

Resource Summary Report

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RAP-DB

RRID:SCR_006610

Type: Tool

Proper Citation

RAP-DB (RRID:SCR_006610)

Resource Information

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

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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: database, data or information resource

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: 20260805T044139+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 664 mentions in open access literature.

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

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.

Adu BG, et al. (2025) Transcriptome and gene co-expression network analysis revealed a putative regulatory mechanism of low nitrogen response in rice seedlings. *Frontiers in plant science*, 16, 1547897.

Aung MH, et al. (2025) Comprehensive characterization and diversity analysis of the *HIS1* gene family in rice subpopulations for herbicide resistance. *BMC plant biology*, 25(1), 371.

Consorti E, et al. (2025) Co-Cultivation with *Azolla* Affects the Metabolome of Whole Rice Plant Beyond Canonical Inorganic Nitrogen Fertilization. *Rice (New York, N.Y.)*, 18(1), 49.

Hua H, et al. (2025) A Novel Non-functional *RFT1* Allele Delays Heading Date in Rice. *Rice (New York, N.Y.)*, 18(1), 106.

Lubba KM, et al. (2025) Haplotype shifts in the lipid-related *OsGELP* gene family underpin rice adaptation to high latitudes. *Scientific reports*, 15(1), 32293.

Hori K, et al. (2025) QTN detection and candidate gene identification for improved eating and cooking quality in rice using GWAS and PLS regression analysis. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(3), 58.

Yamaguchi M, et al. (2025) *LIPID RICH 1* modulates allocation of carbon between starch and triacylglycerol in *Arabidopsis* leaves. *Journal of experimental botany*, 76(8), 2144.

Ying S, et al. (2025) Get the ball rolling: update and perspective on the role of chloroplast plastoglobule-associated proteins under abiotic stress. *Journal of experimental botany*, 76(17), 4735.

Li M, et al. (2025) QTL mapping and candidate gene analysis of element accumulation in rice grains via genome-wide association study and population genetic analysis. *BMC plant biology*, 25(1), 93.

Satrio RD, et al. (2025) Rice QTL hotspots related with seed grain size, shape, weight, and color based on genome wide association study and linkage mapping. *Scientific reports*, 15(1), 21470.

Hu Q, et al. (2025) Natural variation of GNP2 enhances grain number to benefit rice yield. *Nature communications*, 16(1), 8848.

Marti-Jerez K, et al. (2025) Unveiling novel QTLs for nitrogen use efficiency in temperate Japonica rice. *BMC plant biology*, 25(1), 1470.

Peng X, et al. (2025) Identification of the BBX gene family and SmBBX5 positively regulate anthocyanin accumulation in eggplant (*Solanum melongena* L.). *BMC genomics*, 26(1), 1132.

Nurmansyah , et al. (2025) Unique starch biosynthesis pathways in wild rice revealed by multi-omics analyses. *Plant biotechnology journal*, 23(6), 2429.

Zhao Y, et al. (2025) Elite haplotype of STRONG1 enhances rice yield by improving lodging resistance, panicle and plant architecture. *Nature communications*, 16(1), 5894.

Herbert L, et al. (2025) dCas9-SPO11-1 locally stimulates meiotic recombination in rice. *Frontiers in plant science*, 16, 1580225.

Yogendra K, et al. (2025) Agroinfiltration-mediated transient assay for rapid evaluation of constructs in pigeonpea. *Biotechnology notes (Amsterdam, Netherlands)*, 6, 117.

Jun S, et al. (2025) Mapping QTLs for PHS resistance and development of a deep learning model to measure PHS rate in japonica rice. *The plant genome*, 18(3), e70109.

Liu R, et al. (2025) Natural variation in OsMADS1 transcript splicing affects rice grain thickness and quality by influencing monosaccharide loading to the endosperm. *Plant communications*, 6(1), 101178.