

Resource Summary Report

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PlnTFDB

RRID:SCR_010899

Type: Tool

Proper Citation

PlnTFDB (RRID:SCR_010899)

Resource Information

URL: <http://plntfdb.bio.uni-potsdam.de>

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Description: Public database arising from efforts to identify and catalogue all plant genes involved in transcriptional control. Integrative plant transcription factor database that provides web interface to access large sets of transcription factors of several plant species, currently encompassing *Arabidopsis thaliana* (thale cress), *Populus trichocarpa* (poplar), *Oryza sativa* (rice), *Chlamydomonas reinhardtii* and *Ostreococcus tauri*. Provides access point to its daughter databases of species-centered representation of transcription factors (OstreoTFDB, ChlamyTFDB, ArabTFDB, PoplarTFDB and RiceTFDB). Information including protein sequences, coding regions, genomic sequences, expressed sequence tags, domain architecture and scientific literature is provided for each family.

Synonyms: Plant Transcription Factor Database, PlnTFDB v3.0

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

Defining Citation: [PMID:19858103](#), [PMID:17286856](#)

Keywords: protein model, protein sequence, gene family, protein, transcriptional control, blast, bio.tools, FASEB list

Funding: University of Potsdam ;
Germany ;
German Federal Ministry of Education and Research ;
Fond der Chemischen Industrie

Availability: Free, Freely available

Resource Name: PlnTFDB

Resource ID: SCR_010899

Alternate IDs: biotools:plntfdb, OMICS_00561

Alternate URLs: <http://plntfdb.bio.uni-potsdam.de/v3.0/>, <https://bio.tools/plntfdb>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260805T044249+0000

Ratings and Alerts

No rating or validation information has been found for PInTFDB.

No alerts have been found for PInTFDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 201 mentions in open access literature.

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

Yan S, et al. (2025) Transcriptome Analysis Reveals Critical Genes Involved in the Response of *Stropharia rugosoannulata* to High Temperature and Drought Stress. *Current issues in molecular biology*, 47(10).

Muñoz-Pérez JM, et al. (2025) Gene Co-Expression Networks Highlight Key Nodes Associated With Ammonium Nitrate in Sugarcane. *Physiologia plantarum*, 177(6), e70612.

Lai X, et al. (2025) Dynamic changes in the transcriptome of tropical region-originated king grasses in response to cold stress. *Frontiers in plant science*, 16, 1511466.

Gou C, et al. (2025) Genome wide identification of Dof transcription factors in Carmine radish reveals RsDof33 role in cadmium stress and anthocyanin biosynthesis. *Scientific reports*, 15(1), 4766.

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).

Park S, et al. (2025) Comparative genome-wide characterization and evolutionary insights into the AP2/ERF gene family in three *Coffea* species (*C. canephora*, *C. eugenoides*, and *C. arabica*). *BMC genomics*, 26(1), 653.

Yu J, et al. (2025) Physiological mechanism of lodging resistance of oat stalk and analysis of transcriptome differences. *Frontiers in plant science*, 16, 1532216.

Xu C, et al. (2025) SISPL15: A Negative Regulator Targeted by SlmiR156a Participates in Regulating the Light-Induced Anthocyanin Biosynthesis of Aft Tomato Fruits. *Physiologia plantarum*, 177(5), e70471.

Pan X, et al. (2024) Full-length transcriptome analysis of a bloom-forming dinoflagellate *Prorocentrum shikokuense* (Dinophyceae). *Scientific data*, 11(1), 430.

Yu H, et al. (2024) Transcriptome Expression Profiling Reveals the Molecular Response to Salt Stress in *Gossypium anomalum* Seedlings. *Plants* (Basel, Switzerland), 13(2).

Xia W, et al. (2024) Chromosome-level genome provides new insight into the overwintering process of Korla pear (*Pyrus sinkiangensis* Yu). *BMC plant biology*, 24(1), 773.

Wang Y, et al. (2024) Full-length single-molecule sequencing uncovers novel insight into the global landscape of the cold stress response in trifoliate orange (*Citrus trifoliata*). *Frontiers in plant science*, 15, 1506414.

Zhu X, et al. (2024) Genome-wide analysis and expression profile of the bZIP gene family in *Neopyropia yezoensis*. *Frontiers in plant science*, 15, 1461922.

Xu H, et al. (2024) Study on molecular response of alfalfa to low temperature stress based on transcriptomic analysis. *BMC plant biology*, 24(1), 1244.

Ji W, et al. (2023) Transcriptome Profiling of *Gossypium anomalum* Seedlings Reveals Key Regulators and Metabolic Pathways in Response to Drought Stress. *Plants* (Basel, Switzerland), 12(2).

Hu J, et al. (2023) PearMODB: a multiomics database for pear (*Pyrus*) genomics, genetics and breeding study. *Database : the journal of biological databases and curation*, 2023.

Zafar UB, et al. (2023) De novo transcriptome assembly of *Dalbergia sissoo* Roxb. (Fabaceae) under *Botryodiplodia theobromae*-induced dieback disease. *Scientific reports*, 13(1), 20503.

Yang S, et al. (2023) Global Responses of Autopolyploid Sugarcane Badila (*Saccharum officinarum* L.) to Drought Stress Based on Comparative Transcriptome and Metabolome Profiling. *International journal of molecular sciences*, 24(4).

Zhou P, et al. (2023) Omics analyses of *Rehmannia glutinosa* dedifferentiated and cambial meristematic cells reveal mechanisms of catalpol and indole alkaloid biosynthesis. *BMC plant biology*, 23(1), 463.

Yang Y, et al. (2023) Metabolome combined with transcriptome profiling reveals the dynamic changes in flavonoids in red and green leaves of *Populus × euramericana* 'Zhonghuahongye'. *Frontiers in plant science*, 14, 1274700.