

SNP-Seek database of SNPs derived from 3000 rice genes

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Challenging regulations: Managing risks in crop biotechnology. Food and Energy Security, 2015, 4, 87-91.	2.0	19
2	Genome-Wide Association of Rice Blast Disease Resistance and Yield-Related Components of Rice. Molecular Plant-Microbe Interactions, 2015, 28, 1383-1392.	1.4	68
3	Drought susceptibility of modern rice varieties: an effect of linkage of drought tolerance with undesirable traits. Scientific Reports, 2015, 5, 14799.	1.6	145
4	A trehalose-6-phosphate phosphatase enhances anaerobic germination tolerance in rice. Nature Plants, 2015, 1, 15124.	4.7	263
5	A knowledge-based molecular screen uncovers a broad spectrum <i>O</i> s<sup>14</sup>/i> resistance allele to bacterial blight from wild rice. Plant Journal, 2015, 84, 694-703.	2.8	181
6	MorTAL Kombat: the story of defense against TAL effectors through loss-of-susceptibility. Frontiers in Plant Science, 2015, 6, 535.	1.7	94
7	Assessing the genetic diversity of rice originating from Bangladesh, Assam and West Bengal. Rice, 2015, 8, 35.	1.7	63
8	Marker-Assisted Breeding. , 2015, , 95-144.		12
9	Current Technologies in Plant Molecular Breeding. , 2015, , .		6
10	Allele mining and enhanced genetic recombination for rice breeding. Rice, 2015, 8, 34.	1.7	57
11	Joint Mapping and Allele Mining of the Rolled Leaf Trait in Rice ( <i>Oryza sativa</i> L.). PLoS ONE, 2016, 11, e0158246.	1.1	24
12	An Efficient Strategy Combining SSR Markers- and Advanced QTL-seq-driven QTL Mapping Unravels Candidate Genes Regulating Grain Weight in Rice. Frontiers in Plant Science, 2016, 7, 1535.	1.7	21
13	Genetic Diversity and Population Structure of Rice Varieties Cultivated in Temperate Regions. Rice, 2016, 9, 58.	1.7	32
14	Genetic and root phenotype diversity in Sri Lankan rice landraces may be related to drought resistance. Rice, 2016, 9, 24.	1.7	5
15	Databases and bioinformatics tools for rice research. Current Plant Biology, 2016, 7-8, 39-52.	2.3	18
16	SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . Current Plant Biology, 2016, 7-8, 16-25.	2.3	48
17	Advances in breeding for high grain Zinc in Rice. Rice, 2016, 9, 49.	1.7	205
18	Self-similar characteristics of single nucleotide polymorphisms in the rice genome. Journal of the Korean Physical Society, 2016, 69, 1591-1596.	0.3	0

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19	Translational genomics for plant breeding with the genome sequence explosion. <i>Plant Biotechnology Journal</i> , 2016, 14, 1057-1069.	4.1	46
20	From promise to application: root traits for enhanced nutrient capture in rice breeding. <i>Journal of Experimental Botany</i> , 2016, 67, 3605-3615.	2.4	79
21	JBrowse: a dynamic web platform for genome visualization and analysis. <i>Genome Biology</i> , 2016, 17, 66.	3.8	690
22	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016, 9, 975-985.	3.9	102
23	Flood and drought tolerance in rice: opposite but may coexist. <i>Food and Energy Security</i> , 2016, 5, 76-88.	2.0	52
24	The Argonaute binding platform of <i>NRPE1</i> evolves through modulation of intrinsically disordered repeats. <i>New Phytologist</i> , 2016, 212, 1094-1105.	3.5	16
25	Genetic factors underlying boron toxicity tolerance in rice: genome-wide association study and transcriptomic analysis. <i>Journal of Experimental Botany</i> , 2017, 68, erw423.	2.4	31
26	Nucleotide diversity analysis highlights functionally important genomic regions. <i>Scientific Reports</i> , 2016, 6, 35730.	1.6	48
27	Updated Rice Kinase Database RKD 2.0: enabling transcriptome and functional analysis of rice kinase genes. <i>Rice</i> , 2016, 9, 40.	1.7	20
28	GigaGenotype investigator for genome-wide analyses. <i>GigaScience</i> , 2016, 5, 25.	3.3	20
29	Ricebase: a breeding and genetics platform for rice, integrating individual molecular markers, pedigrees and whole-genome-based data. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw107.	1.4	30
30	SNP-based analysis of genetic diversity reveals important alleles associated with seed size in rice. <i>BMC Plant Biology</i> , 2016, 16, 93.	1.6	42
31	Genome-wide DNA polymorphism in the <i>indica</i> rice varieties RGD-7S and Taifeng B as revealed by whole genome re-sequencing. <i>Genome</i> , 2016, 59, 197-207.	0.9	13
32	Developing maps of fitness consequences for plant genomes. <i>Current Opinion in Plant Biology</i> , 2016, 30, 101-107.	3.5	13
33	The role of root size versus root efficiency in phosphorus acquisition in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 1179-1189.	2.4	101
34	Rice Improvement Through Genome-Based Functional Analysis and Molecular Breeding in India. <i>Rice</i> , 2016, 9, 1.	1.7	111
35	Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. <i>Heredity</i> , 2016, 116, 395-408.	1.2	296
36	Information Commons for Rice (IC4R). <i>Nucleic Acids Research</i> , 2016, 44, D1172-D1180.	6.5	41

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37	Increased novel single nucleotide polymorphisms in weedy rice populations associated with the change of farming styles: Implications in adaptive mutation and evolution. <i>Journal of Systematics and Evolution</i> , 2017, 55, 149-157.	1.6	3
38	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	3.5	68
39	RPAN: rice pan-genome browser for ~¼3000 rice genomes. <i>Nucleic Acids Research</i> , 2017, 45, 597-605.	6.5	156
40	Genetic Architecture of a Rice Nested Association Mapping Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1913-1926.	0.8	71
41	Genome-wide Association Analysis Tracks Bacterial Leaf Blight Resistance Loci In Rice Diverse Germplasm. <i>Rice</i> , 2017, 10, 8.	1.7	49
42	Genome-wide association study of salt tolerance at the seed germination stage in rice. <i>BMC Plant Biology</i> , 2017, 17, 92.	1.6	120
43	Evolutionary relationships and expression analysis of EUL domain proteins in rice ( <i>Oryza sativa</i> ). <i>Rice</i> , 2017, 10, 26.	1.7	31
44	Past and Future Use of Wild Relatives in Crop Breeding. <i>Crop Science</i> , 2017, 57, 1070-1082.	0.8	446
45	OsLG3 contributing to rice grain length and yield was mined by Ho-LAMap. <i>BMC Biology</i> , 2017, 15, 28.	1.7	100
46	A natural tandem array alleviates epigenetic repression of IPA1 and leads to superior yielding rice. <i>Nature Communications</i> , 2017, 8, 14789.	5.8	149
47	Translating knowledge about abiotic stress tolerance to breeding programmes. <i>Plant Journal</i> , 2017, 90, 898-917.	2.8	154
48	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <i>Scientific Reports</i> , 2017, 7, 12478.	1.6	69
49	Engineering species-like barriers to sexual reproduction. <i>Nature Communications</i> , 2017, 8, 883.	5.8	41
50	Crosstalk between diurnal rhythm and water stress reveals an altered primary carbon flux into soluble sugars in drought-treated rice leaves. <i>Scientific Reports</i> , 2017, 7, 8214.	1.6	15
51	Allelic variation of the rice blast resistance gene <i>Pid3</i> in cultivated rice worldwide. <i>Scientific Reports</i> , 2017, 7, 10362.	1.6	19
52	The Genetics of Plant Metabolism. <i>Annual Review of Genetics</i> , 2017, 51, 287-310.	3.2	118
53	Approaches in Characterizing Genetic Structure and Mapping in a Rice Multiparental Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1721-1730.	0.8	28
54	Genome-wide and gene-based association mapping for rice eating and cooking characteristics and protein content. <i>Scientific Reports</i> , 2017, 7, 17203.	1.6	60

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55	A single base change explains the independent origin of and selection for the nonshattering gene in African rice domestication. <i>New Phytologist</i> , 2017, 213, 1925-1935.	3.5	23
56	Predicting rice hybrid performance using univariate and multivariate GBLUP models based on North Carolina mating design II. <i>Heredity</i> , 2017, 118, 302-310.	1.2	99
57	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081.	6.5	290
58	New Candidate Genes Affecting Rice Grain Appearance and Milling Quality Detected by Genome-Wide and Gene-Based Association Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1998.	1.7	55
59	Regional Association Analysis of MetaQTLs Delineates Candidate Grain Size Genes in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 807.	1.7	36
60	Simultaneous Improvement and Genetic Dissection of Salt Tolerance of Rice ( <i>Oryza sativa</i> L.) by Designed QTL Pyramiding. <i>Frontiers in Plant Science</i> , 2017, 8, 1275.	1.7	45
61	Toward Genomics-Based Breeding in C3 Cool-Season Perennial Grasses. <i>Frontiers in Plant Science</i> , 2017, 8, 1317.	1.7	11
62	Nucleotide patterns aiding in prediction of eukaryotic promoters. <i>PLoS ONE</i> , 2017, 12, e0187243.	1.1	19
63	Allelic variants of <i>OsHKT1;1</i> underlie the divergence between indica and japonica subspecies of rice ( <i>Oryza sativa</i> ) for root sodium content. <i>PLoS Genetics</i> , 2017, 13, e1006823.	1.5	118
64	Genome-wide association mapping for root cone angle in rice. <i>Rice</i> , 2017, 10, 45.	1.7	25
65	Single-base resolution map of evolutionary constraints and annotation of conserved elements across major grass genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 473-488.	1.1	11
66	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
67	Databases for Rice Omics Studies. , 2018, , 541-554.		1
68	Characterization of <i>OglDREB2A</i> gene from African rice ( <i>Oryza glaberrima</i> ), comparative analysis and its transcriptional regulation under salinity stress. <i>3 Biotech</i> , 2018, 8, 91.	1.1	10
69	Overexpression of miR164b-resistant <i>OsNAC2</i> improves plant architecture and grain yield in rice. <i>Journal of Experimental Botany</i> , 2018, 69, 1533-1543.	2.4	66
70	Natural variation reveals that <i>OsSAP16</i> controls low-temperature germination in rice. <i>Journal of Experimental Botany</i> , 2018, 69, 413-421.	2.4	81
71	Preferential Geographic Distribution Pattern of Abiotic Stress Tolerant Rice. <i>Rice</i> , 2018, 11, 10.	1.7	21
72	Novel sequences, structural variations and gene presence variations of Asian cultivated rice. <i>Scientific Data</i> , 2018, 5, 180079.	2.4	14

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73	QTL mapping and candidate gene analysis of peduncle vascular bundle related traits in rice by genome-wide association study. <i>Rice</i> , 2018, 11, 13.	1.7	45
74	Rice Genomics: over the Past Two Decades and into the Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 397-404.	3.0	46
75	Comparative whole genome re-sequencing analysis in upland New Rice for Africa: insights into the breeding history and respective genome compositions. <i>Rice</i> , 2018, 11, 33.	1.7	9
76	A simple way to visualize detailed phylogenetic tree of huge genome-wide SNP data constructed by SNPhylo. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1972-1978.	1.7	5
77	Predicting Rice Phenotypes with Meta-learning. <i>Lecture Notes in Computer Science</i> , 2018, , 144-158.	1.0	2
78	The Application of Multi-Locus GWAS for the Detection of Salt-Tolerance Loci in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 1464.	1.7	94
79	Physiological characterization and allelic diversity of selected drought tolerant traditional rice ( <i>Oryza sativa</i> L.) landraces of Koraput, India. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 1035-1046.	1.4	35
80	DNA fingerprinting at farm level maps rice biodiversity across Bangladesh and reveals regional varietal preferences. <i>Scientific Reports</i> , 2018, 8, 14920.	1.6	20
81	An imputation platform to enhance integration of rice genetic resources. <i>Nature Communications</i> , 2018, 9, 3519.	5.8	65
82	Association mapping in rice: basic concepts and perspectives for molecular breeding. <i>Plant Production Science</i> , 2018, 21, 159-176.	0.9	28
83	Genetic Architecture and Candidate Genes for Deep-Sowing Tolerance in Rice Revealed by Non-syn GWAS. <i>Frontiers in Plant Science</i> , 2018, 9, 332.	1.7	49
84	Genetic Basis Underlying Correlations Among Growth Duration and Yield Traits Revealed by GWAS in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 650.	1.7	28
85	MCRiceRepGP: a framework for the identification of genes associated with sexual reproduction in rice. <i>Plant Journal</i> , 2018, 96, 188-202.	2.8	13
86	Genome-wide association and gene validation studies for early root vigour to improve direct seeding of rice. <i>Plant, Cell and Environment</i> , 2018, 41, 2731-2743.	2.8	35
87	Genome-wide association study of seedling stage salinity tolerance in temperate japonica rice germplasm. <i>BMC Genetics</i> , 2018, 19, 2.	2.7	39
88	Identification of novel mutations in the rice starch branching enzyme I gene via TILLING by sequencing. <i>Euphytica</i> , 2018, 214, 1.	0.6	10
89	Genome-wide association mapping of aluminum toxicity tolerance and fine mapping of a candidate gene for Nrat1 in rice. <i>PLoS ONE</i> , 2018, 13, e0198589.	1.1	24
90	High-resolution mapping and characterization of <i>Xa42</i> , a resistance gene against multiple <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> races in rice ( <i>Oryza sativa</i> L.). <i>Breeding Science</i> , 2018, 68, 188-199.	0.9	8

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91	Rice with reduced stomatal density conserves water and has improved drought tolerance under future climate conditions. <i>New Phytologist</i> , 2019, 221, 371-384.	3.5	330
92	Genetic Interactions Among Ghd7, Ghd8, OsPRR37 and Hd1 Contribute to Large Variation in Heading Date in Rice. <i>Rice</i> , 2019, 12, 48.	1.7	57
93	Infrastructures of systems biology that facilitate functional genomic study in rice. <i>Rice</i> , 2019, 12, 15.	1.7	21
94	1k-RiCA (1K-Rice Custom Amplicon) a novel genotyping amplicon-based SNP assay for genetics and breeding applications in rice. <i>Rice</i> , 2019, 12, 55.	1.7	46
95	MaizeSNPDB: A comprehensive database for efficient retrieve and analysis of SNPs among 1210 maize lines. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1377-1383.	1.9	12
96	Discovery of Functional SNPs via Genome-Wide Exploration of Malaysian Pigmented Rice Varieties. <i>International Journal of Genomics</i> , 2019, 2019, 1-12.	0.8	4
97	Identification of Superior Alleles for Seedling Stage Salt Tolerance in the USDA Rice Mini-Core Collection. <i>Plants</i> , 2019, 8, 472.	1.6	23
98	Mapping of genomic regions associated with arsenic toxicity stress in a backcross breeding populations of rice ( <i>Oryza sativa</i> L.). <i>Rice</i> , 2019, 12, 61.	1.7	31
99	Benchmarking database systems for Genomic Selection implementation. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	7
100	Association analysis of rice grain traits with single nucleotide polymorphisms in a Brassinosteroid-insensitive 1 (BR1)-associated receptor kinase 1-like gene. <i>Plant Gene</i> , 2019, 19, 100188.	1.4	1
101	Molecular characterization and expression dynamics of MTP genes under various spatio-temporal stages and metal stress conditions in rice. <i>PLoS ONE</i> , 2019, 14, e0217360.	1.1	34
102	Dissecting the genome-wide genetic variants of milling and appearance quality traits in rice. <i>Journal of Experimental Botany</i> , 2019, 70, 5115-5130.	2.4	30
103	Development of introgression lines of AA genome <i>Oryza</i> species, <i>O. glaberrima</i> , <i>O. rufipogon</i> , and <i>O. nivara</i> , in the genetic background of <i>O. sativa</i> L. cv. Taichung 65. <i>Breeding Science</i> , 2019, 69, 359-363.	0.9	8
104	Rice Galaxy: an open resource for plant science. <i>GigaScience</i> , 2019, 8, .	3.3	11
105	Genome-wide association study and linkage analysis on resistance to rice black-streaked dwarf virus disease. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	11
106	Development of a core SNP arrays based on the KASP method for molecular breeding of rice. <i>Rice</i> , 2019, 12, 21.	1.7	60
107	Gigva v2"Extended and improved genotype investigator. <i>GigaScience</i> , 2019, 8, .	3.3	20
109	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880.	2.4	112

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110	Identification of novel mutations in genes involved in silicon and arsenic uptake and accumulation in rice. <i>Euphytica</i> , 2019, 215, 1.	0.6	1
111	Genotypic differences in shoot silicon concentration and the impact on grain arsenic concentration in rice. <i>Journal of Plant Nutrition and Soil Science</i> , 2019, 182, 265-276.	1.1	13
112	Tracking the origin of two genetic components associated with transposable element bursts in domesticated rice. <i>Nature Communications</i> , 2019, 10, 641.	5.8	34
113	Identification of genes for salt tolerance and yield-related traits in rice plants grown hydroponically and under saline field conditions by genome-wide association study. <i>Rice</i> , 2019, 12, 88.	1.7	105
114	Harmonizing technological advances in phenomics and genomics for enhanced salt tolerance in rice from a practical perspective. <i>Rice</i> , 2019, 12, 89.	1.7	24
115	Rice Stress-Resistant SNP Database. <i>Rice</i> , 2019, 12, 97.	1.7	9
116	Genome-wide associated study identifies NAC42-activated nitrate transporter conferring high nitrogen use efficiency in rice. <i>Nature Communications</i> , 2019, 10, 5279.	5.8	153
117	Haplotype Characterization of the sd1 Semidwarf Gene in United States Rice. <i>Plant Genome</i> , 2019, 12, 190010.	1.6	16
118	Next-Generation Sequencing Accelerates Crop Gene Discovery. <i>Trends in Plant Science</i> , 2019, 24, 263-274.	4.3	111
119	NGS sequencing reveals that many of the genetic variations in transgenic rice plants match the variations found in natural rice population. <i>Genes and Genomics</i> , 2019, 41, 213-222.	0.5	8
120	Origin, taxonomy, and phylogenetics of rice. , 2019, , 1-29.		6
121	Translational genomics and multi-omics integrated approaches as a useful strategy for crop breeding. <i>Genes and Genomics</i> , 2019, 41, 133-146.	0.5	34
122	Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019, 20, 565-571.	3.2	4
123	Hybrid breeding of rice via genomic selection. <i>Plant Biotechnology Journal</i> , 2020, 18, 57-67.	4.1	87
124	Towards a deeper haplotype mining of complex traits in rice with <sc>RFGB</sc> v2.0. <i>Plant Biotechnology Journal</i> , 2020, 18, 14-16.	4.1	78
125	The Green Revolution shaped the population structure of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i>. <i>ISME Journal</i> , 2020, 14, 492-505.	4.4	29
126	An evaluation of machine-learning for predicting phenotype: studies in yeast, rice, and wheat. <i>Machine Learning</i> , 2020, 109, 251-277.	3.4	88
127	Identification of genetic loci for leaf hair development in rice through genome-wide association study. <i>Plant Growth Regulation</i> , 2020, 90, 101-108.	1.8	1



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128	Applications and challenges for efficient exploration of omics interventions for the enhancement of nutritional quality in rice ( <i>Oryza sativa</i> L.). <i>Critical Reviews in Food Science and Nutrition</i> , 2020, 60, 3304-3320.	5.4	29
129	Genome-wide association study identifies QTLs conferring salt tolerance in rice. <i>Plant Breeding</i> , 2020, 139, 73-82.	1.0	19
130	Cloning and characterization of a gene encoding MIZ1, a domain of unknown function protein and its role in salt and drought stress in rice. <i>Protoplasma</i> , 2020, 257, 475-487.	1.0	18
131	Time for a paradigm shift in the use of plant genetic resources. <i>Genome</i> , 2020, 63, 189-194.	0.9	13
132	Rapid prediction of head rice yield and grain shape for genome-wide association study in indica rice. <i>Journal of Cereal Science</i> , 2020, 96, 103091.	1.8	12
133	Genetic architecture to cause dynamic change in tiller and panicle numbers revealed by genome-wide association study and transcriptome profile in rice. <i>Plant Journal</i> , 2020, 104, 1603-1616.	2.8	12
134	Presence of the HPPD Inhibitor Sensitive 1 Gene and ALSS653N Mutation in Weedy <i>Oryza sativa</i> Sensitive to Benzobicyclon. <i>Plants</i> , 2020, 9, 1576.	1.6	4
135	Resequencing of a Core Rice Mutant Population Induced by Gamma-Ray Irradiation and Its Application in a Genome-Wide Association Study. <i>Journal of Plant Biology</i> , 2020, 63, 463-472.	0.9	14
136	Predicting rice phenotypes with meta and multi-target learning. <i>Machine Learning</i> , 2020, 109, 2195-2212.	3.4	3
137	Breeding and biotechnological interventions for trait improvement: status and prospects. <i>Planta</i> , 2020, 252, 54.	1.6	48
138	Identify QTLs and candidate genes underlying source-, sink-, and grain yield-related traits in rice by integrated analysis of bi-parental and natural populations. <i>PLoS ONE</i> , 2020, 15, e0237774.	1.1	6
139	BarleyVarDB: a database of barley genomic variation. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	13
140	Epistasis and Quantitative Resistance to <i>Pyricularia oryzae</i> Revealed by GWAS in Advanced Rice Breeding Populations. <i>Agriculture (Switzerland)</i> , 2020, 10, 622.	1.4	1
141	Choosing the optimal population for a genome-wide association study: A simulation of whole-genome sequences from rice. <i>Plant Genome</i> , 2020, 13, e20005.	1.6	9
142	Genome-wide analysis of polymorphisms identified domestication-associated long low-diversity region carrying important rice grain size/weight quantitative trait loci. <i>Plant Journal</i> , 2020, 103, 1525-1547.	2.8	9
143	Designing a Mini-Core Collection Effectively Representing 3004 Diverse Rice Accessions. <i>Plant Communications</i> , 2020, 1, 100049.	3.6	21
144	A novel intragenic marker targeting the ectodomain of bacterial blight-resistance gene <i>Xa21</i> for marker-assisted selection in rice. <i>Journal of Crop Improvement</i> , 2020, 34, 824-841.	0.9	1
145	Differentiation, evolution and utilization of natural alleles for cold adaptability at the reproductive stage in rice. <i>Plant Biotechnology Journal</i> , 2020, 18, 2491-2503.	4.1	27

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146	Over-Expression of HDA710 Delays Leaf Senescence in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 471.	2.0	10
147	Characterization of the transcriptional divergence between the subspecies of cultivated rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.2	16
148	Transcriptional regulation of genes bearing intronic heterochromatin in the rice genome. <i>PLoS Genetics</i> , 2020, 16, e1008637.	1.5	23
149	uORFlight: a vehicle toward uORF-mediated translational regulation mechanisms in eukaryotes. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	24
150	Combination of DNA markers and eQTL information for introgression of multiple salt-tolerance traits in rice. , 2020, , 1-22.		0
151	RAINBOW: Haplotype-based genome-wide association study using a novel SNP-set method. <i>PLoS Computational Biology</i> , 2020, 16, e1007663.	1.5	46
152	Glycosyltransferase OsUGT90A1 helps protect the plasma membrane during chilling stress in rice. <i>Journal of Experimental Botany</i> , 2020, 71, 2723-2739.	2.4	36
153	Nucleotide variations of 9-cis-epoxycarotenoid dioxygenase 2 (NCED2) and pericarp coloration genes (Rc and Rd) from upland rice varieties. <i>3 Biotech</i> , 2020, 10, 105.	1.1	4
154	Comparative population genomic analysis provides insights into breeding of modern indica rice in China. <i>Gene</i> , 2021, 768, 145303.	1.0	1
155	Evolution and diversification of reproductive phased small interfering RNAs in <i>Oryza</i> species. <i>New Phytologist</i> , 2021, 229, 2970-2983.	3.5	12
156	Genome-Wide Association Study on Resistance to Rice Black-Streaked Dwarf Disease Caused by Rice black-streaked dwarf virus. <i>Plant Disease</i> , 2021, 105, 607-615.	0.7	11
157	Review of Dimension Reduction Methods. <i>Journal of Data Analysis and Information Processing</i> , 2021, 09, 189-231.	0.7	17
158	Genomic Designing for Biotic Stress Resistant Rice. , 2021, , 1-58.		0
159	Exploring Natural Allelic Variations of the Î²-Triketone Herbicide Resistance Gene HIS1 for Application in indica Rice and Particularly in Two-Line Hybrid Rice. <i>Rice</i> , 2021, 14, 7.	1.7	5
160	Introduction of the Databases of Rice. , 2021, , 51-69.		0
161	Omics Approaches for Elucidating Abiotic Stress Responses in Plants. , 2021, , 169-189.		1
162	OsTPR boosts the superior grains through increase in upper secondary rachis branches without incurring a grain quality penalty. <i>Plant Biotechnology Journal</i> , 2021, 19, 1396-1411.	4.1	9
163	Genetic dissection of rice appearance quality and cooked rice elongation by genome-wide association study. <i>Crop Journal</i> , 2021, 9, 1470-1480.	2.3	10

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164	Nitrogen Challenges and Opportunities for Agricultural and Environmental Science in India. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	1.8	29
165	Computational Analysis of Rice Transcriptomic and Genomic Datasets in Search for SNPs Involved in Flavonoid Biosynthesis. , 0, , .		0
166	OryzaGenome2.1: Database of Diverse Genotypes in Wild Oryza Species. <i>Rice</i> , 2021, 14, 24.	1.7	17
167	Strategies to Modulate Specialized Metabolism in Mediterranean Crops: From Molecular Aspects to Field. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2887.	1.8	29
169	Drought Tolerance in Rice: Focus on Recent Mechanisms and Approaches. <i>Rice Science</i> , 2021, 28, 119-132.	1.7	129
170	Genome-Wide Association Study Reveals the QTLs for Seed Storability in World Rice Core Collections. <i>Plants</i> , 2021, 10, 812.	1.6	9
171	Identification and mapping of a novel resistance gene to the rice pathogen, <i>Cercospora janseana</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 2221-2234.	1.8	6
172	Emerging Molecular Strategies for Improving Rice Drought Tolerance. <i>Current Genomics</i> , 2021, 22, 16-25.	0.7	6
173	A drought-responsive rice amidohydrolase is the elusive plant guanine deaminase with the potential to modulate the epigenome. <i>Physiologia Plantarum</i> , 2021, 172, 1853-1866.	2.6	2
174	Enriched-GWAS and Transcriptome Analysis to Refine and Characterize a Major QTL for Anaerobic Germination Tolerance in Rice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4445.	1.8	7
175	Smart Breeding for Climate Resilient Agriculture. , 0, , .		2
176	Estimation of the Genetic Diversity and Population Structure of Thailand's Rice Landraces Using SNP Markers. <i>Agronomy</i> , 2021, 11, 995.	1.3	13
177	Genetic Variability through Induced Mutation. , 0, , .		1
178	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
179	Unraveling regulatory divergence, heterotic malleability, and allelic imbalance switching in rice due to drought stress. <i>Scientific Reports</i> , 2021, 11, 13489.	1.6	3
180	The New Is Old: Novel Germination Strategy Evolved From Standing Genetic Variation in Weedy Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 699464.	1.7	5
181	Genome-Wide Association Study of the Genetic Basis of Effective Tiller Number in Rice. <i>Rice</i> , 2021, 14, 56.	1.7	14
182	Genomic Prediction across Structured Hybrid Populations and Environments in Maize. <i>Plants</i> , 2021, 10, 1174.	1.6	5

#	ARTICLE	IF	CITATIONS
183	Identification and analysis of the structure, expression and nucleotide polymorphism of the GPAT gene family in rice. <i>Plant Gene</i> , 2021, 26, 100290.	1.4	7
184	Rewilding crops for climate resilience: economic analysis and <i>de novo</i> domestication strategies. <i>Journal of Experimental Botany</i> , 2021, 72, 6123-6139.	2.4	52
185	Identification of quantitative trait loci associated with resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> pathotypes prevalent in South China. <i>Crop Journal</i> , 2022, 10, 498-507.	2.3	4
186	Rice Blast Disease in India: Present Status and Future Challenges. , 0, , .		5
187	<i>OsPDCD5</i> negatively regulates plant architecture and grain yield in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	17
188	Identification and allele mining of new candidate genes underlying rice grain weight and grain shape by genome-wide association study. <i>BMC Genomics</i> , 2021, 22, 602.	1.2	13
189	Validation of Genes Affecting Rice Grain Zinc Content Through Candidate Gene-Based Association Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 701658.	1.1	4
190	Identification of SNPs in rice GPAT genes and in silico analysis of their functional impact on GPAT proteins. <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2021, 49, 12346.	0.5	0
191	An inferred functional impact map of genetic variants in rice. <i>Molecular Plant</i> , 2021, 14, 1584-1599.	3.9	48
192	Enhancing genetic gains through marker-assisted recurrent selection: from phenotyping to genotyping. <i>Cereal Research Communications</i> , 2022, 50, 523-538.	0.8	5
193	Omics for the Improvement of Abiotic, Biotic, and Agronomic Traits in Major Cereal Crops: Applications, Challenges, and Prospects. <i>Plants</i> , 2021, 10, 1989.	1.6	39
194	Prototype for developing SNP markers from GWAS and biparental QTL for rice panicle and grain traits. <i>Agricultural and Environmental Letters</i> , 2021, 6, e20047.	0.8	5
195	Genomic basis of geographical adaptation to soil nitrogen in rice. <i>Nature</i> , 2021, 590, 600-605.	13.7	204
196	Genomics-Assisted Breeding of Climate-Smart Inbred and Hybrid Rice Varieties. , 2020, , 1-43.		1
197	Genomics-Assisted Breeding for Improving Stress Tolerance of Gramineous Crops to Biotic and Abiotic Stresses: Progress and Prospects. , 2017, , 59-81.		6
198	Integrating the Bioinformatics and Omics Tools for Systems Analysis of Abiotic Stress Tolerance in <i>Oryza sativa</i> (L.). , 2019, , 59-77.		3
199	<i>In silico</i> analysis of the fragrance gene ( <i>badh2</i> ) in Asian rice ( <i>Oryza sativa</i> L.) germplasm and validation of allele specific markers. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 71-80.	0.4	7
203	Genome-Wide Association Analysis of the Genetic Basis for Sheath Blight Resistance in Rice. <i>Rice</i> , 2019, 12, 93.	1.7	25

#	ARTICLE	IF	CITATIONS
204	Overexpression of the Transcription Factor Gene OsSTAP1 Increases Salt Tolerance in Rice. <i>Rice</i> , 2020, 13, 50.	1.7	28
205	Genetic architecture of cold tolerance in rice ( <i>Oryza sativa</i> ) determined through high resolution genome-wide analysis. <i>PLoS ONE</i> , 2017, 12, e0172133.	1.1	107
206	Promoter variants of Xa23 alleles affect bacterial blight resistance and evolutionary pattern. <i>PLoS ONE</i> , 2017, 12, e0185925.	1.1	9
207	Whole genome sequencing of <i>Oryza sativa</i> L. cv. Seeragasamba identifies a new fragrance allele in rice. <i>PLoS ONE</i> , 2017, 12, e0188920.	1.1	27
208	Breeding green super rice (GSR) varieties for sustainable rice cultivation. <i>Burleigh Dodds Series in Agricultural Science</i> , 2017, , 109-130.	0.1	10
209	Transforming Rice Breeding: Re-Designing the Irrigated Breeding Pipeline at the International Rice Research Institute (IRRI). , 0, , .		16
210	Identifying a Candidate Mutation Underlying a Reduced Cuticle Wax Mutant of Rice Using Targeted Exon Capture and Sequencing. <i>Plant Breeding and Biotechnology</i> , 2019, 7, 1-11.	0.3	5
211	Toward Integrated Multi-Omics Intervention: Rice Trait Improvement and Stress Management. <i>Frontiers in Plant Science</i> , 2021, 12, 741419.	1.7	14
212	Genome-wide in silico analysis of long intergenic non-coding RNAs from rice peduncles at the heading stage. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2389-2406.	1.4	1
213	NABIC SNP: an integrated database for SNP markers. <i>Bioinformatics</i> , 2015, 11, 369-372.	0.2	1
214	Throughput Rice Molecular Breeding System Development at IRRI. <i>Journal of the Korean Society of International Agriculture</i> , 2015, 27, 551-563.	0.1	0
217	Gene expression and SNP identification related to leaf angle traits using a genome-wide association study in rice ( <i>Oryza sativa</i> L.). <i>Journal of Plant Biotechnology</i> , 2018, 45, 17-29.	0.1	0
219	Rice Epigenetic Pathways: Great Genetic Variation and Implication for Rapid Rice Breeding. <i>Journal of Plant Genetics and Crop Research</i> , 2018, 1, 40-46.	0.0	0
226	Photorespiration Regulates Carbon-Nitrogen Metabolism by Magnesium Chelatase D Subunit in Rice. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 112-125.	2.4	15
227	Genetic and Genomic Resources and Their Exploitation for Unlocking Genetic Potential from the Wild Relatives. , 2020, , 193-210.		3
228	Genome-Wide Association Analysis Dissects the Genetic Basis of the Grain Carbon and Nitrogen Contents in Milled Rice. <i>Rice</i> , 2019, 12, 101.	1.7	8
229	Development of SNP markers for grain yield screening of Brazilian rice cultivars. <i>Pesquisa Agropecuaria Brasileira</i> , 0, 55, .	0.9	1
230	Genome-wide association study on agronomic traits of temperate japonica rice ( <i>Oryza sativa</i> L.). <i>Crop Breeding and Applied Biotechnology</i> , 2020, 20, .	0.1	5

#	ARTICLE	IF	CITATIONS
231	Identification of Rice Mutants with Altered Grain Alkali Digestion Trait. <i>Plant Breeding and Biotechnology</i> , 2020, 8, 19-27.	0.3	2
232	Plant-ImputeDB: an integrated multiple plant reference panel database for genotype imputation. <i>Nucleic Acids Research</i> , 2021, 49, D1480-D1488.	6.5	16
234	OsVDE, a xanthophyll cycle key enzyme, mediates abscisic acid biosynthesis and negatively regulates salinity tolerance in rice. <i>Planta</i> , 2022, 255, 6.	1.6	17
235	Laboratory phenomics predicts field performance and identifies superior indica haplotypes for early seedling vigour in dry direct-seeded rice. <i>Genomics</i> , 2021, 113, 4227-4236.	1.3	5
236	Natural Variation in OsMKK3 Contributes to Grain Size and Chalkiness in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 784037.	1.7	12
237	GC content of plant genes is linked to past gene duplications. <i>PLoS ONE</i> , 2022, 17, e0261748.	1.1	6
238	Aus rice root architecture variation contributing to grain yield under drought suggests a key role of nodal root diameter class. <i>Plant, Cell and Environment</i> , 2022, 45, 854-870.	2.8	10
240	Identification of Candidate Genes for Salinity and Anaerobic Tolerance at the Germination Stage in Rice by Genome-Wide Association Analyses. <i>Frontiers in Genetics</i> , 2022, 13, 822516.	1.1	12
242	Genetic Bases of Flow- and Sink-Related Traits in Rice Revealed by Genome-Wide Association Study. <i>Agronomy</i> , 2022, 12, 776.	1.3	1
243	Combining Genome-Wide Association Study and Gene-Based Haplotype Analysis to Identify Candidate Genes for Alkali Tolerance at the Germination Stage in Rice. <i>Frontiers in Plant Science</i> , 2022, 13, 887239.	1.7	9
245	Molecular Docking and Interaction Studies of Identified Abscisic Acid Receptors in <i>Oryza sativa</i> : An In-Silico Perspective on Comprehending Stress Tolerance Mechanisms. <i>Current Genomics</i> , 2021, 22, 607-619.	0.7	8
246	Alternative splicing of <i>OsGS1;1</i> affects nitrogen use efficiency, grain development, and amylose content in rice. <i>Plant Journal</i> , 2022, 110, 1751-1762.	2.8	18
311	Deciphering comparative and structural variation that regulates abiotic stress response. , 2022, , 561-586.		0
312	Autophagy targets Hd1 for vacuolar degradation to regulate rice flowering. <i>Molecular Plant</i> , 2022, 15, 1137-1156.	3.9	13
313	Phenotyping of a rice ( <i>Oryza sativa</i> L.) association panel identifies loci associated with tolerance to low soil fertility on smallholder farm conditions in Madagascar. <i>PLoS ONE</i> , 2022, 17, e0262707.	1.1	0
314	Overview of developed core and mini core collections and their effective utilization in cultivated rice and its related species ( <i>Oryza</i> sp.)—A review. <i>Plant Breeding</i> , 2022, 141, 501-512.	1.0	5
315	Natural alleles of <i>CIRCADIAN CLOCK ASSOCIATED1</i> contribute to rice cultivation by fine-tuning flowering time. <i>Plant Physiology</i> , 2022, 190, 640-656.	2.3	12
316	Genome-edited ATP BINDING CASSETTE B1 transporter SD8 knockouts show optimized rice architecture without yield penalty. <i>Plant Communications</i> , 2022, 3, 100347.	3.6	5

#	ARTICLE	IF	CITATIONS
317	Genetic architecture of seed glycerolipids in Asian cultivated rice. <i>Plant, Cell and Environment</i> , 0, , .	2.8	9
318	Genetic basis underlying tiller angle in rice ( <i>Oryza sativa</i> L.) by genome-wide association study. <i>Plant Cell Reports</i> , 0, , .	2.8	4
319	The brassinosteroid biosynthesis gene TaD11-2A controls grain size and its elite haplotype improves wheat grain yields. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2907-2923.	1.8	17
320	Discovery and Validation of Grain Shape Loci in U.S. Rice Germplasm Through Haplotype Characterization. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
321	Global identification of quantitative trait loci and candidate genes for cold stress and chilling acclimation in rice through GWAS and RNA-seq. <i>Planta</i> , 2022, 256, .	1.6	4
322	<i>Large Vascular Bundle Phloem Area 4</i> enhances grain yield and quality in rice via source-sink flow. <i>Plant Physiology</i> , 2023, 191, 317-334.	2.3	8
323	Uncovering the Genetic of Cadmium Accumulation in the Rice 3K Panel. <i>Plants</i> , 2022, 11, 2813.	1.6	1
324	Development of SNP Markers from GWAS for Selecting Seed Coat and Aleurone Layers in Brown Rice ( <i>Oryza sativa</i> L.). <i>Genes</i> , 2022, 13, 1805.	1.0	6
325	Genome-Wide Association Mapping Identifies New Candidate Genes for Cold Stress and Chilling Acclimation at Seedling Stage in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 13208.	1.8	4
326	Distribution characteristics of selenium, cadmium and arsenic in rice grains and their genetic dissection by genome-wide association study. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
327	Spectrum and Density of Gamma and X-ray Induced Mutations in a Non-Model Rice Cultivar. <i>Plants</i> , 2022, 11, 3232.	1.6	3
328	Stress-induced F-box protein-coding gene <i>OsFBX257</i> modulates drought stress adaptations and ABA responses in rice. <i>Plant, Cell and Environment</i> , 2023, 46, 1207-1231.	2.8	11
329	Selection of a CTAB protocol for high-quality DNA extraction in <i>Oryza sativa</i> L. validated for application in genotyping process based on Illumina sequencing. <i>Journal of Crop Science and Biotechnology</i> , 0, , .	0.7	0
330	Integrating GWAS and transcriptomics to identify candidate genes conferring heat tolerance in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
331	Combined genome-wide association study and epistasis analysis reveal multifaceted genetic architectures of plant height in Asian cultivated rice. <i>Plant, Cell and Environment</i> , 2023, 46, 1295-1311.	2.8	5
332	Pan-genome inversion index reveals evolutionary insights into the subpopulation structure of Asian rice. <i>Nature Communications</i> , 2023, 14, .	5.8	13
333	Identification and validation of new MADS-box homologous genes in 3010 rice pan-genome. <i>Plant Cell Reports</i> , 0, , .	2.8	1
339	Revisiting the Genomic Approaches in the Cereals and the Path Forward. , 2023, , 1-40.		1

#	ARTICLE	IF	CITATIONS
345	Breeding Strategies for Improvement of Drought Tolerance in Rice: Recent Approaches, and Future Outlooks., 0, , .		0