

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

ASPicDB

RRID:SCR_002102

Type: Tool

Proper Citation

ASPicDB (RRID:SCR_002102)

Resource Information

URL: <http://srv00.recas.ba.infn.it/ASPicDB/>

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Description: A database to access reliable annotations of the alternative splicing pattern of human genes, obtained by ASPic algorithm (Castrignano et al. 2006), and to the functional annotation of predicted isoforms. Users may select and extract specific sets of data related to genes, transcripts and introns fulfilling a combination of user-defined criteria. Several tabular and graphical views of the results are presented, providing a comprehensive assessment of the functional implication of alternative splicing in the gene set under investigation. ASPicDB also includes information on tissue-specific splicing patterns of normal and cancer cells, based on available EST data and their library source annotation.

Abbreviations: ASPicDB

Synonyms: Alternative Splicing Prediction Data Base, ASPicDB - A Database tool for alternative splicing analysis

Resource Type: data or information resource, database

Defining Citation: [PMID:21051348](#), [PMID:18388144](#)

Keywords: annotation, splicing pattern, gene, transcript, intron, protein, variant, alternative splicing, splicing, blast, exon, u2, u12, isoform

Related Condition: Normal, Cancer

Availability: Free, Freely available

Resource Name: ASPicDB

Resource ID: SCR_002102

Alternate IDs: OMICS_01882

Old URLs: <http://srv00.ibbe.cnr.it/ASPicDB/>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260829T182921+0000

Ratings and Alerts

No rating or validation information has been found for ASPicDB.

No alerts have been found for ASPicDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Monti M, et al. (2022) Clinical Significance and Regulation of ERK5 Expression and Function in Cancer. *Cancers*, 14(2).

Yang WJ, et al. (2020) Further identification of a 140bp sequence from amid intron 9 of human FMR1 gene as a new exon. *BMC genetics*, 21(1), 63.

Diez-Hernando S, et al. (2020) Control of the neuroprotective Lipocalin Apolipoprotein D expression by alternative promoter regions and differentially expressed mRNA 5' UTR variants. *PloS one*, 15(6), e0234857.

Mejias A, et al. (2019) Characterization of mammalian Lipocalin UTRs in silico: Predictions for their role in post-transcriptional regulation. *PloS one*, 14(3), e0213206.

Chang JY, et al. (2018) Dynamics of alternative polyadenylation in human preimplantation embryos. *Biochemical and biophysical research communications*, 504(4), 727.

Pfau T, et al. (2016) Towards improved genome-scale metabolic network reconstructions: unification, transcript specificity and beyond. *Briefings in bioinformatics*, 17(6), 1060.

Fuzio P, et al. (2015) Clusterin transcript variants expression in thyroid tumor: a potential marker of malignancy? *BMC cancer*, 15, 349.

Martelli PL, et al. (2011) ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing. *Nucleic acids research*, 39(Database issue), D80.