

# Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

## STIFDB

RRID:SCR\_002131

Type: Tool

### Proper Citation

STIFDB (RRID:SCR\_002131)

### Resource Information

**URL:** <http://caps.ncbs.res.in/stifdb2/>

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**Description:** Database of biotic and abiotic stress responsive genes in Arabidopsis thaliana and Oryza sativa L. with options to identify probable Transcription Factor Binding Sites in their promoters. In the response to biotic stress like Bacteria and abiotic stresses like ABA, drought, cold, salinity, dehydration, UV-B, high light, heat, heavy metals etc, ten specific families of transcription factors in Arabidopsis thaliana and six in Oryza sativa L. are known to be involved. HMM-based models are used to identify binding sites of transcription factors belonging to these families. They have also consulted literature reports to cross-validate the Transcription Factor Binding Sites predicted by the method.

**Abbreviations:** STIFDB

**Synonyms:** Stress Responsive Transcription Factor Database

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

**Defining Citation:** [PMID:23314754](#), [PMID:19841686](#)

**Keywords:** stress responsive, transcription factor, biotic, abiotic, gene, transcription factor binding site, promoter, stress, chromosome, blast

**Availability:** Free, Freely Available

**Resource Name:** STIFDB

**Resource ID:** SCR\_002131

**Alternate IDs:** OMICS\_01866

**Record Creation Time:** 20220129T080211+0000

**Record Last Update:** 20260829T182915+0000

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## Ratings and Alerts

No rating or validation information has been found for STIFDB.

No alerts have been found for STIFDB.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Wu X, et al. (2022) A microRNA-microRNA crosstalk network inferred from genome-wide single nucleotide polymorphism variants in natural populations of *Arabidopsis thaliana*. *Frontiers in plant science*, 13, 958520.

Kumari S, et al. (2021) Meta-Analysis of Yield-Related and N-Responsive Genes Reveals Chromosomal Hotspots, Key Processes and Candidate Genes for Nitrogen-Use Efficiency in Rice. *Frontiers in plant science*, 12, 627955.

Ke L, et al. (2020) Genome-wide identification of cold responsive transcription factors in *Brassica napus* L. *BMC plant biology*, 20(1), 62.

Hong WJ, et al. (2019) Infrastructures of systems biology that facilitate functional genomic study in rice. *Rice (New York, N.Y.)*, 12(1), 15.

Pradhan SK, et al. (2019) Genes, pathways and transcription factors involved in seedling stage chilling stress tolerance in indica rice through RNA-Seq analysis. *BMC plant biology*, 19(1), 352.

Prasad KVSK, et al. (2018) Vascular Plant One-Zinc-Finger (VOZ) Transcription Factors Are Positive Regulators of Salt Tolerance in *Arabidopsis*. *International journal of molecular sciences*, 19(12).

Thirunavukkarasu N, et al. (2017) Genomewide Expression and Functional Interactions of Genes under Drought Stress in Maize. *International journal of genomics*, 2017, 2568706.

Agarwal P, et al. (2016) Rice Improvement Through Genome-Based Functional Analysis and Molecular Breeding in India. *Rice (New York, N.Y.)*, 9(1), 1.

Prasad KVSK, et al. (2016) Global gene expression analysis using RNA-seq uncovered a new role for SR1/CAMTA3 transcription factor in salt stress. *Scientific reports*, 6, 27021.

Muthuramalingam M, et al. (2015) A GCC-box motif in the promoter of nudix hydrolase 7 (*AtNUDT7*) gene plays a role in ozone response of *Arabidopsis* ecotypes. *Genomics*, 105(1), 31.

Zhu L, et al. (2014) *Gleditsia sinensis*: transcriptome sequencing, construction, and application of its protein-protein interaction network. *BioMed research international*, 2014, 404578.