

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

RAP-DB

RRID:SCR_006610

Type: Tool

Proper Citation

RAP-DB (RRID:SCR_006610)

Resource Information

URL: <http://rapdb.dna.affrc.go.jp/>

Proper Citation: RAP-DB (RRID:SCR_006610)

Description: Database that provides the genome sequence assembly of the International Rice Genome Sequencing Project (IRGSP), manually curated annotation of the sequence, and other genomics information that could be useful for comprehensive understanding of the rice biology. RAP-DB contains clone positions, structures and functions of genes validated by cDNAs, RNA genes detected by massively parallel signature sequencing (MPSS) technology and sequence similarity, flanking sequences of mutant lines, transposable elements, etc. Other annotation data such as Gnomon can be displayed along with those of RAP for comparison.

Abbreviations: RAP-DB

Synonyms: Rice Annotation Project, Rice Annotation Project Database

Resource Type: data or information resource, database

Defining Citation: [PMID:23299411](#), [PMID:18089549](#)

Keywords: genome sequence assembly, International Rice Genome Sequencing Project, manually curated annotation, sequence, genomics information,

Funding: Japanese Ministry of Education Culture Sports Science and Technology MEXT NT05-3 42996

Availability: Free, Freely available

Resource Name: RAP-DB

Resource ID: SCR_006610

Alternate IDs: SCR_015062, nif-0000-03385

Old URLs: <http://rapdb.lab.nig.ac.jp/>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260912T200143+0000

Ratings and Alerts

No rating or validation information has been found for RAP-DB.

No alerts have been found for RAP-DB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 837 mentions in open access literature.

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

Hu J, et al. (2026) OsSTK-Mediated Sakuranetin Biosynthesis and Carbon Flux Orchestrate Growth and Defence in Rice. *Plant biotechnology journal*, 24(2), 455.

Lu W, et al. (2026) Genomic Selection for Lodging-Related Traits in Double-Cropping Rice. *Plants (Basel, Switzerland)*, 15(5).

Naing NNZN, et al. (2026) Unraveling the Genetic Architecture of Photoperiod Sensitivity in Myanmar Rice Landraces Through Integrated GWAS and Transcriptome Analysis. *International journal of molecular sciences*, 27(4).

Lu J, et al. (2026) Heat Shock Transcription Factor OsHsf1a Enhances Rice Seedling Thermotolerance by Regulating OsMFT1 and Preserving Chloroplast Structure Under Heat Stress. *Plant biotechnology journal*, 24(3), 1898.

Wang D, et al. (2026) The transcription factor OsMADS61 positively regulates root elongation and nitrogen use efficiency in rice. *Plant communications*, 7(2), 101630.

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).

Tao H, et al. (2026) Pan-genome of wild and cultivated rice uncovers genetic diversity, lost and selected sequences during rice domestication. *Rice (New York, N.Y.)*, 19(1).

- Jaiswal S, et al. (2026) Genomic dissection of iron toxicity tolerance in rice identifies key loci, candidate genes, and associated haplotypes. *Scientific reports*, 16(1).
- Sruthi SR, et al. (2026) GWAS and Regularised Regression Identify SNPs Associated with Candidate Genes for Stage-Specific Salinity Tolerance in Rice. *Plants (Basel, Switzerland)*, 15(7).
- Yang H, et al. (2026) The OsGSK1-OsBZR3-OsJAZ4 module integrates nitrate signaling with brassinosteroid and jasmonic acid crosstalk to drive cell wall remodeling for salt recovery in rice. *Plant communications*, 7(6), 101874.
- Darmagaru S, et al. (2026) Genome-wide association studies for identifying SNPs and candidate genes associated with grain quality traits in rice (*Oryza sativa* L.). *The plant genome*, 19(2), e70190.
- Guan S, et al. (2026) Multiplex Gene Editing and Effect Analysis of Yield, Fragrance, and Blast Resistance Genes in Rice. *Genes*, 17(1).
- Lee CJ, et al. (2026) A new genetic architecture for PHS resistance in rice: deciphering the epistatic interactions of three major QTL. *Frontiers in plant science*, 17, 1778741.
- Fang H, et al. (2026) Genome-wide identification and functional characterization of the Magnesium Transporter (MGT) gene family and its expression patterns to different anionic magnesium stresses in *Yinshania henryi*. *BMC genomics*, 27(1).
- Kim MS, et al. (2026) Transcriptional Divergence of Conserved Starch Metabolism Genes During Grain Filling in Indica and Japonica Rice. *Current issues in molecular biology*, 48(5).
- Zeng Y, et al. (2026) Endophyte *Acrocalymma vagum* establishes the holobiont with rice to attract beneficial microorganisms and promote disease resistance. *Journal of advanced research*, 79, 161.
- Qu M, et al. (2026) Impairment of the Uroporphyrinogen Decarboxylase 2 Gene Induces Lesion Mimicry and Downregulates Tetrapyrrole Biosynthesis Pathway Genes in Rice. *Rice (New York, N.Y.)*, 19(1).
- Das S, et al. (2026) Genome-wide association analysis to identify QTLs and candidate genes associated with grain yield and its related traits under low light conditions in rice (*Oryza sativa* L.). *The plant genome*, 19(1), e70191.
- Yamazaki K, et al. (2026) OsAux1 is required for nutritropism in rice roots. *The Plant journal : for cell and molecular biology*, 125(5), e70779.