

Resource Summary Report

Generated by [nidm-terms](#) on Jul 30, 2026

Extended Alternatively Spliced EST Database

RRID:SCR_008186

Type: Tool

Proper Citation

Extended Alternatively Spliced EST Database (RRID:SCR_008186)

Resource Information

URL: <http://www.bioinf.mdc-berlin.de/splice/db/>

Proper Citation: Extended Alternatively Spliced EST Database (RRID:SCR_008186)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. An online available compendium of alternative splice forms for several organisms (*Arabidopsis thaliana*, *Bos taurus*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Danio rerio*, *Homo sapiens*, *Mus musculus*, *Rattus norvegicus*, *Xenopus laevis*). Alternative splice forms are defined by comparing high-scoring ESTs to mRNA sequences (both from GenBank) with known exon-intron information (from ENSEMBL database) using BLAST. Repetitive sequences of all mRNAs have beforehand been masked by MaskerAid. Filtering programs with defined parameters compare the ends of each aligned sequence pair for deletions or insertions in the EST sequence, which suggest the existence of alternative splice forms. The database is accessible by typing in accession numbers (ACC) or keywords like description, gene names, organism or other keywords. (If more than one hit was found a list of all results is given.) And the result page is divided into 4 major parts. The first part (General Information About The Entry) summarizes the most important information as database ids, organism, and description. The so called alternative splice profile (ASP) of each human sequence is shown in the second part (Alternative Splice Frequency). The ASP indicates the number of alternatively spliced ESTs (NAE), the number of constitutively spliced ESTs (NCE) as well as the number of alternative splice sites (NSS) per mRNA. NAE and NCE corresponds to the EST coverage and can be used as a quality value for the predicted alternative splice variants. The NSS value specifies the splice propensity of a gene. Moreover the number of ESTs from cancerous tissues is shown. The histological source and the developmental stages are illustrated with several colors to enables the user to get an overview of the origins of the matching ESTs. Also, the Splice Site View shows graphically all alternative splice sites for the whole transcript.

Abbreviations: EASED

Synonyms: Extended Alternatively Spliced EST Database

Resource Type: data or information resource, database

Keywords: drosophila melanogaster, est, exon, filtering, form, gene structure, aligned, alternative, arabidopsis thaliana, bos taurus, caenorhabditis elegans, cancerous, color, danio rerio, deletion, developmental, histological, homo sapien, insertion, intron, mrna, mus musculus, nucleotide sequence, organism, pair, rattus norvegicus, sequence, splice, splice sites databases, stage, tissue, xenopus laevis

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Extended Alternatively Spliced EST Database

Resource ID: SCR_008186

Alternate IDs: nif-0000-21138

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260729T044202+0000

Ratings and Alerts

No rating or validation information has been found for Extended Alternatively Spliced EST Database.

No alerts have been found for Extended Alternatively Spliced EST Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.