

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Database of Rice Transcription Factors

RRID:SCR_002413

Type: Tool

Proper Citation

Database of Rice Transcription Factors (RRID:SCR_002413)

Resource Information

URL: <http://drtf.cbi.pku.edu.cn/>

Proper Citation: Database of Rice Transcription Factors (RRID:SCR_002413)

Description: Database collection of known and predicted transcription factors of *Oryza sativa* L. ssp. indica and *Oryza sativa* L. ssp. japonica. DRTF currently contains 2,025 putative transcription factors (TF) gene models in indica and 2,384 in japonica, distributed in 63 families. THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 13, 2026.

Abbreviations: DRTF

Resource Type: data or information resource, database

Defining Citation: [PMID:16551659](#)

Keywords: oryza sativa indica, oryza sativa japonica, rice transcription, rice, transcription factor, gene model, blast

Funding: NSFC 863 Programme 2003CB715900 (973);
NSFC 863 Programme 90408015

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Database of Rice Transcription Factors

Resource ID: SCR_002413

Alternate IDs: OMICS_00554, nif-0000-02771

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260905T133117+0000

Ratings and Alerts

No rating or validation information has been found for Database of Rice Transcription Factors.

No alerts have been found for Database of Rice Transcription Factors.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Kababji AM, et al. (2024) Synthetic directed evolution for targeted engineering of plant traits. *Frontiers in plant science*, 15, 1449579.

Ke S, et al. (2018) Genome-wide transcriptome profiling provides insights into panicle development of rice (*Oryza sativa* L.). *Gene*, 675, 285.

Cho WK, et al. (2015) Time-Course RNA-Seq Analysis Reveals Transcriptional Changes in Rice Plants Triggered by Rice stripe virus Infection. *PloS one*, 10(8), e0136736.

Yang YW, et al. (2015) Comparative Transcriptome Analysis of Shoots and Roots of TNG67 and TCN1 Rice Seedlings under Cold Stress and Following Subsequent Recovery: Insights into Metabolic Pathways, Phytohormones, and Transcription Factors. *PloS one*, 10(7), e0131391.

Hou Y, et al. (2015) A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. *BMC plant biology*, 15, 163.

Chen YA, et al. (2014) Transcriptome profiling and physiological studies reveal a major role for aromatic amino acids in mercury stress tolerance in rice seedlings. *PloS one*, 9(5), e95163.

Chi WC, et al. (2013) Autotoxicity mechanism of *Oryza sativa*: transcriptome response in rice roots exposed to ferulic acid. *BMC genomics*, 14, 351.

Priya P, et al. (2013) RiceSRTFDB: a database of rice transcription factors containing comprehensive expression, cis-regulatory element and mutant information to facilitate gene function analysis. *Database : the journal of biological databases and curation*, 2013, bat027.

Ya H, et al. (2012) Gene expression profiles in promoted-growth rice seedlings that germinated from the seeds implanted by low-energy N⁺ beam. *Journal of radiation research*, 53(4), 558.

Xu H, et al. (2012) Transcriptomic analysis of rice (*Oryza sativa*) developing embryos using the RNA-Seq technique. *PloS one*, 7(2), e30646.

Schnable JC, et al. (2011) Dose-sensitivity, conserved non-coding sequences, and duplicate gene retention through multiple tetraploidies in the grasses. *Frontiers in plant science*, 2, 2.

Filichkin SA, et al. (2011) Global profiling of rice and poplar transcriptomes highlights key conserved circadian-controlled pathways and cis-regulatory modules. *PloS one*, 6(6), e16907.

Mochida K, et al. (2010) Genomics and bioinformatics resources for crop improvement. *Plant & cell physiology*, 51(4), 497.

Mochida K, et al. (2009) In silico analysis of transcription factor repertoire and prediction of stress responsive transcription factors in soybean. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 16(6), 353.

Yang B, et al. (2009) Identification and expression analysis of WRKY transcription factor genes in canola (*Brassica napus* L.) in response to fungal pathogens and hormone treatments. *BMC plant biology*, 9, 68.

Ramirez SR, et al. (2009) Comparative analyses of plant transcription factor databases. *Current genomics*, 10(1), 10.