

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on Apr 10, 2025

Splicing Express

RRID:SCR_016498

Type: Tool

Proper Citation

Splicing Express (RRID:SCR_016498)

Resource Information

URL: <https://omictools.com/splicing-express-tool>

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Description: Software suite for Alternative Splicing Events (ASEs) analysis from transcriptome sequencing data in any transcriptome. Used for identification, annotation and visualization. Written in Perl and suitable to run only in UNIX-like systems.

Resource Type: software application, data processing software, data visualization software, software resource, data analysis software

Defining Citation: [PMID:26618088](https://pubmed.ncbi.nlm.nih.gov/26618088/)

Keywords: alternative, splicing, analysis, next, generation, sequencing, data, transcriptome, identify, annotate, visualize, Perl, UNIX, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Splicing Express

Resource ID: SCR_016498

Alternate IDs: biotools:splicing_express

Alternate URLs: https://bio.tools/splicing_express

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250410T070753+0000

Ratings and Alerts

No rating or validation information has been found for Splicing Express.

No alerts have been found for Splicing Express.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Feng W, et al. (2020) Profiling Novel Alternative Splicing within Multiple Tissues Provides Useful Insights into Porcine Genome Annotation. *Genes*, 11(12).

Nogueira VB, et al. (2018) Sex-biased gene expression in the frontal cortex of common marmosets (*Callithrix jacchus*) and potential behavioral correlates. *Brain and behavior*, 8(12), e01148.

Cardoso TF, et al. (2018) Differential expression of mRNA isoforms in the skeletal muscle of pigs with distinct growth and fatness profiles. *BMC genomics*, 19(1), 145.