

Resource Summary Report

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[funRiceGenes](#)

RRID:SCR_015778

Type: Tool

Proper Citation

funRiceGenes (RRID:SCR_015778)

Resource Information

URL: <https://funricegenes.github.io/>

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Description: Dataset of functionally characterized rice genes and members of different gene families. The dataset was created by integrating data from available databases and reviewing publications of rice functional genomic studies.

Synonyms: RICENCODE

Resource Type: data or information resource, data set, database

Keywords: rice, functional genomics, interaction network, genetic improvement, gene, data integration

Funding: National Key Research and Development Program of China 2016YFD0100903; National Natural Science Foundation of China 31771873 and National Natural Science Foundation of China; Outstanding Young Talents Program

Availability: Freely available, Public, Available for download, Free

Resource Name: funRiceGenes

Resource ID: SCR_015778

Alternate URLs: <https://github.com/venyao/RICENCODE>, <http://funricegenes.ncpgr.cn/>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260811T043527+0000

Ratings and Alerts

No rating or validation information has been found for funRiceGenes.

No alerts have been found for funRiceGenes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

Jia J, et al. (2025) Transposable elements drive the subgenomic divergence of homoeologous genes to shape wheat domestication and improvement. *Plant communications*, 6(6), 101341.

Liu C, et al. (2025) A multi-layered regulatory model uncovers the central role of OsPPR37 in coordinating multiple agronomic traits. *BMC plant biology*, 26(1), 134.

Sheng W, et al. (2024) Candidate genes for alkali tolerance identified by genome-wide association study at the seedling stage in rice (*Oryza sativa* L.). *Scientific reports*, 14(1), 30063.

Shi H, et al. (2024) Identification of Candidate Genes for Cold Tolerance at Seedling Stage by GWAS in Rice (*Oryza sativa* L.). *Biology*, 13(10).

Jiao A, et al. (2024) Linkage Mapping and Discovery of Candidate Genes for Drought Tolerance in Rice During the Vegetative Growth Period. *Rice (New York, N.Y.)*, 17(1), 53.

Yoo YH, et al. (2024) Characterization of the Regulatory Network under Waterlogging Stress in Soybean Roots via Transcriptome Analysis. *Plants (Basel, Switzerland)*, 13(18).

Hwang W, et al. (2024) The Rice Online Expression Profiles Array Database Version 2 (ROADv2): An Interactive Atlas for Rice Functional Genomics. *Rice (New York, N.Y.)*, 17(1), 75.

Lian S, et al. (2024) Functional differentiation and genetic diversity of rice cation exchanger (CAX) genes and their potential use in rice improvement. *Scientific reports*, 14(1), 8642.

Satasiya P, et al. (2024) Meta-analysis of identified genomic regions and candidate genes underlying salinity tolerance in rice (*Oryza sativa* L.). *Scientific reports*, 14(1), 5730.

Long W, et al. (2024) Genome evolution and diversity of wild and cultivated rice species. *Nature communications*, 15(1), 9994.

Rahimi Y, et al. (2023) Genome-wide association study to identify genomic loci associated with early vigor in bread wheat under simulated water deficit complemented with

quantitative trait loci meta-analysis. G3 (Bethesda, Md.), 13(2).

Zeng W, et al. (2023) Functional characterization and allelic mining of OsGLR genes for potential uses in rice improvement. *Frontiers in plant science*, 14, 1236251.

Wang X, et al. (2023) Identification of the CNGC Gene Family in Rice and Mining of Alleles for Application in Rice Improvement. *Plants (Basel, Switzerland)*, 12(24).

Jiang X, et al. (2023) Genome-Wide Identification and Analysis of Collar Region-Preferential Genes in Rice. *Plants (Basel, Switzerland)*, 12(16).

Sun Z, et al. (2023) Dissecting the genetic basis of heterosis in elite super-hybrid rice. *Plant physiology*, 192(1), 307.

Mahto A, et al. (2023) Cytological, transcriptome and miRNome temporal landscapes decode enhancement of rice grain size. *BMC biology*, 21(1), 91.

Adam H, et al. (2023) Genomic introgressions from African rice (*Oryza glaberrima*) in Asian rice (*O. sativa*) lead to the identification of key QTLs for panicle architecture. *BMC genomics*, 24(1), 587.

Abdirad S, et al. (2022) Genome-Wide Expression Analysis of Root Tips in Contrasting Rice Genotypes Revealed Novel Candidate Genes for Water Stress Adaptation. *Frontiers in plant science*, 13, 792079.

Cross A, et al. (2022) Grain dispersal mechanism in cereals arose from a genome duplication followed by changes in spatial expression of genes involved in pollen development. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 135(4), 1263.

Chen Y, et al. (2022) The *Triticum ispahanicum* elongated glume locus P2 maps to chromosome 6A and is associated with the ectopic expression of SVP-A1. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 135(7), 2313.