Resource Summary Report

Generated by dkNET on Apr 29, 2025

Database of Poplar Transcription Factors

RRID:SCR_007080
Type: Tool

Proper Citation

Database of Poplar Transcription Factors (RRID:SCR_007080)

Resource Information

URL: http://dptf.cbi.pku.edu.cn/

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Description: Database of collected known and predicted transcription factors (TF) of the black cottonwood tree, Populus trichocarpa. They have made extensive annotations, including similarity searches against major databases (Uniprot, RefSeq, EMBL, TRANSFAC et al) and EST expression information extraction from UniGene clusters and microarray expression, to provide comprehensive information for the putative TFs. In addition, multiple alignment of the DNA-binding domain of each family, Neighbor-Joining phylogenetic tree of each family, the GO annotation, homolog with the Database of Arabidopsis Transcription Factors (DATF), the Database of Rice Transcription Factors (DRTF) are included.

Abbreviations: DPTF

Resource Type: data or information resource, database

Defining Citation: PMID:17392330

Keywords: transcription factor

Funding:

Availability: Free, Acknowledgement requested

Resource Name: Database of Poplar Transcription Factors

Resource ID: SCR_007080

Alternate IDs: OMICS_00553

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250429T055129+0000

Ratings and Alerts

No rating or validation information has been found for Database of Poplar Transcription Factors.

No alerts have been found for Database of Poplar Transcription Factors.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Kababji AM, et al. (2024) Synthetic directed evolution for targeted engineering of plant traits. Frontiers in plant science, 15, 1449579.

Chai G, et al. (2012) Comprehensive analysis of CCCH zinc finger family in poplar (Populus trichocarpa). BMC genomics, 13, 253.

Filichkin SA, et al. (2011) Global profiling of rice and poplar transcriptomes highlights key conserved circadian-controlled pathways and cis-regulatory modules. PloS one, 6(6), e16907.

Dharmawardhana P, et al. (2010) Genome-wide transcriptome analysis of the transition from primary to secondary stem development in Populus trichocarpa. BMC genomics, 11, 150.

Mochida K, et al. (2010) Genomics and bioinformatics resources for crop improvement. Plant & cell physiology, 51(4), 497.

Hu R, et al. (2010) Comprehensive analysis of NAC domain transcription factor gene family in Populus trichocarpa. BMC plant biology, 10, 145.

Ramirez SR, et al. (2009) Comparative analyses of plant transcription factor databases. Current genomics, 10(1), 10.