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 analysis service, service resource, database, analysis service resource, data or information resource, production 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: 20250430T055448+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 1400 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Li J, et al. (2025) Nymphal feeding suppresses oviposition-induced indirect plant defense in

rice. Nature communications, 16(1), 508.

Tong C, et al. (2025) Pangenome and pantranscriptome as the new reference for genefamily 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.

Gawande ND, et al. (2024) Genome wide characterization and expression analysis of CrRLK1L gene family in wheat unravels their roles in development and stress-specific responses. Frontiers in plant science, 15, 1345774.

Fan W, et al. (2024) Genome-wide identification and expression profiling of MST, SUT and SWEET transporters in Dendrobium catenatum. BMC genomics, 25(1), 1213.

Kobayashi A, et al. (2024) How have breeders adapted rice flowering to the growing region? Journal of integrative plant biology, 66(12), 2736.

Zheng X, et al. (2024) OsCSD2 and OsCSD3 Enhance Seed Storability by Modulating Antioxidant Enzymes and Abscisic Acid in Rice. Plants (Basel, Switzerland), 13(2).

Hickey K, et al. (2024) Genotype-Specific Activation of Autophagy during Heat Wave in Wheat. Cells, 13(14).

Liang Z, et al. (2024) Genome-wide identification and analysis of ascorbate peroxidase (APX) gene family in hemp (Cannabis sativa L.) under various abiotic stresses. PeerJ, 12, e17249.

Miao Y, et al. (2024) RETINOBLASTOMA RELATED 1 switches mitosis to meiosis in rice. Plant communications, 5(6), 100857.

Sandhu N, et al. (2024) Development of Novel KASP Markers for Improved Germination in Deep-Sown Direct Seeded Rice. Rice (New York, N.Y.), 17(1), 33.

Zou Z, et al. (2024) TIP aquaporins in Cyperus esculentus: genome-wide identification, expression profiles, subcellular localizations, and interaction patterns. BMC plant biology, 24(1), 298.

Xie T, et al. (2024) Allantoate Amidohydrolase OsAAH is Essential for Preharvest Sprouting Resistance in Rice. Rice (New York, N.Y.), 17(1), 28.

Zhao S, et al. (2024) OsUGT88C3 Encodes a UDP-Glycosyltransferase Responsible for Biosynthesis of Malvidin 3-O-Galactoside in Rice. Plants (Basel, Switzerland), 13(5).

Mu F, et al. (2024) Genome-wide systematic survey and analysis of the RNA helicase gene family and their response to abiotic stress in sweetpotato. BMC plant biology, 24(1), 193.

Li K, et al. (2024) Analysis of genome-wide association studies of low-temperature

germination in Xian and Geng rice. Frontiers in plant science, 15, 1404879.

Ding R, et al. (2024) Molecular traits of MAPK kinases and the regulatory mechanism of GhMAPKK5 alleviating drought/salt stress in cotton. Plant physiology, 196(3), 2030.

He A, et al. (2024) Genome-wide identification and expression analysis of the SPL gene family and its response to abiotic stress in barley (Hordeum vulgare L.). BMC genomics, 25(1), 846.

Wu W, et al. (2024) The elite haplotype OsGATA8-H coordinates nitrogen uptake and productive tiller formation in rice. Nature genetics, 56(7), 1516.

Zhang J, et al. (2024) Transcriptome- and genome-wide systematic identification of expansin gene family and their expression in tuberous root development and stress responses in sweetpotato (Ipomoea batatas). Frontiers in plant science, 15, 1412540.