Resource Summary Report

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Human Transcriptome Database for Alternative Splicing

RRID:SCR_013305
Type: Tool

Proper Citation

Human Transcriptome Database for Alternative Splicing (RRID:SCR_013305)

Resource Information

URL: http://jbirc.jbic.or.jp/h-dbas/

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Description: A specialized database for human alternative splicing (AS) based on H-Invitational full-length cDNAs. H-DBAS offers unique data and viewer for human Alternative Splicing (AS) analysis. It contains: * Genome-wide representative alternative splicing variants (RASVs) identified from following datasets * H-Inv full-length cDNAs (resource summary): H-Invitational cDNA dataset * H-Inv all transcripts (resource summary): Published human mRNA dataset * Mouse full-length cDNAs (resource summary): Mouse cDNA dataset * RASVs affecting protein functions such as protein motif, GO, subcellular localization signal and transmembrane domain * Conserved RASVs compared with mouse genome and the full-length cDNAs (H-Inv full-length cDNAs only)

Abbreviations: H-DBAS

Synonyms: H-DBAS - Human-transcriptome DataBase for Alternative Splicing

Resource Type: database, data or information resource

Defining Citation: PMID:19969536, PMID:17130147

Keywords: alternative splicing, alternative splicing variant, cdna, transcriptome, h-invitational, rna-seq, rna, comparative genomics

Funding:

Resource Name: Human Transcriptome Database for Alternative Splicing

Resource ID: SCR_013305

Alternate IDs: nif-0000-02935, OMICS_01887

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250412T055716+0000

Ratings and Alerts

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

No alerts have been found for Human Transcriptome Database for Alternative Splicing.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.