Resource Summary Report

Generated by T1D on Aug 5, 2026

Transcription Regulatory Regions Database

RRID:SCR_005723
Type: Tool

Proper Citation

Transcription Regulatory Regions Database (RRID:SCR_005723)

Resource Information

URL: http://www.bionet.nsc.ru/trrd/

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Description: TRRD is a unique information resource, accumulating information on structural and functional organization of transcription regulatory regions of eukaryotic genes. Only experimentally confirmed information is included into TRRD. Transcription Regulatory Regions Database (TRRD) is developed for accumulation of experimental information on the structure-function features of regulatory regions of eukaryotic genes. Each entry of TRRD corresponds to a particular gene. The annotated part of an entry includes the structure-function description of gene regulatory regions composed by regulatory units (promoters, silencers, enhancers, etc.), individual transcription factor binding sites that constitute these regulatory units, and transcription factors that bind to these sites. In addition, the entry contains the gene expression patterns and references to original publications.

Synonyms: TRRD

Resource Type: database, data or information resource

Defining Citation: PMID:11752324

Resource Name: Transcription Regulatory Regions Database

Resource ID: SCR_005723

Alternate IDs: nif-0000-03594

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260805T044126+0000

Ratings and Alerts

No rating or validation information has been found for Transcription Regulatory Regions Database.

No alerts have been found for Transcription Regulatory Regions Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Zhang B, et al. (2020) Study on the Antibreast Cancer Mechanism and Bioactive Components of Si-Wu-Tang by Cell Type-Specific Molecular Network. Evidence-based complementary and alternative medicine : eCAM, 2020, 2345970.

H??rhold F, et al. (2020) Reprogramming of macrophages employing gene regulatory and metabolic network models. PLoS computational biology, 16(2), e1007657.

Poos AM, et al. (2019) Modelling TERT regulation across 19 different cancer types based on the MIPRIP 2.0 gene regulatory network approach. BMC bioinformatics, 20(1), 737.

Xu WW, et al. (2017) Cancer cell-secreted IGF2 instigates fibroblasts and bone marrow-derived vascular progenitor cells to promote cancer progression. Nature communications, 8, 14399.

Vafaee F, et al. (2016) ORTI: An Open-Access Repository of Transcriptional Interactions for Interrogating Mammalian Gene Expression Data. PloS one, 11(10), e0164535.

He YH, et al. (2016) Improved lipids, diastolic pressure and kidney function are potential contributors to familial longevity: a study on 60 Chinese centenarian families. Scientific reports, 6, 21962.

Xie Y, et al. (2013) Bcrp1 transcription in mouse testis is controlled by a promoter upstream of a novel first exon (E1U) regulated by steroidogenic factor-1. Biochimica et biophysica acta, 1829(12), 1288.

Coulibaly I, et al. (2008) Bioinformatic tools for inferring functional information from plant microarray data II: Analysis beyond single gene. International journal of plant genomics, 2008, 893941.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.