

Resource Summary Report

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The Alternative Splicing Database

RRID:SCR_001883

Type: Tool

Proper Citation

The Alternative Splicing Database (RRID:SCR_001883)

Resource Information

URL: <http://www.ebi.ac.uk/astd/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23, 2022. The Alternative Splicing and Transcript Diversity (ASTD) database project is creating a database of alternative splice events and transcripts of genes from human, mouse and rat. Full length transcripts are generated with the aim of understanding the mechanism of alternative splicing on a genome-wide scale. The current release of the human genome consists of: 16715 genes, 14101 have more than one splice isoform, with an average of 5.6 splice patterns per gene. 10831 transcripts are annotated as full length with a transcription start site and a poly(A). The current release of the mouse genome consists of: 16491 genes, 13028 have more than one splice isoform, with an average of 4 splice patterns per gene. 6011 transcripts are annotated as full length with a transcription start site and a poly(A). The current release of the rat genome consists of: 10424 genes, 6344 have more than one splice isoform, with an average of 2.6 splice patterns per gene. 1250 transcripts are annotated as full length with a transcription start site and a poly(A). Sponsors: The ASTD project at EBI is supported by a grant from the EC: Eurasnet Network of Excellence (LSHG-CT-2005-518238). It was also supported by the ASD grant from the EC (QLRT-CT-2001-02062) until November 2005 and the ATD grant from the EC (LSHG-CT-2003-503329) until May 2007.

Synonyms: ASTD

Resource Type: data or information resource, database

Defining Citation: [PMID:19059335](#)

Keywords: exon, exon splice site, gene, gene structure, alternative splicing, human genome, intron, intron splice site, mouse genome, nucleotide sequence database, rat genome, splice isoform, transcript, transcription, transcription diversity, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: The Alternative Splicing Database

Resource ID: SCR_001883

Alternate IDs: nif-0000-02579, biotools:astd

Alternate URLs: <https://bio.tools/astd>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260801T190906+0000

Ratings and Alerts

No rating or validation information has been found for The Alternative Splicing Database.

No alerts have been found for The Alternative Splicing Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Fu XG, et al. (2020) Splicing of exon 9a in FMR1 transcripts results in a truncated FMRP with altered subcellular distribution. Gene, 731, 144359.

Pappas JJ, et al. (2014) The multidrug resistance 1 gene Abcb1 in brain and placenta: comparative analysis in human and guinea pig. PloS one, 9(10), e111135.

Lovett DH, et al. (2012) A novel intracellular isoform of matrix metalloproteinase-2 induced by oxidative stress activates innate immunity. PloS one, 7(4), e34177.

Laderas TG, et al. (2011) Computational detection of alternative exon usage. Frontiers in neuroscience, 5, 69.

Chen L, et al. (2010) A global comparison between nuclear and cytosolic transcriptomes reveals differential compartmentalization of alternative transcript isoforms. Nucleic acids research, 38(4), 1086.