

Zhiqiang Chen

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

866
citations

516710

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h-index

552781

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40
docs citations

40
times ranked

925
citing authors

#	ARTICLE	IF	CITATIONS
1	Low-temperature stress affects reactive oxygen species, osmotic adjustment substances, and antioxidants in rice (<i>Oryza sativa</i> L.) at the reproductive stage. <i>Scientific Reports</i> , 2022, 12, 6224.	3.3	15
2	The Class III peroxidase gene <i>OsPrx30</i> , transcriptionally modulated by the AT-hook protein <i>OsATH1</i> , mediates rice bacterial blight-induced ROS accumulation. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 393-408.	8.5	34
3	Identification of QTL and candidate genes involved in early seedling growth in rice via high-density genetic mapping and RNA-seq. <i>Crop Journal</i> , 2021, 9, 360-371.	5.2	14
4	Dynamic genome-wide association analysis and identification of candidate genes involved in anaerobic germination tolerance in rice. <i>Rice</i> , 2021, 14, 1.	4.0	48
5	Identification and candidate gene screening of qCIR9.1, a novel QTL associated with anther culturability in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2097-2111.	3.6	6
6	Genome-wide association study reveals early seedling vigour-associated quantitative trait loci in indica rice. <i>Euphytica</i> , 2021, 217, 1.	1.2	1
7	Time Course Analysis of Genome-Wide Identification of Mutations Induced by and Genes Expressed in Response to Carbon Ion Beam Irradiation in Rice (<i>Oryza sativa</i> L.). <i>Genes</i> , 2021, 12, 1391.	2.4	5
8	Genome-wide association study reveals novel genetic loci contributing to cold tolerance at the germination stage in indica rice. <i>Plant Science</i> , 2020, 301, 110669.	3.6	11
9	Global analysis of differentially expressed genes between two Japonica rice varieties induced by low temperature during the booting stage by RNA-Seq. <i>Royal Society Open Science</i> , 2020, 7, 192243.	2.4	12
10	Dynamic transcriptome and metabolome analyses of two types of rice during the seed germination and young seedling growth stages. <i>BMC Genomics</i> , 2020, 21, 603.	2.8	20
11	QTL mapping and haplotype analysis revealed candidate genes for grain thickness in rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314rgBT /Over	2.1	2
12	Identification of QTLs involved in cold tolerance during the germination and bud stages of rice (<i>Oryza sativa</i> L.) via a high-density genetic map. <i>Breeding Science</i> , 2020, 70, 292-302.	1.9	17
13	A single nucleotide mutation in the fourth exon of RBH1 is responsible for brown hull phenotype in rice. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	2
14	Identification of candidate genes controlling chilling tolerance of rice in the cold region at the booting stage by BSA-Seq and RNA-Seq. <i>Royal Society Open Science</i> , 2020, 7, 201081.	2.4	15
15	Metabolic profile analysis and identification of key metabolites during rice seed germination under low-temperature stress. <i>Plant Science</i> , 2019, 289, 110282.	3.6	75
16	Quantitative Trait Locus Analysis of Seed Germination and Early Seedling Growth in Rice. <i>Frontiers in Plant Science</i> , 2019, 10, 1582.	3.6	15
17	Genome-Wide Comparisons of Mutations Induced by Carbon-Ion Beam and Gamma-Rays Irradiation in Rice via Resequencing Multiple Mutants. <i>Frontiers in Plant Science</i> , 2019, 10, 1514.	3.6	27
18	Improvement of rice blast resistance by developing monogenic lines, two-gene pyramids and three-gene pyramid through MAS. <i>Rice</i> , 2019, 12, 78.	4.0	19

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19	Integrating GWAS, QTL, mapping and RNA-seq to identify candidate genes for seed vigor in rice (<i>Oryza</i>) Tj ETQq1 1,0,784314,rgBT /O	2.1	44
20	Development of a core SNP arrays based on the KASP method for molecular breeding of rice. <i>Rice</i> , 2019, 12, 21.	4.0	60
21	Identification of stable QTLs and candidate genes involved in anaerobic germination tolerance in rice via high-density genetic mapping and RNA-Seq. <i>BMC Genomics</i> , 2019, 20, 355.	2.8	39
22	Comparative Transcriptome Profile Analysis of Anther Development in Reproductive Stage of Rice in Cold Region Under Cold Stress. <i>Plant Molecular Biology Reporter</i> , 2019, 37, 129-145.	1.8	12
23	Development and utilization of functional KASP markers to improve rice eating and cooking quality through MAS breeding. <i>Euphytica</i> , 2019, 215, 1.	1.2	14
24	Characterization and Fine Mapping of a Leaf Wilt Mutant, <i>lwm3</i> , Induced by Heavy Ion Irradiation of Rice. <i>Crop Science</i> , 2019, 59, 2679-2688.	1.8	5
25	Identification of <i>Magnaporthe oryzae</i> -elicited rice novel miRNAs and their targets by miRNA and degradome sequencing. <i>European Journal of Plant Pathology</i> , 2018, 151, 629-647.	1.7	10
26	Pasting properties, grain-filling characteristics and allelic variation linked to the grain quality in diverse rice. <i>Euphytica</i> , 2017, 213, 1.	1.2	6
27	Marker-assisted selection for rice blast resistance genes <i>Pi2</i> and <i>Pi9</i> through high-resolution melting of a gene-targeted amplicon. <i>Plant Breeding</i> , 2017, 136, 67-73.	1.9	20
28	Analysis of a major rice blast resistance gene in the rice restorer line Hanghui 1179. <i>Euphytica</i> , 2017, 213, 1.	1.2	3
29	NBS-LRR Protein <i>Pik-H4</i> Interacts with <i>OsBIHD1</i> to Balance Rice Blast Resistance and Growth by Coordinating Ethylene-Brassinosteroid Pathway. <i>Frontiers in Plant Science</i> , 2017, 8, 127.	3.6	32
30	CONSTANS-Like 9 (<i>OsCOL9</i>) Interacts with Receptor for Activated C-Kinase 1 (<i>OsRACK1</i>) to Regulate Blast Resistance through Salicylic Acid and Ethylene Signaling Pathways. <i>PLoS ONE</i> , 2016, 11, e0166249.	2.5	30
31	Quantitative trait loci identification and meta-analysis for rice panicle-related traits. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1927-1940.	2.1	39
32	CONSTANS-like 9 (<i>COL9</i>) delays the flowering time in <i>Oryza sativa</i> by repressing the <i>Ehd1</i> pathway. <i>Biochemical and Biophysical Research Communications</i> , 2016, 479, 173-178.	2.1	40
33	High-resolution QTL mapping for grain appearance traits and co-localization of chalkiness-associated differentially expressed candidate genes in rice. <i>Rice</i> , 2016, 9, 48.	4.0	56
34	A genotyping platform assembled with high-throughput DNA extraction, codominant functional markers, and automated CE system to accelerate marker-assisted improvement of rice. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	6
35	Chromosome mapping, molecular cloning and expression analysis of a novel gene response for leaf width in rice. <i>Biochemical and Biophysical Research Communications</i> , 2016, 480, 394-401.	2.1	10
36	4-Coumarate-CoA Ligase-Like Gene <i>OsAAE3</i> Negatively Mediates the Rice Blast Resistance, Floret Development and Lignin Biosynthesis. <i>Frontiers in Plant Science</i> , 2016, 7, 2041.	3.6	41

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37	Identification of three major R genes responsible for broad-spectrum blast resistance in an indica rice accession. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	11
38	Stacking of five favorable alleles for amylase content, fragrance and disease resistance into elite lines in rice (<i>Oryza sativa</i>) by using four HRM-based markers and a linked gel-based marker. <i>Molecular Breeding</i> , 2014, 34, 805-815.	2.1	9
39	Identification and fine mapping of a major R gene to <i>Magnaporthe oryzae</i> in a broad-spectrum resistant germplasm in rice. <i>Molecular Breeding</i> , 2012, 30, 1715-1726.	2.1	10
40	Identification and fine mapping of a resistance gene to <i>Magnaporthe oryzae</i> in a space-induced rice mutant. <i>Molecular Breeding</i> , 2011, 28, 303-312.	2.1	27