

Resource Summary Report

Generated by [RRID](#) on Aug 7, 2026

PlantTFcat

RRID:SCR_010898

Type: Tool

Proper Citation

PlantTFcat (RRID:SCR_010898)

Resource Information

URL: <http://plantgrn.noble.org/PlantTFcat/>

Proper Citation: PlantTFcat (RRID:SCR_010898)

Description: A web-based analysis tool that is designed to identify and categorize plant TF/TR/CR genes from genome-scale protein and nucleic acid sequences by systematically analyzing InterProScan domain patterns in protein sequences., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PlantTFcat

Synonyms: PlantTFcat: An Online Plant Transcription Factor and Transcriptional Regulator Categorization and Analysis Tool

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Defining Citation: [PMID:24219505](#)

Keywords: bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PlantTFcat

Resource ID: SCR_010898

Alternate IDs: biotools:planttfcat, OMICS_00559

Alternate URLs: <https://bio.tools/planttfcat>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260807T042745+0000

Ratings and Alerts

No rating or validation information has been found for PlantTFcat.

No alerts have been found for PlantTFcat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Jiang Q, et al. (2026) Comprehensive analysis of salt tolerance mechanisms in forage maize: physiological adaptation, transcriptional regulation, and key gene identification. BMC plant biology, 26(1), 211.

Ko?cielniak P, et al. (2025) Comparative RNA sequencing-based transcriptome profiling of *Quercus robur*: specific sets of genes involved in taproot and lateral roots emergence. Tree physiology, 45(6).

Naim D, et al. (2024) Genome-wide identification and in silico characterization of major RNAi gene families in date palm (*Phoenix dactylifera*). BMC genomic data, 25(1), 31.

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.

Liu G, et al. (2023) Genes expression profiles in vascular cambium of *Eucalyptus urophylla* × *Eucalyptus grandis* at different ages. BMC plant biology, 23(1), 500.

Coe K, et al. (2023) Population genomics identifies genetic signatures of carrot domestication and improvement and uncovers the origin of high-carotenoid orange carrots. Nature plants, 9(10), 1643.

Wang C, et al. (2022) Transcriptome analysis and differential gene expression profiling of wucaï (*Brassica campestris* L.) in response to cold stress. BMC genomics, 23(1), 137.

Ko?cielniak P, et al. (2022) OakRootRNADB-a consolidated RNA-seq database for coding and noncoding RNA in roots of pedunculate oak (*Quercus robur*). Database : the journal of biological databases and curation, 2022.

Liu P, et al. (2022) Integrated analysis of long non-coding RNAs and mRNAs reveals the regulatory network of maize seedling root responding to salt stress. BMC genomics, 23(1), 50.

Maibam A, et al. (2022) Transcriptome Analysis of *Pennisetum glaucum* (L.) R. Br. Provides Insight Into Heat Stress Responses. Frontiers in genetics, 13, 884106.

Kadri SUT, et al. (2022) Transcriptome-wide identification and computational insights into protein modeling and docking of CAMTA transcription factors in *Eleusine coracana* L (finger millet). *International journal of biological macromolecules*, 206, 768.

Rohilla M, et al. (2022) Genome-wide identification and development of miniature inverted-repeat transposable elements and intron length polymorphic markers in tea plant (*Camellia sinensis*). *Scientific reports*, 12(1), 16233.

Sohrabi SS, et al. (2022) Identification of key genes and molecular mechanisms associated with temperature stress in lentil. *Gene*, 807, 145952.

Sathasivam M, et al. (2022) Insights into the molecular basis of hypergravity-induced root growth phenotype in bread wheat (*Triticum aestivum* L.). *Genomics*, 114(2), 110307.

Larriba E, et al. (2022) Identification of Transcriptional Networks Involved in De Novo Organ Formation in Tomato Hypocotyl Explants. *International journal of molecular sciences*, 23(24).

Rahimi Y, et al. (2021) Characterization of Dynamic Regulatory Gene and Protein Networks in Wheat Roots Upon Perceiving Water Deficit Through Comparative Transcriptomics Survey. *Frontiers in plant science*, 12, 710867.

Alam P, et al. (2021) Functional annotations of ESTs of *Stevia rebaudiana* involved in abiotic stress signaling through computational approach. *Saudi journal of biological sciences*, 28(4), 2602.

Ghosh Dasgupta M, et al. (2021) Draft genome of *Korthalsia laciniosa* (Griff.) Mart., a climbing rattan elucidates its phylogenetic position. *Genomics*, 113(4), 2010.

Kashyap SP, et al. (2020) Understanding salt tolerance mechanism using transcriptome profiling and de novo assembly of wild tomato *Solanum chilense*. *Scientific reports*, 10(1), 15835.

Lamelas L, et al. (2020) Integrative analysis of the nuclear proteome in *Pinus radiata* reveals thermoprimering coupled to epigenetic regulation. *Journal of experimental botany*, 71(6), 2040.