

# A Draft Sequence of the Rice Genome (*Oryza sativa* L. ss

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Current methods of gene prediction, their strengths and weaknesses. <i>Nucleic Acids Research</i> , 2002, 30, 4103-4117.	6.5	374
2	The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between Arabidopsis and Rice. <i>Genome Research</i> , 2002, 12, 1792-1801.	2.4	127
3	THE RICE GENOME: Opening the Door to Comparative Plant Biology. <i>Science</i> , 2002, 296, 60-63.	6.0	76
4	Genome-Wide Identification of Nodule-Specific Transcripts in the Model Legume <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2002, 130, 519-537.	2.3	229
5	Beyond the Arabidopsis Genome: Opportunities for Comparative Genomics. <i>Plant Physiology</i> , 2002, 129, 1439-1447.	2.3	70
6	Rice Functional Genomics by T-DNA Insertional Mutagenesis. <i>Asia Pacific Biotech News</i> , 2002, 06, 926-929.	0.5	0
7	An International Campaign for Agricultural and Livestock Genomics (CALG). <i>Asia Pacific Biotech News</i> , 2002, 06, 958-965.	0.5	0
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10	Rice Genome Organization: the Centromere and Genome Interactions. <i>Annals of Botany</i> , 2002, 90, 427-435.	1.4	34
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15	THE RICE GENOME: The Most Precious Things Are Not Jade and Pearls.... <i>Science</i> , 2002, 296, 58-59.	6.0	24
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18	Chlorophyll-deficient Mutants of Rice Demonstrated the Deletion of a DNA Fragment by Heavy-ion Irradiation. <i>Journal of Radiation Research</i> , 2002, 43, S157-S161.	0.8	49

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20	Diversity in Nucleotide Binding Site-Leucine-Rich Repeat Genes in Cereals. <i>Genome Research</i> , 2002, 12, 1871-1884.	2.4	292
21	Abscisic Acid-Induced Transcription Is Mediated by Phosphorylation of an Abscisic Acid Response Element Binding Factor, TRAB1. <i>Plant Cell</i> , 2002, 14, 3177-3189.	3.1	196
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1479	The Plant Organelles Database 2 (PODB2): An Updated Resource Containing Movie Data of Plant Organelle Dynamics. <i>Plant and Cell Physiology</i> , 2011, 52, 244-253.	1.5	18
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1803	Genetics of Tillering in Rice and Barley. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0032.	1.6	75
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1833	Genome Sequencing. <i>Agronomy</i> , 2015, , 289-302.	0.2	3
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1835	Unlimited Thirst for Genome Sequencing, Data Interpretation, and Database Usage in Genomic Era: The Road towards Fast-Track Crop Plant Improvement. <i>Genetics Research International</i> , 2015, 2015, 1-15.	2.0	18
1836	Identification of Immune Related LRR-Containing Genes in Maize ( <i>Zea mays</i> L.) by Genome-Wide Sequence Analysis. <i>International Journal of Genomics</i> , 2015, 2015, 1-11.	0.8	47
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1848	Genome-wide identification and characterization of R2R3-MYB transcription factors in pear. <i>Scientia Horticulturae</i> , 2015, 197, 176-182.	1.7	18
1849	Mutant-Based Reverse Genetics for Functional Genomics of Non-model Crops. , 2015, , 473-487.		1
1850	Next-Generation Sequencing (NGS) Tools and Impact in Plant Breeding. , 2015, , 563-612.		8
1851	Investigating the MicroRNAomes of Two Developmental Phases of <i>Dendrocalamus latiflorus</i> (Poaceae:). Tj ETQq1 1 0,784314 rgBT /Over 1.0 6		
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1853	Multilocus species tree analyses resolve the ancient radiation of the subtribe Zizaniinae (Poaceae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 232-239.	1.2	18
1854	Constructing the barley model for genetic transformation in Triticeae. <i>Journal of Integrative Agriculture</i> , 2015, 14, 453-468.	1.7	11
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1857	Whole-genome resequencing: changing the paradigms of SNP detection, molecular mapping and gene discovery. Molecular Breeding, 2015, 35, 1.	1.0	35
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1860	Integrated genome sequence and linkage map of physic nut (<i>Jatropha curcas</i> L.), a biodiesel plant. Plant Journal, 2015, 81, 810-821.	2.8	149
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1868	Brassinosteroid insensitive 1-associated kinase 1 (OsI-BAK1) is associated with grain filling and leaf development in rice. Journal of Plant Physiology, 2015, 182, 23-32.	1.6	28
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1870	Food Proteins and Peptides. Comprehensive Analytical Chemistry, 2015, 68, 309-357.	0.7	9
1871	Genome-wide analysis of potential cross-reactive endogenous allergens in rice (<i>Oryza sativa</i> L.). Toxicology Reports, 2015, 2, 1233-1245.	1.6	10
1872	The rice endophyte <i>Harpophora oryzae</i> genome reveals evolution from a pathogen to a mutualistic endophyte. Scientific Reports, 2014, 4, 5783.	1.6	66
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1877	Bigenic epistasis between QTLs for heading date in rice analyzed using single segment substitution lines. <i>Field Crops Research</i> , 2015, 178, 16-25.	2.3	10
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1882	De novo assembly, gene annotation, and marker development of mulberry ( <i>Morus atropurpurea</i> ) transcriptome. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	19
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1885	Next-generation sequencing (NGS) transcriptomes reveal association of multiple genes and pathways contributing to secondary metabolites accumulation in tuberous roots of <i>Aconitum heterophyllum</i> Wall.. <i>Planta</i> , 2015, 242, 239-258.	1.6	34
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1889	A Gene Expression Profiling of Early Rice Stamen Development that Reveals Inhibition of Photosynthetic Genes by OsMADS58. <i>Molecular Plant</i> , 2015, 8, 1069-1089.	3.9	29
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1891	Plant Proteomics: Technologies and Applications. , 2015, , 213-256.		3
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1895	Development of genome-wide insertion/deletion markers in rice based on graphic pipeline platform. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 980-991.	4.1	41
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1900	Genome-wide mapping of 5-hydroxymethylcytosine in three rice cultivars reveals its preferential localization in transcriptionally silent transposable element genes. <i>Journal of Experimental Botany</i> , 2015, 66, 6651-6663.	2.4	26
1901	Achieving Crop Stress Tolerance and Improvement—An Overview of Genomic Techniques. <i>Applied Biochemistry and Biotechnology</i> , 2015, 177, 1395-1408.	1.4	6
1902	2D-DIGE-based proteome expression changes in leaves of rice seedlings exposed to low-level gamma radiation at Iitate village, Fukushima. <i>Plant Signaling and Behavior</i> , 2015, 10, e1103406.	1.2	30
1903	Genomics and Bioinformatics Resources. , 2015, , 117-153.		1
1904	Metabolic responses of rice leaves and seeds under transgenic backcross breeding and pesticide stress by pseudotargeted metabolomics. <i>Metabolomics</i> , 2015, 11, 1802-1814.	1.4	16
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1907	<i>OsSIZ1</i> , a SUMO E3 Ligase Gene, is Involved in the Regulation of the Responses to Phosphate and Nitrogen in Rice. <i>Plant and Cell Physiology</i> , 2015, 56, 2381-2395.	1.5	59
1908	Unraveling the light-specific metabolic and regulatory signatures of rice through combined in silico modeling and multi-omics analysis. <i>Plant Physiology</i> , 2015, 169, pp.01379.2015.	2.3	68
1909	The Brachypodium distachyon Reference Genome. <i>Plant Genetics and Genomics: Crops and Models</i> , 2015, , 55-70.	0.3	2
1910	Mutational bias is the driving force for shaping the synonymous codon usage pattern of alternatively spliced genes in rice ( <i>Oryza sativa</i> L.). <i>Molecular Genetics and Genomics</i> , 2015, 290, 649-660.	1.0	18

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1912	Genome Evolution in Maize: From Genomes Back to Genes. <i>Annual Review of Plant Biology</i> , 2015, 66, 329-343.	8.6	65
1913	Rice terpene synthase 20 ( <i>OsTPS20</i> ) plays an important role in producing terpene volatiles in response to abiotic stresses. <i>Protoplasma</i> , 2015, 252, 997-1007.	1.0	46
1914	Protein domain evolution is associated with reproductive diversification and adaptive radiation in the genus <i>Eucalyptus</i> . <i>New Phytologist</i> , 2015, 206, 1328-1336.	3.5	19
1915	Heat shock factors in carrot: genome-wide identification, classification, and expression profiles response to abiotic stress. <i>Molecular Biology Reports</i> , 2015, 42, 893-905.	1.0	54
1916	Full-genome identification and characterization of NBS-encoding disease resistance genes in wheat. <i>Molecular Genetics and Genomics</i> , 2015, 290, 257-271.	1.0	21
1917	Evaluation of Sample Preparation Methods from Rice Seeds and Seedlings Suitable for Two-Dimensional Gel Electrophoresis. <i>Applied Biochemistry and Biotechnology</i> , 2015, 175, 1035-1051.	1.4	9
1918	De novo transcriptome characterization of <i>Lilium Sorbonne</i> ™ and key enzymes related to the flavonoid biosynthesis. <i>Molecular Genetics and Genomics</i> , 2015, 290, 399-412.	1.0	39
1919	Expression profiling of NBS-encoding genes in a triploid white poplar. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2015, 24, 283-291.	0.9	1
1920	Loss of Function of the Cytochrome P450 Gene <i>CYP78B5</i> Causes Giant Embryos in Rice. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 69-83.	1.0	26
1921	Targeted Discovery of Single Nucleotide Polymorphisms in an Unmarked Wheat Chromosomal Region Containing the Hessian Fly Resistance Gene <i>H33</i> . <i>Crop Science</i> , 2016, 56, 1106-1114.	0.8	8
1922	Genome-wide expression analysis of a rice mutant line under salt stress. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	17
1923	Integration of Next-generation Sequencing Technologies with Comparative Genomics in Cereals. , 2016, , .		2
1925	Barley. , 2016, , 125-157.		3
1926	Innovation for Sustainable Agriculture and Food Production. , 2016, , .		3
1927	Improvement of Salinity Stress Tolerance in Rice: Challenges and Opportunities. <i>Agronomy</i> , 2016, 6, 54.	1.3	177
1928	Anthocyanin Accumulation in Muscadine Berry Skins Is Influenced by the Expression of the MYB Transcription Factors, <i>MybA1</i> , and <i>MYBCS1</i> . <i>Antioxidants</i> , 2016, 5, 35.	2.2	16
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1931	Transcriptomic Analysis for Different Sex Types of <i>Ricinus communis</i> L. during Development from Apical Buds to Inflorescences by Digital Gene Expression Profiling. <i>Frontiers in Plant Science</i> , 2015, 6, 1208.	1.7	21
1932	Analyses of Old Prokaryotic Proteins Indicate Functional Diversification in <i>Arabidopsis</i> and <i>Oryza sativa</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 304.	1.7	1
1933	Emerging Genomic Tools for Legume Breeding: Current Status and Future Prospects. <i>Frontiers in Plant Science</i> , 2016, 7, 455.	1.7	180
1934	Trait Specific Expression Profiling of Salt Stress Responsive Genes in Diverse Rice Genotypes as Determined by Modified Significance Analysis of Microarrays. <i>Frontiers in Plant Science</i> , 2016, 7, 567.	1.7	23
1935	Isolation and Functional Characterization of Bidirectional Promoters in Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 766.	1.7	14
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1937	Genome-Wide QTL Mapping for Wheat Processing Quality Parameters in a Gaocheng 8901/Zhoumai 16 Recombinant Inbred Line Population. <i>Frontiers in Plant Science</i> , 2016, 7, 1032.	1.7	84
1938	High-Throughput Sequencing Reveals Single Nucleotide Variants in Longer-Kernel Bread Wheat. <i>Frontiers in Plant Science</i> , 2016, 7, 1193.	1.7	7
1939	Genetic Architecture of Flowering Phenology in Cereals and Opportunities for Crop Improvement. <i>Frontiers in Plant Science</i> , 2016, 7, 1906.	1.7	90
1940	Transposon Activation Tagging in Plants for Gene Function Discovery. <i>Progress in Botany Fortschritte Der Botanik</i> , 2016, , 265-289.	0.1	1
1941	Transcriptome shock in an interspecific F1 triploid hybrid of <i>Oryza</i> revealed by RNA sequencing. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 150-164.	4.1	38
1942	A genetic delineation of Patchouli ( <i>Pogostemon cablin</i> ) revealed by specific locus amplified fragment sequencing. <i>Journal of Systematics and Evolution</i> , 2016, 54, 491-501.	1.6	16
1943	The Rice Pentatricopeptide Repeat Gene TCD10 is Needed for Chloroplast Development under Cold Stress. <i>Rice</i> , 2016, 9, 67.	1.7	62
1944	Simple and rapid detection of <i>Tilletia horrida</i> causing rice kernel smut in rice seeds. <i>Scientific Reports</i> , 2016, 6, 33258.	1.6	20
1945	Genome-wide identification, phylogeny, and expression analysis of pectin methylesterases reveal their major role in cotton fiber development. <i>BMC Genomics</i> , 2016, 17, 1000.	1.2	42
1946	Genetic regulation of day length adaptation and bulb formation in onion ( <i>Allium cepa</i> L.). <i>Acta Horticulturae</i> , 2016, , 7-14.	0.1	1
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1949	Acyl-CoA-Binding Proteins (ACBPs) in Plant Development. <i>Sub-Cellular Biochemistry</i> , 2016, 86, 363-404.	1.0	15
1950	QTLs for Genetic Improvement Under Global Climate Changes. , 2016, , 471-513.		1
1951	Role of Genomics in Enhancing Nutrition Content of Cereals. , 2016, , 77-96.		1
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1954	Progress in Botany 77. <i>Progress in Botany Fortschritte Der Botanik</i> , 2016, , .	0.1	2
1955	Goals and hurdles for a successful implementation of genomic selection in breeding programme for selected annual and perennial crops. <i>Biotechnology and Genetic Engineering Reviews</i> , 2016, 32, 18-42.	2.4	10
1956	Quantitative proteomic analysis of two different rice varieties reveals that drought tolerance is correlated with reduced abundance of photosynthetic machinery and increased abundance of ClpD1 protease. <i>Journal of Proteomics</i> , 2016, 143, 73-82.	1.2	50
1957	A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. <i>DNA Research</i> , 2016, 23, 241-251.	1.5	18
1958	Understanding and utilizing crop genome diversity via high-resolution genotyping. <i>Plant Biotechnology Journal</i> , 2016, 14, 1086-1094.	4.1	95
1959	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
1960	Bulked sample analysis in genetics, genomics and crop improvement. <i>Plant Biotechnology Journal</i> , 2016, 14, 1941-1955.	4.1	239
1961	Pooled mapping: an efficient method of calling variations for population samples with low-depth resequencing data. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	13
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1963	Indica rice genome assembly, annotation and mining of blast disease resistance genes. <i>BMC Genomics</i> , 2016, 17, 242.	1.2	51
1964	RNA-Seq Library Construction Methods for Transcriptome Analysis. <i>Current Protocols in Plant Biology</i> , 2016, 1, 197-215.	2.8	8
1965	A meta-analysis of potential candidate genes associated with salinity stress tolerance in rice. <i>Agri Gene</i> , 2016, 1, 126-134.	1.9	6
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1968	Identification and fine mapping of <i>lemma-distortion1</i> , a single recessive gene playing an essential role in the development of lemma in rice. <i>Journal of Agricultural Science</i> , 2016, 154, 989-1001.	0.6	2
1970	Rice caryopsis development I: Dynamic changes in different cell layers. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 772-785.	4.1	62
1971	The effects of fresh and rapid desiccated tissue on estimates of Ophiopogoneae genome size. <i>Plant Diversity</i> , 2016, 38, 190-193.	1.8	6
1972	The Genome of a Southern Hemisphere Seagrass Species ( <i>Zostera muelleri</i> ). <i>Plant Physiology</i> , 2016, 172, 272-283.	2.3	88
1973	- New Farm Management Strategy to Enhance Sustainable Rice Production in Japan and Indonesia. , 2016, , 342-361.		0
1974	Proteomics of Flooding-Stressed Plants. , 2016, , 71-95.		0
1975	Applications of Quantitative Proteomics in Plant Research. , 2016, , 1-29.		5
1976	Localization of Low-Copy DNA Sequences on Mitotic Chromosomes by FISH. <i>Methods in Molecular Biology</i> , 2016, 1429, 49-64.	0.4	14
1977	The Sequencing: How it was Done and What it Produced. <i>Compendium of Plant Genomes</i> , 2016, , 95-109.	0.3	0
1978	Genomic identification of WRKY transcription factors in carrot ( <i>Daucus carota</i> ) and analysis of evolution and homologous groups for plants. <i>Scientific Reports</i> , 2016, 6, 23101.	1.6	68
1979	Draft genome sequence of an elite <i>Dura</i> palm and whole-genome patterns of DNA variation in oil palm. <i>DNA Research</i> , 2016, 23, 527-533.	1.5	34
1981	Broadening the Genetic Base of Grain Cereals. , 2016, , .		16
1982	Genome Analysis of Plants. , 2016, , 1-27.		0
1983	Comparison of molecular genetic utilities of TD, AFLP, and MSAP among the accessions of japonica, indica, and Tongil of <i>Oryza sativa</i> L.. <i>Genes and Genomics</i> , 2016, 38, 819-830.	0.5	8
1984	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016, 25, 5267-5281.	2.0	16
1986	Activation tagging in <i>indica</i> rice identifies ribosomal proteins as potential targets for manipulation of water-use efficiency and abiotic stress tolerance in plants. <i>Plant, Cell and Environment</i> , 2016, 39, 2440-2459.	2.8	41
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1991	Diversity and Evolution of Disease Resistance Genes in Barley ( <i>Hordeum vulgare</i> L.). <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S38085.	0.6	27
1992	Novel green tissue-specific synthetic promoters and cis-regulatory elements in rice. <i>Scientific Reports</i> , 2016, 5, 18256.	1.6	28
1993	Economic importance, taxonomic representation and scientific priority as drivers of genome sequencing projects. <i>BMC Genomics</i> , 2016, 17, 782.	1.2	13
1994	Rice Chloroplast Genome Variation Architecture and Phylogenetic Dissection in Diverse <i>Oryza</i> Species Assessed by Whole-Genome Resequencing. <i>Rice</i> , 2016, 9, 57.	1.7	63
1995	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
1997	Genome-Wide Identification and Analysis of the MYB Transcription Factor Superfamily in <i>Solanum lycopersicum</i> . <i>Plant and Cell Physiology</i> , 2016, 57, 1657-1677.	1.5	117
1998	Quantitative evaluation of influence of PROSTRATE GROWTH 1 gene on rice canopy structure based on three-dimensional structure model. <i>Field Crops Research</i> , 2016, 194, 65-74.	2.3	10
1999	Bioinformatics resources for pollen. <i>Plant Reproduction</i> , 2016, 29, 133-147.	1.3	6
2000	The Rice TCM5 Gene Encoding a Novel Deg Protease Protein is Essential for Chloroplast Development under High Temperatures. <i>Rice</i> , 2016, 9, 13.	1.7	42
2001	Rice: The First Crop Genome. <i>Rice</i> , 2016, 9, 14.	1.7	66
2002	The post-genomics era of cotton. <i>Science China Life Sciences</i> , 2016, 59, 109-111.	2.3	6
2003	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. <i>Plant Science</i> , 2016, 242, 47-64.	1.7	60
2004	Cloning and functional analysis of pale-green leaf (PGL10) in rice ( <i>Oryza sativa</i> L.). <i>Plant Growth Regulation</i> , 2016, 78, 69-77.	1.8	28
2005	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016, 48, 109-111.	9.4	184
2006	A transgenic, visual screenable marker for soybean seeds. <i>Transgenic Research</i> , 2016, 25, 187-193.	1.3	1
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2010	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
2011	Efficiency and Inheritance of Targeted Mutagenesis in Maize Using CRISPR-Cas9. <i>Journal of Genetics and Genomics</i> , 2016, 43, 25-36.	1.7	171
2012	Mass Spectrometry in Plant-omics. <i>Analytical Chemistry</i> , 2016, 88, 3422-3434.	3.2	68
2013	Transporters involved in mineral nutrient uptake in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 3645-3653.	2.4	99
2014	Breeding high-yield superior quality hybrid super rice by rational design. <i>National Science Review</i> , 2016, 3, 283-294.	4.6	179
2015	The Genome of the Model Moss <i>Physcomitrella patens</i> . <i>Advances in Botanical Research</i> , 2016, 78, 97-140.	0.5	9
2016	Complete Chloroplast Genome Sequence and Annotation of the Tropical japonica Group of Asian Cultivated Rice ( <i>Oryza sativa</i> L.). <i>Genome Announcements</i> , 2016, 4, .	0.8	0
2017	What makes up plant genomes: The vanishing line between transposable elements and genes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 366-380.	0.9	67
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2024	What Do We Know about Homeodomain Leucine Zipper I Transcription Factors? Functional and Biotechnological Considerations. , 2016, , 343-356.		3
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2028	Tandem duplications of receptor-like kinase genes reshaped the homologous chromosome 1 regions in <i>Oryza sativa</i> ssp. <i>indica</i> and <i>japonica</i> and their possible ancestral genomes. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	0
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2042	Maintenance of phosphate homeostasis and root development are coordinately regulated by MYB1, an R2R3-type MYB transcription factor in rice. <i>Journal of Experimental Botany</i> , 2017, 68, 3603-3615.	2.4	71
2043	Genome-wide association mapping for phenotypic plasticity in rice. <i>Plant, Cell and Environment</i> , 2017, 40, 1565-1575.	2.8	45
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2049	The genome draft of coconut ( <i>Cocos nucifera</i> ). <i>GigaScience</i> , 2017, 6, 1-11.	3.3	96
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2054	Evolutionarily Conserved Alternative Splicing Across Monocots. <i>Genetics</i> , 2017, 207, 465-480.	1.2	47
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2059	An atypical strictosidine synthase, <i>OsSTRL2</i> , plays key roles in anther development and pollen wall formation in rice. <i>Scientific Reports</i> , 2017, 7, 6863.	1.6	42
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2111	Transport System of Mineral Elements in Rice. , 2018, , 223-240.		11
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2200	<i>OsDCL1a</i> activation impairs phytoalexin biosynthesis and compromises disease resistance in rice. Annals of Botany, 2019, 123, 79-93.	1.4	15
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2290	Cloning of long sterile lemma ( <i>lsl2</i> ), a single recessive gene that regulates spike germination in rice ( <i>Oryza sativa</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 561.	1.6	3
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2293	The draft genome sequence of an upland wild rice species, <i>Oryza granulata</i> . <i>Scientific Data</i> , 2020, 7, 131.	2.4	21
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2325	A chromosome-level genome assembly of the wild rice <i>Oryza rufipogon</i> facilitates tracing the origins of Asian cultivated rice. <i>Science China Life Sciences</i> , 2021, 64, 282-293.	2.3	24
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2336	Genetics and Genomics Resources of Millets: Availability, Advancements, and Applications. , 2021, , 153-166.		0
2337	Mutagenic Effects of Ethyl Methanesulfonate on Morpho-Physiological Traits of Local Rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT <sub>0</sub> /Overlook	0.3	0
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2341	Bamboo Transposon Research: Current Status and Perspectives. <i>Methods in Molecular Biology</i> , 2021, 2250, 257-270.	0.4	3
2342	Bioinformaticsâ€™ role in studying microbeâ€™mediated biotic and abiotic stress tolerance. , 2021, , 203-219.		0
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2347	Chromosome-level &lt;i>de novo&/i> genome assemblies of over 100 plant species. <i>Breeding Science</i> , 2021, 71, 117-124.	0.9	19
2348	Possibility of Uncoding Structural Organization of Genome in Rice Research: Prospects and Approaches by 3D Genome Sequencing. , 2021, , 3-28.		0
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2350	Metabolomics in Rice Improvement. , 2021, , 83-103.		0
2351	The Genetic Basis of Plant-Herbivore Interactions. , 2021, , 59-91.		1



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