

Resource Summary Report

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Transcriptional Regulatory Relationships Unrevealed by Sentence based Text mining database

RRID:SCR_022554

Type: Tool

Proper Citation

Transcriptional Regulatory Relationships Unrevealed by Sentence based Text mining database (RRID:SCR_022554)

Resource Information

URL: <https://www.grnpedia.org/trrust/>

Proper Citation: Transcriptional Regulatory Relationships Unrevealed by Sentence based Text mining database (RRID:SCR_022554)

Description: TRUSST is reference database of human transcriptional regulatory interactions. TRRUST v2 is manually curated expanded reference database of human and mouse transcriptional regulatory interactions.

Abbreviations: TRRUST

Synonyms: TRRUST database, TRRUSTv2

Resource Type: database, data or information resource

Defining Citation: [PMID:26066708](#), [DOI:10.1093/nar/gkx1013](#)

Keywords: human and mouse transcriptional regulatory interactions, regulatory networks, transcriptional regulatory networks, human, mouse

Funding: National Research Foundation of Korea ;
Brain Korea 21 PLUS program

Availability: Restricted

Resource Name: Transcriptional Regulatory Relationships Unrevealed by Sentence based Text mining database

Resource ID: SCR_022554

Alternate URLs: <https://www.grnpedia.org/trrust/v1/>

Record Creation Time: 20220713T050151+0000

Record Last Update: 20260805T044503+0000

Ratings and Alerts

No rating or validation information has been found for Transcriptional Regulatory Relationships Unrevealed by Sentence based Text mining database.

No alerts have been found for Transcriptional Regulatory Relationships Unrevealed by Sentence based Text mining database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 140 mentions in open access literature.

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

He X, et al. (2025) FOSL2 activates TGF- β 1-mediated GLUT1/mTOR signaling to promote diabetic kidney disease. Journal of diabetes investigation, 16(2), 187.

Hashemi Karoii D, et al. (2025) Analysis of microarray and single-cell RNA-seq identifies gene co-expression, cell-cell communication, and tumor environment associated with metabolite interconversion enzyme in prostate cancer. Discover oncology, 16(1), 177.

Shi D, et al. (2025) Identification and validation of diagnostic biomarkers for temporal lobe epilepsy related to ferroptosis and potential therapeutic targets. Scientific reports, 15(1), 4908.

Cai D, et al. (2025) Integrated Analysis of Ferroptosis and Immune Infiltration in Ulcerative Colitis Based on Bioinformatics. Journal of inflammation research, 18, 3535.

Yang Y, et al. (2025) Evaluation of FXR Activity in Pollutants Identified in Sewage Sludge and Subsequent in Vitro and in Vivo Characterization of Metabolic Effects of Triphenyl Phosphate. Environmental health perspectives, 133(3-4), 47005.

Lin J, et al. (2025) Prunella vulgaris: A potential molecule for the treatment of hepatocellular carcinoma. Medicine, 104(17), e42267.

Yuan Y, et al. (2025) Integrative bioinformatics analysis and experimental validation reveals key genes and regulatory mechanisms in the development of gout. Frontiers in genetics, 16, 1598835.

Aras S, et al. (2025) Transcriptome Analysis of the Effects of X-Ray Radiotherapy on Non-small-cell Lung Cancer Using Next-generation Sequencing. *In vivo* (Athens, Greece), 39(5), 2711.

Xue C, et al. (2025) Unraveling the mechanism of curcumin in coronary slow flow phenomenon through network pharmacology and molecular docking. *Scientific reports*, 15(1), 44551.

Huang Y, et al. (2025) Proteomic analysis of Burkitt lymphoma tissues: insights into the impact of age and EBV infection on protein expression and molecular characteristics. *Discover oncology*, 16(1), 2132.

Wan J, et al. (2025) Exploration of the shared gene signatures and comorbidity mechanisms of primary aldosteronism and atrial fibrillation. *Endocrine connections*, 14(1).

Zhang J, et al. (2025) Integrated bioinformatics analysis of the effects of chronic pain on patients with spinal cord injury. *Frontiers in cellular neuroscience*, 19, 1457740.

Zhao M, et al. (2025) Integrated multiomics signatures to optimize the accurate diagnosis of lung cancer. *Nature communications*, 16(1), 84.

Yan S, et al. (2025) Metabolic landscape uncovers remodeling of T cell immunity affected by fatty acid desaturase in Parkinson's disease at single-cell resolution. *BMC biology*, 23(1), 245.

Sun T, et al. (2025) Glucocorticoid receptor inhibits Th2 immune responses by down-regulating Pparg and Gata3 in schistosomiasis. *Frontiers in immunology*, 16, 1518586.

Yuan Z, et al. (2025) Investigating the mechanisms by which low NAT1 expression in tumor cells contributes to chemo-resistance in colorectal cancer. *Clinical epigenetics*, 17(1), 77.

Alwadi D, et al. (2025) RNA-Seq Uncovers Association of Endocrine-Disrupting Chemicals with Hub Genes and Transcription Factors in Aggressive Prostate Cancer. *International journal of molecular sciences*, 26(12).

Feng L, et al. (2025) Transcriptomic insights into the mechanism of action of telomere-related biomarkers in rheumatoid arthritis. *Frontiers in immunology*, 16, 1585895.

Zeng L, et al. (2025) Machine learning identifies exosome related gene signatures for early prediction of non-small cell lung cancer. *Scientific reports*, 15(1), 37274.

Kalaki NS, et al. (2025) PDCD1 as a targetable immune checkpoint hub: therapeutic insights for ibrutinib-resistant CLL management. *Clinical and experimental medicine*, 26(1), 19.