

Resource Summary Report

Generated by T1D on Aug 1, 2026

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: data analysis service, data or information resource, database, service resource, production service resource, analysis 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 ;
NSFC ;
China 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: 20260801T042532+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 1109 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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.

Sun T, et al. (2026) Conserved spatial patterning of gene expression in independent lineages of C4 plants. *The New phytologist*, 249(1), 24.

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Zhang J, et al. (2025) Evolution of HD-ZIP transcription factors and their function in cabbage leafy head formation. *Frontiers in plant science*, 16, 1583110.

Yue L, et al. (2025) Metabolomic and transcriptomic analyses of drought resistance mechanisms in sorghum varieties. *PeerJ*, 13, e19596.

Sheng Y, et al. (2025) Single-nucleus multi-omics reveals the impact of drought stress on the development of soybean endosperm. *Plant communications*, 6(10), 101495.

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

Ji M, et al. (2025) Maize leaves salt-responsive genes revealed by comparative transcriptome of salt-tolerant and salt-sensitive cultivars during the seedling stage. *PeerJ*, 13, e19268.

Pab??n-Mora N, et al. (2025) The floral ABCs of *Hydnora*, one of the most bizarre parasitic plants in the world, and its autotrophic relatives of the order Piperales. *EvoDevo*, 16(1), 16.

Wu J, et al. (2025) Comparative phenotypic and transcriptomic analyses reveal the potential molecular basis of forming bigger leaf blade in autotetraploid castor bean. *BMC plant biology*, 25(1), 1223.

Lu P, et al. (2025) SnRK-PP2C-PYL Gene Families in *Citrus sinensis*: Genomic Characterization and Regulatory Roles in Carotenoid Metabolism. *Metabolites*, 15(9).

Geng S, et al. (2025) Genome-wide identification and analysis of paclobutrazol-resistance gene family in cotton and the positive role of GhPRE3 in salt stress and drought stress resistance. *Functional & integrative genomics*, 25(1), 201.

Zhang X, et al. (2025) Transcriptomic analysis reveals the growth of *Populus Schneideri* in different light qualities. *BMC genomics*, 26(1), 871.

Shen Z, et al. (2025) The SNL Histone Deacetylase-Binding Factor GmHE13 Is a Novel Regulator of Soybean Hypocotyl Elongation. *Plant biotechnology journal*, 23(12), 5353.

Korek M, et al. (2025) The cost of survival: mutation in a barley Strigolactone repressor HvD53A impairs photosynthesis but increases drought tolerance. *Plant & cell physiology*, 66(10), 1426.

Su Q, et al. (2025) Transcriptome analysis reveals that regulation network of the genes related to unique double flowers in tropical viviparous water lily. *Scientific reports*, 15(1), 29561.

Wang C, et al. (2025) Genome-wide identification of GATA family genes in sweet potato (*Ipomoea batatas* L.) and their expression patterns under abiotic stress. *Frontiers in genetics*, 16, 1635749.

Jin Z, et al. (2025) Natural variation in PtobZIP18 confers the trade-off between stem growth and drought tolerance in *Populus*. *Plant biotechnology journal*, 23(10), 4633.

Sun H, et al. (2025) Transcriptome profiling reveals key genes in eggplant (*Solanum melongena*) roots under salt stress. *BMC genomics*, 26(1), 635.