of the thioredoxin protein gene family in rice. <i>Molecular Genetics and Genomics</i> , 2008, 280, 139-51.	1.0	58
79	KT/HAK/KUP potassium transporters gene family and their whole-life cycle expression profile in rice (<i>Oryza sativa</i>). <i>Molecular Genetics and Genomics</i> , 2008, 280, 437-52.	1.0	129
80	Systematic sequence analysis and identification of tissue-specific or stress-responsive genes of NAC transcription factor family in rice. <i>Molecular Genetics and Genomics</i> , 2008, 280, 547-563.	1.0	411
81	Comprehensive sequence and expression profile analysis of PEX11 gene family in rice. <i>Gene</i> , 2008, 412, 59-70.	1.0	29
82	Rice Gene Network Inferred from Expression Profiling of Plants Overexpressing OsWRKY13, a Positive Regulator of Disease Resistance. <i>Molecular Plant</i> , 2008, 1, 538-551.	3.9	52
83	Rice Gene Network Inferred from Expression Profiling of Plants Overexpressing OsWRKY13, a Positive Regulator of Disease Resistance. <i>Molecular Plant</i> , 2008, 1, 538-551.	3.9	131