

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

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

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

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

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: 20260821T193926+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 218 mentions in open access literature.

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

Wang Y, et al. (2026) Transcriptomic Profiling Across Developmental Stages of *Camellia petelotii* (Merr.) Sealy Flower. *Metabolites*, 16(2).

Zhang Y, et al. (2026) Comparative transcriptomics unveils the role of DELLA protein GAIP-B in cold tolerance of mango (*Mangifera indica* L.). *BMC plant biology*, 26(1).

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.

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).

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.

Zhang S, et al. (2025) Transcriptomic Analysis of Leaves from Two Maize Hybrids Under Heat Stress During the Early Generative Stage. *Genes*, 16(5).

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. eugenioides*, and *C. arabica*). *BMC genomics*, 26(1), 653.

Zhao R, et al. (2025) Evaluating the accumulation of organic acids and fatty acids under different environmental stresses in *Dendrobium nobile*. *BMC plant biology*, 26(1), 189.

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.

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

Tian J, et al. (2025) Evolutionary Dynamics and Expression Divergence of the MADS-Box Gene Family During Recent Speciation of AA-Genome *Oryza* Species. *Plants (Basel, Switzerland)*, 14(3).

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

Zhao R, et al. (2024) Metabolic and Transcriptomic Profile Revealing the Differential Accumulating Mechanism in Different Parts of *Dendrobium nobile*. *International journal of molecular sciences*, 25(10).

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.

Zhang R, et al. (2024) Dynamic evolution of MADS-box genes in extant ferns via large-scale phylogenomic analysis. *Frontiers in plant science*, 15, 1410554.