

Resource Summary Report

Generated by [dkNET](#) on Aug 18, 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 [dkNET](#) .

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.