

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

Database of Transcribed Sequences

RRID:SCR_002334

Type: Tool

Proper Citation

Database of Transcribed Sequences (RRID:SCR_002334)

Resource Information

URL: <http://www.allgenes.org/>

Proper Citation: Database of Transcribed Sequences (RRID:SCR_002334)

Description: DoTS (Database Of Transcribed Sequences) is a human and mouse transcript index created from all publicly available transcript sequences. The input sequences are clustered and assembled to form the DoTS Consensus Transcripts that comprise the index. These transcripts are assigned stable identifiers of the form DT.123456 (and are often referred to as dots). The transcripts are in turn clustered to form putative DoTS Genes. These are assigned stable identifiers of the form DG.1234356. As of September 1, 2004, the DoTS annotation team has manually annotated 43,164 human and 78,054 mouse DoTS Transcripts (DTs), corresponding to 3,939 human and 7,752 mouse DoTS Genes (DGs). Use the manually annotated gene query to see the DoTS Transcripts that have been manually annotated. The focus of the DoTS project is integrating the various types of data (e.g., EST sequences, genomic sequence, expression data, functional annotation) in a structured manner which facilitates sophisticated queries that are otherwise not easy to perform. DoTS is built on the GUS Platform which includes a relational database that uses controlled vocabularies and ontologies to ensure that biologically meaningful queries can be posed in a uniform fashion. An easy way to start using the site is to search for DoTS Transcripts using an existing cDNA or mRNA sequence. Click on the BLAST tab at the top of the page and enter your sequence in the form provided. All the transcripts with significant sequence similarity to your query sequence will be displayed. Or use one of the provided queries to retrieve transcripts using a number of criteria. These queries are listed on the query page, which can also be reached by clicking on the tab marked query at the top of the page. Finally, the boolean query page allows these queries to be combined in a variety of ways. Sponsors: Funding provided by -NIH grant RO1-HG-01539-03 -DOE grant DE-FG02-00ER62893

Synonyms: DoTs

Resource Type: data or information resource, database

Keywords: expression, functional, gene, annotation, biological, cdna, genomic, human, index, model organisms and comparative genomics databases, mouse, mrna, sequence, structure, transcribed, transcript

Resource Name: Database of Transcribed Sequences

Resource ID: SCR_002334

Alternate IDs: nif-0000-21125

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260804T043139+0000

Ratings and Alerts

No rating or validation information has been found for Database of Transcribed Sequences.

No alerts have been found for Database of Transcribed Sequences.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Noonan HR, et al. (2024) A chronic signaling TGFb zebrafish reporter identifies immune response in melanoma. eLife, 13.

Aghaeinezhadfirouzja S, et al. (2018) Practical 3-D Beam Pattern Based Channel Modeling for Multi-Polarized Massive MIMO Systems. Sensors (Basel, Switzerland), 18(4).

Qian G, et al. (2014) Sequencing and comparative genomics analysis in Senecio scandens Buch.-Ham. Ex D. Don, based on full-length cDNA library. Biotechnology, biotechnological equipment, 28(5), 805.

Mazzarelli JM, et al. (2007) EPConDB: a web resource for gene expression related to pancreatic development, beta-cell function and diabetes. Nucleic acids research, 35(Database issue), D751.

Bichutskiy VY, et al. (2007) Heterogeneous biomedical database integration using a hybrid strategy: a p53 cancer research database. Cancer informatics, 2, 277.

Perera HK, et al. (2006) Expression and shifting subcellular localization of the transcription factor, Foxd3, in embryonic and adult pancreas. Gene expression patterns : GEP, 6(8),

Kong YM, et al. (2006) A comprehensive survey of DNA-binding transcription factor gene expression in human fetal and adult organs. *Gene expression patterns : GEP*, 6(7), 678.

Schug J, et al. (2005) Promoter features related to tissue specificity as measured by Shannon entropy. *Genome biology*, 6(4), R33.

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

Shklar M, et al. (2005) GeneTide--Terra Incognita Discovery Endeavor: a new transcriptome focused member of the GeneCards/GeneNote suite of databases. *Nucleic acids research*, 33(Database issue), D556.

Kasukawa T, et al. (2004) Construction of representative transcript and protein sets of human, mouse, and rat as a platform for their transcriptome and proteome analysis. *Genomics*, 84(6), 913.

Wjst M, et al. (2004) Target SNP selection in complex disease association studies. *BMC bioinformatics*, 5, 92.

Mir AA, et al. (2003) A search for candidate genes for lipodystrophy, obesity and diabetes via gene expression analysis of A-ZIP/F-1 mice. *Genomics*, 81(4), 378.

Zhu Y, et al. (2003) Integrating computationally assembled mouse transcript sequences with the Mouse Genome Informatics (MGI) database. *Genome biology*, 4(2), R16.

Denny P, et al. (2001) What use is the human genome for understanding the mouse? *Genome biology*, 2(11), COMMENT2009.