

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: data or information resource, database

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

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

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

Availability: Restricted

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

Resource ID: SCR_022554

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

Record Creation Time: 20220713T050151+0000

Record Last Update: 20260905T133218+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 269 mentions in open access literature.

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

Chianese U, et al. (2026) Glycolytic heterogeneity drives metabolic-targeted therapy in pancreatic ductal adenocarcinoma. Signal transduction and targeted therapy, 11(1), 25.

Chen Q, et al. (2026) Mechanisms of cellular senescence combined with molecular docking strategies: A biomarker study of potential therapeutic targets for allergic rhinitis. PloS one, 21(1), e0338309.

Bai Y, et al. (2026) CCL chemokines as prognostic and immunotherapeutic markers in prostate cancer: a comprehensive analysis. World journal of surgical oncology, 24(1).

Xu L, et al. (2026) Single-nucleus atlas provides insights into changes in the evolution of the pig hippocampus. BMC biology, 24(1).

Xiang Z, et al. (2026) Integrative multi-omics analysis reveals inflammation-related molecular networks in acute mountain sickness. Frontiers in immunology, 17, 1745433.

Qing G, et al. (2026) Identification of shared oxidative stress related hub genes in NAFLD and atherosclerosis using bioinformatics and machine learning. Scientific reports, 16(1), 4644.

Gu Y, et al. (2026) Targeted gene sequencing and bioinformatics analysis of a patient with gallbladder adenosquamous carcinoma: a case report. Frontiers in oncology, 16, 1697015.

Huang J, et al. (2026) An exosome-related gene signature predicts prognosis, immune suppression, and therapeutic sensitivity in luminal breast cancer. Discover oncology,

17(1).

Khonsari YN, et al. (2026) Brucella abortus outer membrane protein modulates host immunity via B-cell receptor-associated protein. *AMB Express*, 16(1).

Xu H, et al. (2026) Preliminary Exploration of Fluvastatin Inhibiting Proliferation, Migration and Invasion of Lung Cancer Cells and Reversing Paclitaxel Resistance: Mechanism Exploration Based on Multi-Omics Analysis. *Drug design, development and therapy*, 20, 579427.

Roger E, et al. (2026) ATM Deficiency Induces TGF β -Mediated Stromal Programming in Pancreatic Cancer. *Cancer research*, 86(14), 3412.

Zhang Z, et al. (2026) miR-96-5p antagonizes FOXQ1-driven WNT/ β -catenin signaling to inhibit triple-negative breast cancer. *Scientific reports*, 16(1), 4624.

Gao L, et al. (2026) Integrated bioinformatic identification and translational validation of key biomarkers and therapeutic candidates for preeclampsia-related acute kidney injury. *Archives of gynecology and obstetrics*, 313(1), 22.

Wu S, et al. (2026) Multi-omics analysis and experiments validate the tumor-suppressive role of mitochondrial lipid metabolism gene ACSM5 in lung adenocarcinoma and its impact on the immune microenvironment. *Human genomics*, 20(1).

Yu Z, et al. (2026) Multi-target modulation of the homologous recombination pathway by resveratrol promotes DNA damage repair in POI: integrated network pharmacology, molecular dynamics simulation, and experimental validation. *International journal of surgery (London, England)*, 112(4), 9404.

Ou Z, et al. (2026) Spatial transcriptomics uncovers vasculature-centered cellular interactions driving Japanese encephalitis progression in a mouse model. *Nature communications*, 17(1).

Shuqian Z, et al. (2026) LncRNA-LINC01281 exerts anti-cancer functions via the MYC/VEGF pathway in the progression of cervical cancer. *Journal of cancer research and clinical oncology*, 152(4).

Zhao L, et al. (2026) Identification and validation of platelet activation-related signatures in ulcerative colitis: a study based on machine learning and single-cell transcriptomic analysis. *Frontiers in immunology*, 17, 1855177.

Wang W, et al. (2026) Integrative transcriptomic and machine learning framework reveals candidate genes and potential mechanisms of aflatoxin B1 exposure in breast cancer. *Scientific reports*, 16(1).

Liao P, et al. (2026) Revealing the therapeutic potential of Laminaria japonica polysaccharides against cataract: evidence from transcriptomics, network pharmacology, and in vivo experiments. *International ophthalmology*, 46(1).