

A Draft Sequence of the Rice Genome (*Oryza sativa*)

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Current methods of gene prediction, their strengths and weaknesses. Nucleic Acids Research, 2002, 30, 4103-4117.	14.5	374
2	The Automatic Detection of Homologous Regions (ADHoRe) and Its Application to Microcolinearity Between Arabidopsis and Rice. Genome Research, 2002, 12, 1792-1801.	5.5	127
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20	Diversity in Nucleotide Binding Site-Leucine-Rich Repeat Genes in Cereals. <i>Genome Research</i> , 2002, 12, 1871-1884.	5.5	292
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#	ARTICLE	IF	CITATIONS
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1549	Rice functional genomics research: Progress and implications for crop genetic improvement. <i>Biotechnology Advances</i> , 2012, 30, 1059-1070.	11.7	100
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1552	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. <i>Nature Biotechnology</i> , 2012, 30, 105-111.	17.5	818
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1555	New Polymorphic EST-SSR Markers in Sugarcane. <i>Sugar Tech</i> , 2012, 14, 357-363.	1.8	5
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1559	Extensive Pyrosequencing Reveals Frequent Intra-Genomic Variations of Internal Transcribed Spacer Regions of Nuclear Ribosomal DNA. <i>PLoS ONE</i> , 2012, 7, e43971.	2.5	112
1560	Genome-Wide Identification and Analysis of Grape Aldehyde Dehydrogenase (ALDH) Gene Superfamily. <i>PLoS ONE</i> , 2012, 7, e32153.	2.5	91
1561	Why Assembling Plant Genome Sequences Is So Challenging. <i>Biology</i> , 2012, 1, 439-459.	2.8	123
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1564	Genome-wide analysis of the AP2/ERF superfamily in peach (<i>Prunus persica</i>). <i>Genetics and Molecular Research</i> , 2012, 11, 4789-809.	0.2	75
1565	Assessment and Utilization of the Genetic Diversity in Rice (<i>Oryza sativa</i> L.). , 0, , .		0
1566	Secretome analysis of <i>Magnaporthe oryzae</i> using in vitro systems. <i>Proteomics</i> , 2012, 12, 878-900.	2.2	30
1567	The First Ten Years of Plant Genome Sequencing and Prospects for the Next Decade. , 2012, , 1-15.		4
1568	Centromeres: Sequences, Structure, and Biology. , 2012, , 59-70.		5

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1571	Protein-Protein Interactions in Plants. Plant and Cell Physiology, 2012, 53, 617-625.	3.1	47
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1576	Identification of salt treated proteins in sorghum using gene ontology linkage. Physiology and Molecular Biology of Plants, 2012, 18, 209-216.	3.1	7
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1595	Functional alleles of the flowering time regulator FRIGIDA in the Brassica oleracea genome. <i>BMC Plant Biology</i> , 2012, 12, 21.	3.6	51
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1597	Molecular Cloning, Characterization, and Expression Analysis of Resistance Gene Candidates in <i>Kaempferia galanga</i> L.. <i>Molecular Biotechnology</i> , 2012, 50, 200-210.	2.4	10
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1605	Turning over a new leaf in plant genomics. <i>Genome Biology</i> , 2013, 14, 403.	8.8	4

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1609	Identification, Phylogeny, and Expression Analysis of Pto-like Genes in Pepper. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 901-916.	1.8	2
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1615	Identification of Traits, Genes, and Crops of the Future. , 2013, , 27-177.		1
1616	Reprint of: Using nuclear gene data for plant phylogenetics: Progress and prospects. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 539-550.	2.7	52
1617	There is no common ground between science and religion. <i>Journal of Biosciences</i> , 2013, 38, 181-187.	1.1	1
1618	Identification of MFS proteins in sorghum using semantic similarity. <i>Theory in Biosciences</i> , 2013, 132, 105-113.	1.4	5
1619	Function of wheat phosphate transporter gene TaPHT2;1 in Pi translocation and plant growth regulation under replete and limited Pi supply conditions. <i>Planta</i> , 2013, 237, 1163-1178.	3.2	109
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1621	Rph22: mapping of a novel leaf rust resistance gene introgressed from the non-host <i>Hordeum bulbosum</i> L. into cultivated barley (<i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1613-1625.	3.6	49
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1636	Development of genomics-based genotyping platforms and their applications in rice breeding. Current Opinion in Plant Biology, 2013, 16, 247-254.	7.1	46
1637	Knights in Action: Lectin Receptor-Like Kinases in Plant Development and Stress Responses. Molecular Plant, 2013, 6, 1405-1418.	8.3	132
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1650	Molecular Approaches to Improve Rice Abiotic Stress Tolerance. <i>Methods in Molecular Biology</i> , 2013, 956, 269-283.	0.9	24
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1656	Phosphate transporters expression in rice (<i>Oryza sativa</i> L.) associated with arbuscular mycorrhizal fungi (AMF) colonization under different levels of arsenate stress. <i>Environmental and Experimental Botany</i> , 2013, 87, 92-99.	4.2	43
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1679	Genome Sequencing and Comparative Genomics in Cereals. , 2013, , 101-126.		0
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1685	Tapping the Promise of Genomics in Species with Complex, Nonmodel Genomes. <i>Annual Review of Plant Biology</i> , 2013, 64, 89-110.	18.7	53
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1691	Functional proteomics of barley and barley chloroplasts “ strategies, methods and perspectives. <i>Frontiers in Plant Science</i> , 2013, 4, 52.	3.6	17
1692	Metabolomics of cereals under biotic stress: current knowledge and techniques. <i>Frontiers in Plant Science</i> , 2013, 4, 82.	3.6	126
1693	Proteomics of rice seed germination. <i>Frontiers in Plant Science</i> , 2013, 4, 246.	3.6	108
1694	Taxonomy and systematics are key to biological information: <i>Arabidopsis</i> , <i>Eutrema</i> (<i>Thellungiella</i>), <i>Noccaea</i> and <i>Schrenkiella</i> (<i>Brassicaceae</i>) as examples. <i>Frontiers in Plant Science</i> , 2013, 4, 267.	3.6	78
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1705	Omics-Based Approaches for Rice Improvement. , 2013, , 1-46.		1
1706	- Sensing and Molecular Responses to Low Temperature in Cyanobacteria. , 2013, , 174-189.		2
1707	Next Generation Characterisation of Cereal Genomes for Marker Discovery. <i>Biology</i> , 2013, 2, 1357-1377.	2.8	15
1709	In vitro Screening and Molecular Characterization of a Bacterial BlightResistance Gene in Rice. <i>Rice Research Open Access</i> , 2013, 01, .	0.4	0
1710	The Orphan Legume Genome Whose Time Has Come: Symposium Highlights from the American Peanut Research & Education Society Annual Meeting. <i>Peanut Science</i> , 2013, 40, 66-69.	0.1	6
1712	Evaluation of Genome Sequencing Quality in Selected Plant Species Using Expressed Sequence Tags. <i>PLoS ONE</i> , 2013, 8, e69890.	2.5	29
1713	Genome-Wide Survey and Comparative Analysis of LTR Retrotransposons and Their Captured Genes in Rice and Sorghum. <i>PLoS ONE</i> , 2013, 8, e71118.	2.5	33
1714	Characterisation and Analysis of the <i>Aegilops sharonensis</i> Transcriptome, a Wild Relative of Wheat in the Sitopsis Section. <i>PLoS ONE</i> , 2013, 8, e72782.	2.5	11
1715	Resistance to sap-sucking insects in modern-day agriculture. <i>Frontiers in Plant Science</i> , 2013, 4, 222.	3.6	19
1716	Phylogenomics of MADS-Box Genes in Plants â€” Two Opposing Life Styles in One Gene Family. <i>Biology</i> , 2013, 2, 1150-1164.	2.8	70
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1833	Genome Sequencing. <i>Agronomy</i> , 2015, , 289-302.	0.2	3

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1865	Development of chromosome-specific markers with high polymorphism for allotetraploid cotton based on genome-wide characterization of simple sequence repeats in diploid cottons (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgB7q/Overl	2.4	114
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1869	High-density mapping of the major FHB resistance gene Fhb7 derived from <i>Thinopyrum ponticum</i> and its pyramiding with Fhb1 by marker-assisted selection. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2301-2316.	3.6	113

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1887	Comprehensive analysis of CCCH-type zinc finger family genes facilitates functional gene discovery and reflects recent allopolyploidization event in tetraploid switchgrass. BMC Genomics, 2015, 16, 129.	2.8	38
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1890	Analyses of random BAC clone sequences of Japanese cedar, <i>Cryptomeria japonica</i> . <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	4
1891	Plant Proteomics: Technologies and Applications. , 2015, , 213-256.		3
1892	Interaction between carbon metabolism and phosphate accumulation is revealed by a mutation of a cellulose synthase-like protein, CSLF6. <i>Journal of Experimental Botany</i> , 2015, 66, 2557-2567.	4.8	16
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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.	18.7	65
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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.	2.3	54
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1984	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016, 25, 5267-5281.	3.9	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.	5.7	41
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1990	Mapping light-driven conformational changes within the photosensory module of plant phytochrome B. <i>Scientific Reports</i> , 2016, 6, 34366.	3.3	28
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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.	3.1	117
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2008	Genetics and Genomics of <i>Brachypodium</i> . <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , .	0.3	22
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2015	The Genome of the Model Moss <i>Physcomitrella patens</i> . <i>Advances in Botanical Research</i> , 2016, 78, 97-140.	1.1	9
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2024	What Do We Know about Homeodomainâ€“Leucine Zipper I Transcription Factors? Functional and Biotechnological Considerations. , 2016, , 343-356.		3
2025	Progress and challenges in improving the nutritional quality of rice (<i>Oryza sativa</i> L.). <i>Critical Reviews in Food Science and Nutrition</i> , 2017, 57, 2455-2481.	10.3	110
2026	Genetic diversity in sorghum [<i>Sorghum bicolor</i> (L.) Moench] germplasm from Southern Africa as revealed by microsatellite markers and agro-morphological traits. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 599-610.	1.6	19
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2057	Segmental Duplication of Chromosome 11 and its Implications for Cell Division and Genome-wide Expression in Rice. Scientific Reports, 2017, 7, 2689.	3.3	4
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