

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: 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 [kravitz2](#) .

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.

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

Bousquet L, et al. (2025) Life cycle and morphogenetic differentiation in heteromorphic cell types of a cosmopolitan marine microalga. *The New phytologist*, 245(5), 1969.

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).

Yang X, et al. (2025) Genome-wide identification and characterization of transcription factors involved in defense responses against *Sclerotinia sclerotiorum* in *Brassica juncea*.

Scientific reports, 15(1), 4341.

Wang M, et al. (2025) Comprehensive genome-wide analysis of ARF transcription factors in orchardgrass (*Dactylis glomerata*): the positive regulatory role of DgARF7 in drought resistance. *BMC genomics*, 26(1), 101.

Zhang Y, et al. (2025) Physiological and transcriptomic evidence revealed the role of exogenous GABA in enhancing salt tolerance in strawberry seedlings. *BMC genomics*, 26(1), 196.

Zhao Q, et al. (2025) The high-quality chromosome-level genome assembly of *Dracocephalum rupestre* Hance. *Scientific data*, 12(1), 472.

Yang Y, et al. (2025) Identification and role of CmLhcb2.1 in regulating low-light stress resistance in Chinese chestnut (*Castanea mollissima*). *Frontiers in plant science*, 16, 1552618.

Liu Y, et al. (2025) Constraint of accessible chromatin maps regulatory loci involved in maize speciation and domestication. *Nature communications*, 16(1), 2477.

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.

Jiang Y, et al. (2025) Metabolomic response of *Zizania latifolia* to low-temperature stress and identification of the bZIP transcription factor family. *GM crops & food*, 16(1), 413.

Contreras-Riquelme JS, et al. (2025) Desert-adapted tomato *Solanum pennellii* exhibit unique regulatory elements and stress-ready transcriptome patterns to drought. *PloS one*, 20(5), e0324724.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

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.

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.