

# Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

## DiffSplice

RRID:SCR\_013215

Type: Tool

### Proper Citation

DiffSplice (RRID:SCR\_013215)

### Resource Information

**URL:** <http://www.netlab.uky.edu/p/bioinfo/DiffSplice>

**Proper Citation:** DiffSplice (RRID:SCR\_013215)

**Description:** The Genome-Wide Detection of Differential Splicing Events with RNA-seq.

**Abbreviations:** DiffSplice

**Resource Type:** software resource

**Defining Citation:** [PMID:23155066](#)

**Resource Name:** DiffSplice

**Resource ID:** SCR\_013215

**Alternate IDs:** OMICS\_01330

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20260815T182454+0000

### Ratings and Alerts

No rating or validation information has been found for DiffSplice.

No alerts have been found for DiffSplice.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Shi Z, et al. (2026) Transcriptome and m6A epitranscriptome profiling reveal CCL20 as a key mediator of inflammation in Staphylococcus aureus-induced bovine mastitis. BMC microbiology, 26(1), 133.

Raleigh D, et al. (2026) A proteogenomic RNA processing mechanism drives sex differences in meningioma. Research square.

Caldi Gomes L, et al. (2024) Multiomic ALS signatures highlight subclusters and sex differences suggesting the MAPK pathway as therapeutic target. Nature communications, 15(1), 4893.

Liu X, et al. (2024) Splicing Factor PQBP1 Curtails BAX Expression to Promote Ovarian Cancer Progression. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(15), e2306229.

Peters LA, et al. (2023) A temporal classifier predicts histopathology state and parses acute-chronic phasing in inflammatory bowel disease patients. Communications biology, 6(1), 95.

Lee K, et al. (2022) ASpediaFI: Functional Interaction Analysis of Alternative Splicing Events. Genomics, proteomics & bioinformatics, 20(3), 466.

Postel MD, et al. (2022) Transcriptome analysis provides critical answers to the "variants of uncertain significance" conundrum. Human mutation, 43(11), 1590.

Fahmi NA, et al. (2021) AS-Quant: Detection and Visualization of Alternative Splicing Events with RNA-seq Data. International journal of molecular sciences, 22(9).

Thorstensen MJ, et al. (2021) RNA sequencing describes both population structure and plasticity-selection dynamics in a non-model fish. BMC genomics, 22(1), 273.

Thodberg M, et al. (2019) Comprehensive profiling of the fission yeast transcription start site activity during stress and media response. Nucleic acids research, 47(4), 1671.

Qiu H, et al. (2018) Unexpected conservation of the RNA splicing apparatus in the highly streamlined genome of Galdieria sulphuraria. BMC evolutionary biology, 18(1), 41.

Holik AZ, et al. (2017) RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. Nucleic acids research, 45(5), e30.

Linde J, et al. (2015) Defining the transcriptomic landscape of Candida glabrata by RNA-Seq. Nucleic acids research, 43(3), 1392.

Sheng Z, et al. (2015) Functional Cross-Talking between Differentially Expressed and Alternatively Spliced Genes in Human Liver Cancer Cells Treated with Berberine. PloS one, 10(11), e0143742.

Lhoumaud P, et al. (2014) Insulators recruit histone methyltransferase dMes4 to regulate chromatin of flanking genes. The EMBO journal, 33(14), 1599.