

# Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

## Database of Poplar Transcription Factors

RRID:SCR\_007080

Type: Tool

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### Proper Citation

Database of Poplar Transcription Factors (RRID:SCR\_007080)

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### Resource Information

**URL:** <http://dptf.cbi.pku.edu.cn/>

**Proper Citation:** Database of Poplar Transcription Factors (RRID:SCR\_007080)

**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

**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:** 20260821T193818+0000

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### 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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.

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

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

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