

# Resource Summary Report

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## Rice Genome Annotation

RRID:SCR\_006663

Type: Tool

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### Proper Citation

Rice Genome Annotation (RRID:SCR\_006663)

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### Resource Information

**URL:** <http://rice.plantbiology.msu.edu/>

**Proper Citation:** Rice Genome Annotation (RRID:SCR\_006663)

**Description:** Database and resource that provides sequence and annotation data for the rice genome. This website provides genome sequence from the Nipponbare subspecies of rice and annotation of the 12 rice chromosomes. All structural and functional annotation is viewable through our Rice Genome Browser which currently supports 75 tracks of annotation. Enhanced data access is available through web interfaces, FTP downloads and a Data Extractor tool developed in order to support discrete dataset downloads. Rice is a model species for the monocotyledonous plants and the cereals which are the greatest source of food for the world's population. While rice genome sequence is available through multiple sequencing projects, high quality, uniform annotation is required in order for genome sequence data to be fully utilized by researchers. The existence of a common gene set and uniform annotation allows researchers within the rice community to work from a common resource so that their results can be more easily interpreted by other scientists. The objective of this project has always been to provide high quality annotation for the rice genome. They generated, refined and updated gene models for the estimated 40,000-60,000 total rice genes, provided standardized annotation for each model, linked each model to functional annotation including expression data, gene ontologies, and tagged lines. They have provided a resource to extend the annotation of the rice genome to other plant species by providing comparative alignments to other plant species. Analysis/Tools are available including: BLAST, Locus Name Search, Functional Term Search, Protein Domain Search, Anatomy Expression Viewer, Highly Expressed Genes

**Abbreviations:** Osa1

**Synonyms:** Rice Genome Annotation Project, MSU Rice Genome Annotation Project Database and Resource

**Resource Type:** data analysis service, data or information resource, database, service resource, production service resource, analysis service resource

**Defining Citation:** [PMID:17145706](#)

**Keywords:** rice, oryza sativa, maize, corn, zea mays, wheat, triticum aestivum, gene, genome, annotation, FASEB list

**Funding:** NSF DBI-0321538;  
NSF DBI-0834043

**Availability:** Acknowledgement requested

**Resource Name:** Rice Genome Annotation

**Resource ID:** SCR\_006663

**Alternate IDs:** OMICS\_01563, nif-0000-31459

**Alternate URLs:** <http://rice.tigr.org>

**Old URLs:** <http://rice.plantbiology.msu.edu/pseudomolecules/info.shtml>

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20260801T190311+0000

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## Ratings and Alerts

No rating or validation information has been found for Rice Genome Annotation.

No alerts have been found for Rice Genome Annotation.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1423 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

He Z, et al. (2025) Global identification and functional characterization of Z-DNA in rice. Plant biotechnology journal, 23(4), 1277.

Roy RK, et al. (2025) Genetic dissection of root traits in a rice 'global MAGIC' population for candidate traits to breed for reduced methane emission. Frontiers in plant science, 16, 1616424.

Li X, et al. (2025) Characterization of fatty acid desaturase gene family in Glycine max and their expression patterns in seeds after Fusarium fujikuroi infection. Frontiers in plant science, 16, 1540003.

You SH, et al. (2025) Genome-wide analysis of OPR family genes in *Vitis vinifera* and the role of VvOPR1 in copper, zinc tolerance. *Frontiers in plant science*, 16, 1509472.

Lu X, et al. (2025) Genome-wide association study uncovers a novel gene responsible for rice seedling submergence tolerance. *Plant biotechnology journal*, 23(9), 4092.

Guo D, et al. (2025) A pangenome reference of wild and cultivated rice. *Nature*, 642(8068), 662.

Li Y, et al. (2025) A molecular framework for the GS2-SUG1 module-mediated control of grain size and weight in rice. *Nature communications*, 16(1), 3944.

Meng R, et al. (2025) Tetraspanin OsTET8 acts as a negative regulator of root development in rice. *Rice (New York, N.Y.)*, 18(1), 104.

Singh PT, et al. (2025) Chromosomal deletions in banana somaclonal variants reveal negative regulators of immunity underlying *Fusarium* wilt resistance. *Proceedings of the National Academy of Sciences of the United States of America*, 122(48), e2511842122.

Li J, et al. (2025) Nymphal feeding suppresses oviposition-induced indirect plant defense in rice. *Nature communications*, 16(1), 508.

Li M, et al. (2025) Genome-wide characterization and expression analysis of LBD transcription factors in *Ziziphus jujuba* var. *spinosa*: putative roles in tissue development and abiotic stress adaptation. *Frontiers in plant science*, 16, 1602440.

Wang H, et al. (2025) A receptor-like kinase recognizes viral proteins at the trans-Golgi network/early endosome and inhibits infection in rice. *Cell discovery*, 11(1), 101.

Tong C, et al. (2025) Pangenome and pantranscriptome as the new reference for gene-family characterization: A case study of basic helix-loop-helix (bHLH) genes in barley. *Plant communications*, 6(1), 101190.

Sun H, et al. (2025) Elite Alleles of EPE1 Identified via Genome-wide Association Studies Increase Panicle Elongation Length in Rice. *Rice (New York, N.Y.)*, 18(1), 4.

Xu P, et al. (2025) The OsbZIP35-COR1-OsTCP19 module modulates cell proliferation to regulate grain length and weight in rice. *Science advances*, 11(37), eadx9815.

Xue L, et al. (2025) Identification of key genes associated with mesocotyl length through a genome-wide association study in rice. *Frontiers in plant science*, 16, 1546580.

Gu L, et al. (2025) Comprehensive identification and expression analysis of the CPP gene family in maize (*Zea mays* L.). *BMC plant biology*, 25(1), 731.

Wang SS, et al. (2025) Identification and Candidate Gene Analysis of qCTS11-TK9, a Novel Major Quantitative Trait Locus Associated with Chilling Tolerance in Rice Seedlings. *Rice (New York, N.Y.)*, 18(1), 81.

Yue Y, et al. (2025) Reciprocal control of metabolic and chromatin regulators improves rice tolerance to heat. *Nature communications*, 16(1), 10698.

Shen T, et al. (2025) The class III peroxidase OsPrx20 is a key regulator of stress response and growth in rice. *Plant communications*, 6(10), 101487.