

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

DBD: Transcription factor prediction database

RRID:SCR_002300

Type: Tool

Proper Citation

DBD: Transcription factor prediction database (RRID:SCR_002300)

Resource Information

URL: <http://www.transcriptionfactor.org/index.cgi?Home>

Proper Citation: DBD: Transcription factor prediction database (RRID:SCR_002300)

Description: Database of predicted transcription factors in completely sequenced genomes. The predicted transcription factors all contain assignments to sequence specific DNA-binding domain families. The predictions are based on domain assignments from the SUPERFAMILY and Pfam hidden Markov model libraries. Benchmarks of the transcription factor predictions show they are accurate and have wide coverage on a genomic scale. The DBD consists of predicted transcription factor repertoires for 930 completely sequenced genomes.

Abbreviations: DBD

Synonyms: DNA-binding domain

Resource Type: data or information resource, database, service resource

Defining Citation: [PMID:18073188](#), [PMID:16381970](#)

Keywords: predicted transcription factor, transcription factor, dna-binding domain, proteome, sequence, domain family, protein sequence, genome, prediction

Availability: Acknowledgement requested

Resource Name: DBD: Transcription factor prediction database

Resource ID: SCR_002300

Alternate IDs: nif-0000-02726, OMICS_00531

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260731T042630+0000

Ratings and Alerts

No rating or validation information has been found for DBD: Transcription factor prediction database.

No alerts have been found for DBD: Transcription factor prediction database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Qin J, et al. (2018) Transcription factor networks involved in cell death in the dorsal root ganglia following peripheral nerve injury. *Neural regeneration research*, 13(9), 1622.

Muñoz M, et al. (2018) Identification of Candidate Genes and Regulatory Factors Underlying Intramuscular Fat Content Through Longissimus Dorsi Transcriptome Analyses in Heavy Iberian Pigs. *Frontiers in genetics*, 9, 608.

Muhie S, et al. (2013) Transcriptome characterization of immune suppression from battlefield-like stress. *Genes and immunity*, 14(1), 19.

Li JS, et al. (2011) Transcriptome analysis of adaptive heat shock response of *Streptococcus thermophilus*. *PloS one*, 6(10), e25777.

Zhang S, et al. (2010) Simultaneous prediction of transcription factor binding sites in a group of prokaryotic genomes. *BMC bioinformatics*, 11, 397.

Schröder A, et al. (2010) Predicting DNA-binding specificities of eukaryotic transcription factors. *PloS one*, 5(11), e13876.

Janssen PJ, et al. (2010) The complete genome sequence of *Cupriavidus metallidurans* strain CH34, a master survivalist in harsh and anthropogenic environments. *PloS one*, 5(5), e10433.

Zaparty M, et al. (2010) "Hot standards" for the thermoacidophilic archaeon *Sulfolobus solfataricus*. *Extremophiles : life under extreme conditions*, 14(1), 119.

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

Teichmann SA, et al. (2005) Transcriptional networking. *Genome biology*, 6(9), 344.