

Resource Summary Report

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Rice Genome Annotation

RRID:SCR_006663

Type: Tool

Proper Citation

Rice Genome Annotation (RRID:SCR_006663)

Resource Information

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

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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 or information resource, analysis service resource, database, production service resource, service resource, data analysis service

Defining Citation: [PMID:17145706](#)

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

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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: 20260819T044155+0000

Ratings and Alerts

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

No alerts have been found for Rice Genome Annotation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1600 mentions in open access literature.

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

Hu J, et al. (2026) Cas9-Embedding Hyperactive TadA8e Confers Efficient and Highly Specific A-To-G Base Editing in Rice. Plant biotechnology journal, 24(4), 2576.

Mohamadiaza M, et al. (2026) Analysis of Genetic Variation of Rice Straw Characteristics and Its Influence on Biomass. Plant direct, 10(1), e70134.

Chen HL, et al. (2026) Exogenous Hydrogen Sulfide Enhances Photosynthesis Under Thiocyanate Stress by Regulating Rubisco Energy Metabolism and Activation in Rice Seedlings. International journal of molecular sciences, 27(4).

- Lee SK, et al. (2026) Establishment of fluorescent protein-tagged lines for investigating dynamic localization of organelle and other cell structures in rice pollen tube. *Plant methods*, 22(1).
- Liao S, et al. (2026) OsCPN10a, cooperating with OsCPN20 and OsHSP60-3B negatively regulate ABA signaling and enhance seed storability in rice. *Journal of integrative plant biology*, 68(7), 2242.
- Ma Y, et al. (2026) Polyploidy-driven expansion and regulatory diversification of the Kelch repeat F-box gene family in sweetpotato. *BMC genomics*, 27(1).
- Xiao W, et al. (2026) The OsRALF5-FLR1 Module Regulates Rice Root Development and Provides a Target for Studying Cell-Cell Communication. *Rice (New York, N.Y.)*, 19(1).
- Jia M, et al. (2026) Root development progression involves RALF peptide-mediated ROS signaling and pectin dynamics in rice. *Nature communications*, 17(1).
- Wang X, et al. (2026) Genome-wide characterization of OFP family in soybean reveals the roles of GmOFP genes involved in plant height regulation and salinity tolerance. *BMC genomics*, 27(1), 157.
- Wei X, et al. (2026) Harnessing Endogenous Homeobox Genes for Synthetic Apomixis in Hybrid Rice. *Plant biotechnology journal*, 24(5), 3324.
- Fan Z, et al. (2026) Genome-wide identification, evolution, and expression pattern analysis of the LEA gene family in Tartary Buckwheat (*Fagopyrum tataricum*). *BMC genomics*, 27(1).
- Liu J, et al. (2026) Genetic identification of Pid3-1 and its regulatory role in promoting blast resistance in rice. *G3 (Bethesda, Md.)*, 16(4).
- Zhang Z, et al. (2026) Identification of BvUGT90 Family Members and Analysis of Drought Resistance Gene Screening in Sugar Beet. *Plants (Basel, Switzerland)*, 15(5).
- Zhao X, et al. (2026) Genome-wide analysis and characterization of the rice OsFBA family provides insights into its responses to ABA and cold stress. *BMC plant biology*, 26(1).
- Zhao S, et al. (2026) Fine mapping and transcriptomics reveal OSG function in regulation of grain size and pollen fertility in rice (*Oryza sativa*). *PloS one*, 21(1), e0338401.
- Zhu B, et al. (2026) Premeiotic chromatin states orchestrate gene expression during male gametogenesis in rice. *Genome biology*, 27(1).
- Li Y, et al. (2026) 3D epigenome architecture orchestrates cis and trans regulation of flowering time in rice. *Genome biology*, 27(1).
- Behera L, et al. (2026) An improved Agrobacterium-mediated transformation method for genome editing using CRISPR/Cas9 in elite indica rice (*Oryza sativa* L.). *BMC genomics*, 27(1).
- Cao L, et al. (2026) HSP101-encoding NEO-TETRAPLOID RICE FERTILITY GENE 1 regulates tapetum development through interaction with SAPK2 in polyploid rice. *Journal of integrative plant biology*, 68(7), 2316.

Li L, et al. (2026) Genome-wide identification and expression analysis of heat shock factors in *Plantago fengdouensis* under abiotic stresses. BMC plant biology, 26(1).