Resource Summary Report

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DBTSS: Database of Transcriptional Start Sites

RRID:SCR_002354
Type: Tool

Proper Citation

DBTSS: Database of Transcriptional Start Sites (RRID:SCR_002354)

Resource Information

URL: http://dbtss.hgc.jp/

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Description: Database of transcriptional start sites (TSSs) representing exact positions in the genome based on a unique experimentally validated TSS sequencing method, TSS Seq. A major part of human adult and embryonic tissues are covered. DBTSS contains 491 million TSS tag sequences collected from a total of 20 tissues and 7 cell cultures. Also integrated is generated RNA-seq data of subcellular- fractionated RNAs and ChIP Seq data of histone modifications, RNA polymerase II and several transcriptional regulatory factors in cultured cell lines. Also included is external epigenomic data, such as chromatin map of the ENCODE project. They associated those TSS information with public and original SNV data, in order to identify single nucleotide variations (SNVs) in the regulatory regions.

Abbreviations: DBTSS

Synonyms: DBTSS: Database of Transcriptional Start Sites, DataBase of Transcriptional Start Sites

Resource Type: database, data or information resource

Defining Citation: PMID:22086958, PMID:19910371, PMID:17942421, PMID:16381981, PMID:14681363, PMID:11752328

Keywords: cdna, cdna library, transcriptional start site, transcriptome, transcriptome analysis, tss-seq, genome, adult human, embryonic, cell, rna-seq, subcellular, rna, chip seq data, histone modification, rna polymerase ii, transcriptional regulatory factor, cell line, single nucleotide variation, regulatory region, genetic valuation, transcriptional regulation, bio.tools, FASEB list

Funding: Japan Society for the Promotion of Science ;
Japanese Ministry of Education Culture Sports Science and Technology MEXT

Resource Name: DBTSS: Database of Transcriptional Start Sites

Resource ID: SCR_002354

Alternate IDs: nif-0000-02738, biotools:dbtss, OMICS_01860

Alternate URLs: https://bio.tools/dbtss

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250423T060031+0000

Ratings and Alerts

No rating or validation information has been found for DBTSS: Database of Transcriptional Start Sites.

No alerts have been found for DBTSS: Database of Transcriptional Start Sites.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 124 mentions in open access literature.

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

Kara? K, et al. (2024) Epigenetic regulation of the human GDAP1 gene. Biochemistry and biophysics reports, 40, 101827.

Hsiao YT, et al. (2024) PCPE-1, a brown adipose tissue-derived cytokine, promotes obesity-induced liver fibrosis. The EMBO journal, 43(21), 4846.

Nakajima T, et al. (2024) Fatty acid metabolism constrains Th9 cell differentiation and antitumor immunity via the modulation of retinoic acid receptor signaling. Cellular &

molecular immunology, 21(11), 1266.

Kaushik P, et al. (2024) miR-198 targets TOPORS: implications for oral squamous cell carcinoma pathogenesis. Frontiers in oncology, 14, 1485802.

Sarkar N, et al. (2024) miR-617 interacts with the promoter of DDX27 and positively regulates its expression: implications for cancer therapeutics. Frontiers in oncology, 14, 1411539.

Enokido T, et al. (2024) Distinct microRNA Signature and Suppression of ZFP36L1 Define ASCL1-Positive Lung Adenocarcinoma. Molecular cancer research : MCR, 22(1), 29.

Deng H, et al. (2023) ACT001 inhibited CD133 transcription by targeting and inducing Olig2 ubiquitination degradation. Oncogenesis, 12(1), 19.

Sato N, et al. (2022) Yin Yang 1 regulates ITGAV and ITGB1, contributing to improved prognosis of colorectal cancer. Oncology reports, 47(5).

Juan C, et al. (2022) Knocking down ETS Proto-oncogene 1 (ETS1) alleviates the pyroptosis of renal tubular epithelial cells in patients with acute kidney injury by regulating the NLR family pyrin domain containing 3 (NLRP3) transcription. Bioengineered, 13(5), 12927.

Rajkumar T, et al. (2022) Identification and validation of plasma biomarkers for diagnosis of breast cancer in South Asian women. Scientific reports, 12(1), 100.

Baralle M, et al. (2021) Characterization of the human TARDBP gene promoter. Scientific reports, 11(1), 10438.

Hosokawa K, et al. (2021) Pax5 mediates the transcriptional activation of the CD81 gene. Scientific reports, 11(1), 22919.

Mohamed Sa'dom SAF, et al. (2021) DNA Methylation of Human Choline Kinase Alpha Promoter-Associated CpG Islands in MCF-7 Cells. Genes, 12(6).

Nakajima T, et al. (2021) ACC1-expressing pathogenic T helper 2 cell populations facilitate lung and skin inflammation in mice. The Journal of experimental medicine, 218(12).

Johnson C, et al. (2021) The Sulfotransferase SULT1C2 Is Epigenetically Activated and Transcriptionally Induced by Tobacco Exposure and Is Associated with Patient Outcome in Lung Adenocarcinoma. International journal of environmental research and public health, 19(1).

Fuentes P, et al. (2021) The 40S-LARP1 complex reprograms the cellular translatome upon mTOR inhibition to preserve the protein synthetic capacity. Science advances, 7(48), eabg9275.

Hasegawa-Ogawa M, et al. (2021) Characterization of the upstream and intron promoters of the gene encoding TAR DNA-binding protein. Scientific reports, 11(1), 8720.

Saito K, et al. (2021) PLOD2-driven IL-6/STAT3 signaling promotes the invasion and metastasis of oral squamous cell carcinoma via activation of integrin ?1. International journal of oncology, 58(6).

Aoto S, et al. (2020) Diversification of CpG-Island Promoters Revealed by Comparative Analysis Between Human and Rhesus Monkey Genomes. Mammalian genome : official journal of the International Mammalian Genome Society, 31(7-8), 240.

Rauluseviciute I, et al. (2020) DNA hypermethylation associated with upregulated gene expression in prostate cancer demonstrates the diversity of epigenetic regulation. BMC medical genomics, 13(1), 6.