

Resource Summary Report

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PLANTTFDB

RRID:SCR_003362

Type: Tool

Proper Citation

PLANTTFDB (RRID:SCR_003362)

Resource Information

URL: <http://planttfdb.gao-lab.org/>

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Description: Comprehensive plant transcription factor database. Interface to allow users to search the database by IDs or free texts, to make sequence similarity search against TFs of all or individual species, and to download TF sequences for local analysis. PlantTFDB 3.0: a portal for the functional and evolutionary study of plant transcription factors

Abbreviations: PlantTFDB

Synonyms: , PlantTFDB 2.0, Plant Transcription Factor Database

Resource Type: production service resource, data analysis service, service resource, analysis service resource, database, data or information resource

Defining Citation: [PMID:24174544](#), [PMID:17933783](#), [PMID:21097470](#)

Keywords: transcription factor, expression, regulation, interaction, conserved element, phenotype, function, evolution, bio.tools, FASEB list

Funding: China 863 ;
China 973 ;
NSFC ;
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Availability: Acknowledgement requested, Free

Resource Name: PLANTTFDB

Resource ID: SCR_003362

Alternate IDs: nif-0000-03311, biotools:planttfdb_2.0, OMICS_00560

Alternate URLs: https://bio.tools/planttfdb_2.0

Old URLs: <http://planttfdb.cbi.pku.edu.cn>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250428T053031+0000

Ratings and Alerts

No rating or validation information has been found for PLANTTFDB.

No alerts have been found for PLANTTFDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 976 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Liu Z, et al. (2025) SoIR: a comprehensive Solanaceae information resource for comparative and functional genomic study. *Nucleic acids research*, 53(D1), D1623.

Wang Q, et al. (2025) Comparative transcriptome analyses of different orthosiphon aristatus tissues reveal differentially expressed genes associated with flavonoid biosynthesis. *Scientific reports*, 15(1), 1059.

Huang J, et al. (2025) Identification of the Granule-Bound Starch Synthase (GBSS) Genes Involved in Amylose Biosynthesis in Tartary Buckwheat (*Fagopyrum tataricum* (L.) Gaertn.). *Plants* (Basel, Switzerland), 14(2).

Ribeyre Z, et al. (2025) De novo transcriptome assembly and discovery of drought-responsive genes in white spruce (*Picea glauca*). *PloS one*, 20(1), e0316661.

Liu D, et al. (2025) AMIR: a multi-omics data platform for Asteraceae plants genetics and breeding research. *Nucleic acids research*, 53(D1), D1563.

Wang C, et al. (2025) Identifying Candidate Genes Related to Soybean (*Glycine max*) Seed

Coat Color via RNA-Seq and Coexpression Network Analysis. *Genes*, 16(1).

Wu X, et al. (2025) Identification and Functional Analysis of Candidate Genes Influencing Citrus Leaf Size Through Transcriptome and Coexpression Network Approaches. *Genes*, 16(1).

Qian X, et al. (2025) The Potassium Utilization Gene Network in *Brassica napus* and Functional Validation of *BnaZSHAK5.2* Gene in Response to Potassium Deficiency. *International journal of molecular sciences*, 26(2).

Huan T, et al. (2025) Phylogeny-based comparative analysis of gene expression modulation upon drought stress across three cotton diploids. *BMC plant biology*, 25(1), 31.

Jost R, et al. (2025) Sink strength, nutrient allocation, cannabinoid yield, and associated transcript profiles vary in two drug-type *Cannabis* chemovars. *Journal of experimental botany*, 76(1), 152.

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (*Oryza sativa* L.) and their expression profiles in response to phytohormones. *PloS one*, 20(1), e0317008.

Wang X, et al. (2025) Genome-wide identification and functional roles relating to anthocyanin biosynthesis analysis in maize. *BMC plant biology*, 25(1), 57.

Liu F, et al. (2025) Time-series transcriptome analysis reveals the cascade mechanism of biological processes following the perturbation of the MVA pathway in *Salvia miltiorrhiza*. *Plant molecular biology*, 115(1), 20.

Wang H, et al. (2024) The genomes of *Dahlia pinnata*, *Cosmos bipinnatus*, and *Bidens alba* in tribe Coreopsiadeae provide insights into polyploid evolution and inulin biosynthesis. *GigaScience*, 13.

He Z, et al. (2024) Single-cell transcriptome analysis dissects lncRNA-associated gene networks in *Arabidopsis*. *Plant communications*, 5(2), 100717.

Montesinos Á, et al. (2024) Contrasting plant transcriptome responses between a pierce-sucking and a chewing herbivore go beyond the infestation site. *BMC plant biology*, 24(1), 120.

Jia C, et al. (2024) Integrative metabolomic and transcriptomic analyses reveal the potential regulatory mechanism of unique dihydroxy fatty acid biosynthesis in the seeds of an industrial oilseed crop *Orychophragmus violaceus*. *BMC genomics*, 25(1), 29.

Wang X, et al. (2024) Genome-wide identification and expression characterization of the GH3 gene family of tea plant (*Camellia sinensis*). *BMC genomics*, 25(1), 120.

Zheng K, et al. (2024) Genome-Wide Identification and Expression Analysis of GATA Family Genes in *Dimocarpus longan* Lour. *International journal of molecular sciences*, 25(2).

Cao Y, et al. (2024) *CsCuAO1* Associated with *CsAMADH1* Confers Drought Tolerance by

