

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

Transcriptional Regulatory Element Database

RRID:SCR_005661

Type: Tool

Proper Citation

Transcriptional Regulatory Element Database (RRID:SCR_005661)

Resource Information

URL: <http://rulai.cshl.edu/tred>

Proper Citation: Transcriptional Regulatory Element Database (RRID:SCR_005661)

Description: Collects mammalian cis- and trans-regulatory elements together with experimental evidence. Regulatory elements were mapped on to assembled genomes. Resource for gene regulation and function studies. Users can retrieve primers, search TF target genes, retrieve TF motifs, search Gene Regulatory Networks and orthologs, and make use of sequence analysis tools. Uses databases such as Genbank, EPD and DBTSS, and employ promoter finding program FirstEF combined with mRNA/EST information and cross-species comparisons. Manually curated.

Abbreviations: TRED

Synonyms: Transcriptional Regulatory Element Database

Resource Type: database, data or information resource

Defining Citation: [PMID:17202159](#)

Keywords: Mammalian, cis, trans, regulatory, element, mapped, genome, gene, regulation, function, data, FASEB list

Funding: NCI ;
NHGRI HG001696

Availability: Free, Freely available

Resource Name: Transcriptional Regulatory Element Database

Resource ID: SCR_005661

Alternate IDs: nif-0000-03585

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260805T044124+0000

Ratings and Alerts

No rating or validation information has been found for Transcriptional Regulatory Element Database.

No alerts have been found for Transcriptional Regulatory Element Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Lu YY, et al. (2025) High APEX1 Expression Facilitates Osteosarcoma Cell Proliferation. Asian Pacific journal of cancer prevention : APJCP, 26(2), 453.

Ginno PA, et al. (2024) Single-mitosis dissection of acute and chronic DNA mutagenesis and repair. Nature genetics, 56(5), 913.

Xu G, et al. (2024) GEO dataset mining analysis reveals novel Staphylococcus aureus virulence gene regulatory networks and diagnostic targets in mice. Frontiers in molecular biosciences, 11, 1381334.

Calandria JM, et al. (2023) cRel and Wnt5a/Frizzled 5 Receptor-Mediated Inflammatory Regulation Reveal Novel Neuroprotectin D1 Targets for Neuroprotection. Cellular and molecular neurobiology, 43(3), 1077.

Li ML, et al. (2022) LY395756 promotes NR2B expression via activation of AKT/CREB signaling in the juvenile methylazoxymethanol mice model of schizophrenia. Brain and behavior, 12(2), e2466.

Colitti M, et al. (2022) Transcriptomic analysis of Simpson Golabi Behmel syndrome cells during differentiation exhibit BAT-like function. Tissue & cell, 77, 101822.

Ataei A, et al. (2021) Topological Analysis of Regulatory Networks Reveals Functionally Key Genes and miRNAs Involved in the Differentiation of Mesenchymal Stem Cells. Iranian journal of biotechnology, 19(1), e2565.

Miele E, et al. (2021) Downregulation of miR-326 and its host gene ?-arrestin1 induces pro-survival activity of E2F1 and promotes medulloblastoma growth. Molecular oncology, 15(2), 523.

Cai C, et al. (2021) Identification of novel transcription factor-microRNA-mRNA co-regulatory networks in pulmonary large-cell neuroendocrine carcinoma. *Annals of translational medicine*, 9(2), 133.

Gao L, et al. (2021) Identification of Novel Kinase-Transcription Factor-mRNA-miRNA Regulatory Network in Nasopharyngeal Carcinoma by Bioinformatics Analysis. *International journal of general medicine*, 14, 7453.

Bo C, et al. (2021) Construction of a TF-miRNA-gene feed-forward loop network predicts biomarkers and potential drugs for myasthenia gravis. *Scientific reports*, 11(1), 2416.

Liu ZG, et al. (2020) MicroRNA regulatory pattern in spinal cord ischemia-reperfusion injury. *Neural regeneration research*, 15(11), 2123.

Shi M, et al. (2020) Globally learning gene regulatory networks based on hidden atomic regulators from transcriptomic big data. *BMC genomics*, 21(1), 711.

Lv J, et al. (2019) Biomarker identification and trans-regulatory network analyses in esophageal adenocarcinoma and Barrett's esophagus. *World journal of gastroenterology*, 25(2), 233.

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.

Park HJ, et al. (2019) Transcriptomic analysis of human IL-7 receptor alpha low and high effector memory CD8⁺ T cells reveals an age-associated signature linked to influenza vaccine response in older adults. *Aging cell*, 18(4), e12960.

Chen D, et al. (2019) Identification of a transcription factor-microRNA network in esophageal adenocarcinoma through bioinformatics analysis and validation through qRT-PCR. *Cancer management and research*, 11, 3315.

Hao S, et al. (2019) MicroRNA-related transcription factor regulatory networks in human colorectal cancer. *Medicine*, 98(15), e15158.

Gao L, et al. (2019) The expression, significance and function of cancer susceptibility candidate 9 in lung squamous cell carcinoma: A bioinformatics and in vitro investigation. *International journal of oncology*, 54(5), 1651.

Breunig C, et al. (2018) TGF β 1 regulates HGF-induced cell migration and hepatocyte growth factor receptor MET expression via C-ets-1 and miR-128-3p in basal-like breast cancer. *Molecular oncology*, 12(9), 1447.