# **Resource Summary Report**

Generated by <u>NIF</u> on May 18, 2025

# **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

Funding:

Resource Name: DiffSplice

Resource ID: SCR\_013215

Alternate IDs: OMICS\_01330

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

Record Last Update: 20250420T014636+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 13 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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 acutechronic 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.

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.

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).

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.

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.

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

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