

Resource Summary Report

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OryGenesDB

RRID:SCR_013226

Type: Tool

Proper Citation

OryGenesDB (RRID:SCR_013226)

Resource Information

URL: <http://orygenesdb.cirad.fr/>

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Description: The Oryza sativa database displays sequence information resulting from the research of the Centre de cooperation internationale en recherche agronomique pour le developpement. It also includes related molecular data from external rice molecular resources (cDNA full length, Gene, EST, Markers, Expression data, etc.). Genome Browser (Gbrowse), a Web-based application for displaying genomic annotations and other features, is the core of our database. The reference annotation layer consists in the 12 rice pseudomolecules released by the TIGR (Version 5.0, January 2007). All the data are superposed as annotations layers and positioned with respect to these pseudomolecules. We developed a set of tools around GBrowse to retrieve as exhaustively as possible information related to queries with several starting points. These tools allow a molecular geneticist to readily find insertion lines (T-DNA, Tos17, Ds) in genes of interest and to retrieve all the associated annotations related to these sequences.

Synonyms: OryGenesDB

Resource Type: data or information resource, database

Resource Name: OryGenesDB

Resource ID: SCR_013226

Alternate IDs: nif-0000-03231

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260829T183027+0000

Ratings and Alerts

No rating or validation information has been found for OryGenesDB.

No alerts have been found for OryGenesDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Feng Z, et al. (2025) Natural variation in SBRR1 shows high potential for sheath blight resistance breeding in rice. *Nature genetics*, 57(8), 2004.

Moin M, et al. (2024) Exploration of the pearl millet phospholipase gene family to identify potential candidates for grain quality traits. *BMC genomics*, 25(1), 581.

Lo KL, et al. (2022) Two genomic regions of a sodium azide induced rice mutant confer broad-spectrum and durable resistance to blast disease. *Rice (New York, N.Y.)*, 15(1), 2.

Dutta M, et al. (2021) Genome-Wide Identification, Transcript Profiling and Bioinformatic Analyses of GRAS Transcription Factor Genes in Rice. *Frontiers in plant science*, 12, 777285.

Thudi M, et al. (2021) Genomic resources in plant breeding for sustainable agriculture. *Journal of plant physiology*, 257, 153351.

Liu X, et al. (2021) Plastid caseinolytic protease OsClpR1 regulates chloroplast development and chloroplast RNA editing in rice. *Rice (New York, N.Y.)*, 14(1), 45.

Hu W, et al. (2020) Regulation of monocot and dicot plant development with constitutively active alleles of phytochrome B. *Plant direct*, 4(4), e00210.

Zhou C, et al. (2020) WRKY Transcription Factor OsWRKY29 Represses Seed Dormancy in Rice by Weakening Absciscic Acid Response. *Frontiers in plant science*, 11, 691.

Herbert L, et al. (2020) Beyond Seek and Destroy: how to Generate Allelic Series Using Genome Editing Tools. *Rice (New York, N.Y.)*, 13(1), 5.

Hong WJ, et al. (2019) Infrastructures of systems biology that facilitate functional genomic study in rice. *Rice (New York, N.Y.)*, 12(1), 15.

Ram H, et al. (2019) Insertional Mutagenesis Approaches and Their Use in Rice for Functional Genomics. *Plants (Basel, Switzerland)*, 8(9).

Wang R, et al. (2019) Genome-wide analysis of poplar NF-YB gene family and identified PtNF-YB1 important in regulate flowering timing in transgenic plants. *BMC plant biology*,

19(1), 251.

Venkatesan A, et al. (2018) Agronomic Linked Data (AgroLD): A knowledge-based system to enable integrative biology in agronomy. PloS one, 13(11), e0198270.

Frouin J, et al. (2018) Tolerance to mild salinity stress in japonica rice: A genome-wide association mapping study highlights calcium signaling and metabolism genes. PloS one, 13(1), e0190964.

Yang X, et al. (2018) Overexpression of OsbHLH107, a member of the basic helix-loop-helix transcription factor family, enhances grain size in rice (*Oryza sativa* L.). Rice (New York, N.Y.), 11(1), 41.

Hinrichs M, et al. (2017) An ABC Transporter Is Involved in the Silicon-Induced Formation of Casparian Bands in the Exodermis of Rice. Frontiers in plant science, 8, 671.

Wu HP, et al. (2017) Large-scale phenomics analysis of a T-DNA tagged mutant population. GigaScience, 6(8), 1.

Bettembourg M, et al. (2017) Genome-wide association mapping for root cone angle in rice. Rice (New York, N.Y.), 10(1), 45.

Sandhu M, et al. (2017) RiceMetaSys for salt and drought stress responsive genes in rice: a web interface for crop improvement. BMC bioinformatics, 18(1), 432.

Feng Z, et al. (2016) SLG controls grain size and leaf angle by modulating brassinosteroid homeostasis in rice. Journal of experimental botany, 67(14), 4241.