Resource Summary Report

Generated by dkNET on May 20, 2025

PlantTFcat

RRID:SCR_010898
Type: Tool

Proper Citation

PlantTFcat (RRID:SCR_010898)

Resource Information

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

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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.

Abbreviations: PlantTFcat

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

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

Defining Citation: PMID:24219505

Keywords: bio.tools

Funding:

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: 20250519T204808+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 43 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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 wucai (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.

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.

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.

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

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 thermopriming coupled to epigenetic regulation. Journal of experimental botany, 71(6), 2040.

Tripathi S, et al. (2020) In silico mining and functional analysis of AP2/ERF gene in Withania somnifera. Scientific reports, 10(1), 4877.

Saxena S, et al. (2020) Transcriptome profiling of differentially expressed genes in cytoplasmic male-sterile line and its fertility restorer line in pigeon pea (Cajanus cajan L.). BMC plant biology, 20(1), 74.

Ayachit G, et al. (2019) De novo transcriptome of Gymnema sylvestre identified putative lncRNA and genes regulating terpenoid biosynthesis pathway. Scientific reports, 9(1), 14876.