

Resource Summary Report

Generated by [NIF](#) on Sep 13, 2026

Rice Gene Thresher

RRID:SCR_007893

Type: Tool

Proper Citation

Rice Gene Thresher (RRID:SCR_007893)

Resource Information

URL: <http://rice.kps.ku.ac.th:8080/RiceGeneThresherWeb2>

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Description: A public online resource for mining genes underlying genome regions of interest or quantitative trait loci (QTL) in rice genome. It is a compendium of rice genomic resources consisting of genetic markers, genome annotation, expressed sequence tags (ESTs), protein domains, gene ontology, plant stress-responsive genes, metabolic pathways and prediction of protein-protein interactions. RiceGeneThresher system integrates these diverse data sources and provides powerful web-based applications, and flexible tools for delivering customized set of biological data on rice. Its system supports whole-genome gene mining for QTL by using DNA marker intervals or genomic loci. RiceGeneThresher provides biologically supported evidences that are essential for targeting groups or networks of genes involved in controlling traits underlying QTL. Users can use it to discover and to assign the most promising candidate genes in preparation for the further gene function validation analysis., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Rice Gene Thresher

Resource Type: data or information resource, database

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Rice Gene Thresher

Resource ID: SCR_007893

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260912T200155+0000

Ratings and Alerts

No rating or validation information has been found for Rice Gene Thresher.

No alerts have been found for Rice Gene Thresher.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Asiaee A, et al. (2023) Transcriptome Complexity Disentangled: A Regulatory Molecules Approach. bioRxiv : the preprint server for biology.

Abrams ZB, et al. (2018) Thirty biologically interpretable clusters of transcription factors distinguish cancer type. BMC genomics, 19(1), 738.

Thongjuea S, et al. (2009) RiceGeneThresher: a web-based application for mining genes underlying QTL in rice genome. Nucleic acids research, 37(Database issue), D996.