

Resource Summary Report

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PLANTTFDB

RRID:SCR_003362

Type: Tool

Proper Citation

PLANTTFDB (RRID:SCR_003362)

Resource Information

URL: <https://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: analysis service resource, data analysis service, data or information resource, database, production service resource, service 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 ;
China NSFC ;
NSFC

Availability: Free, Available for download, Freely available

Resource Name: PLANTTFDB

Resource ID: SCR_003362

Alternate IDs: nif-0000-03311, biotools:planttfdb_2.0, OMICS_00560, r3d100010137

Alternate URLs: https://bio.tools/planttfdb_2.0, <https://doi.org/10.17616/R3JG6V>

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

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260905T132502+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 1441 mentions in open access literature.

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

Cheng H, et al. (2026) Comparative single-cell transcriptomic map reveals divergence in leaves between two cotton species at cell type resolution. *Journal of advanced research*, 79, 121.

Shukla V, et al. (2026) Chromatin state architecture governs transcription factor accessibility across plant genomes. *PLoS genetics*, 22(1), e1012015.

Fu L, et al. (2026) S3RL: Enhancing Spatial Single-Cell Transcriptomics With Separable Representation Learning. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(17), e16178.

Chen Y, et al. (2026) Genome-wide identification of the AP2/ERF gene family and its alternative splicing to reveal their expression profiles in different tissues of *Rosa roxburghii*. *BMC plant biology*, 26(1).

Mao W, et al. (2026) Genome-Wide Analysis of Heat Shock Transcription Factors (HSFs) in Kelp (*Saccharina japonica*) and Analysis of Their Expression in Response to Abiotic Stresses. *Plants* (Basel, Switzerland), 15(3).

Chen C, et al. (2026) Genome-Wide Identification of the HSF Genes in Sweet Potato and Functional Role of IbHSF22 in Anthocyanin Accumulation and Salt Stress Tolerance. *Plants* (Basel, Switzerland), 15(2).

Zhang C, et al. (2026) RpnACs transcription factors coordinate leaf margin development in *Rosa persica*. *BMC genomics*, 27(1), 132.

Akotenou G, et al. (2026) MegaPlantTF: a machine learning framework for comprehensive identification and classification of plant transcription factors. *Bioinformatics* (Oxford, England), 42(1).

Zhang C, et al. (2026) The Maize ZmbHLH118 Transcription Factor Regulates Vacuolar Nitrate Loading by the NO₃ - Transporter ZmCLCa. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(25), e20219.

Kim SM, et al. (2026) The C₂H₂-type zinc finger protein SIHair5 acts as a regulatory node coordinating trichome development and leaf morphogenesis in tomato. *Plant cell reports*, 45(4).

Wu W, et al. (2026) Identification and analysis of the MYB transcription factors against seawater tolerance in daylily (*Hemerocallis fulva* L.). *Scientific reports*, 16(1).

Wang S, et al. (2026) Integrated Metabolomics and Transcriptomics Analysis Reveals the Biosynthetic Mechanism of Isoquinoline Alkaloids in Different Tissues of *Hypecoum erectum* L. *Current issues in molecular biology*, 48(3).

Wang M, et al. (2026) A near telomere-to-telomere chromosome-level genome assembly of *Rhodiola yunnanensis* (Crassulaceae). *Scientific data*, 13(1).

Zhang K, et al. (2026) Multi-tissue transcriptomic profiling of foxtail millet in response to drought and rewatering. *BMC plant biology*, 26(1).

Wang C, et al. (2026) Integrative metabolome and transcriptome of different tree size reveal wood formation in *Corymbia citriodora*. *BMC genomics*, 27(1).

Puthanvila Surendrababu S, et al. (2026) A wheat MYB transcription factor activates defense by repressing TaSIZ1 in response to branched-chain amino acid accumulation. *The Plant cell*, 38(5).

Wang X, et al. (2026) A coordinated network of ABA signaling, photorespiratory and proteostasis in EMS-induced maize mutant with enhanced drought resistance. *Frontiers in plant science*, 17, 1828125.

Ma B, et al. (2026) Transcriptomic and Weighted Gene Co-Expression Network Analysis Reveals Molecular Regulatory Mechanisms of Cold Stress in Rice. *Genes*, 17(6).

Li J, et al. (2026) VvERF045 Integrates Ethylene, Brassinosteroid and Absciscic Acid Pathways to Orchestrate Anthocyanin Biosynthesis in Grapevine. *Plant biotechnology journal*, 24(2), 787.

Idrissi Azami A, et al. (2026) Comprehensive re-assembly and annotation dataset for the argan tree (*Argania spinosa* L., Sapotaceae) genome. *Scientific data*, 13(1), 267.