

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

SpliceTrap

RRID:SCR_006728

Type: Tool

Proper Citation

SpliceTrap (RRID:SCR_006728)

Resource Information

URL: <http://rulai.cshl.edu/splicetrap/>

Proper Citation: SpliceTrap (RRID:SCR_006728)

Description: A statistic tool for quantifying exon inclusion ratios in paired-end RNA-seq data, with broad applications for the study of alternative splicing. SpliceTrap approaches to exon inclusion level estimation as a Bayesian inference problem. For every exon it quantifies the extent to which it is included, skipped or subjected to size variations due to alternative 3'/5' splice sites or Intron Retention. In addition, SpliceTrap can quantify alternative splicing within a single cellular condition, with no need of a background set of reads.

Abbreviations: SpliceTrap

Resource Type: software resource

Defining Citation: [PMID:21896509](#)

Keywords: bio.tools

Resource Name: SpliceTrap

Resource ID: SCR_006728

Alternate IDs: biotools:splicetrap, OMICS_01292

Alternate URLs: <https://bio.tools/splicetrap>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260808T185848+0000

Ratings and Alerts

No rating or validation information has been found for SpliceTrap.

No alerts have been found for SpliceTrap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Fronk AD, et al. (2024) Development and validation of AI/ML derived splice-switching oligonucleotides. *Molecular systems biology*, 20(6), 676.

Teng P, et al. (2023) The human lncRNA GOMAFU suppresses neuronal interferon response pathways affected in neuropsychiatric diseases. *Brain, behavior, and immunity*, 112, 175.

Yang P, et al. (2021) Alternative splicing level related to intron size and organism complexity. *BMC genomics*, 22(1), 853.

Vuong CK, et al. (2018) Rbfox1 Regulates Synaptic Transmission through the Inhibitory Neuron-Specific vSNARE Vamp1. *Neuron*, 98(1), 127.

Liu H, et al. (2018) Alternative splicing analysis in human monocytes and macrophages reveals MBNL1 as major regulator. *Nucleic acids research*, 46(12), 6069.

Johnston WL, et al. (2017) C. elegans SUP-46, an HNRNPM family RNA-binding protein that prevents paternally-mediated epigenetic sterility. *BMC biology*, 15(1), 61.

Das DK, et al. (2017) Fibronectin and androgen receptor expression data in prostate cancer obtained from a RNA-sequencing bioinformatics analysis. *Data in brief*, 11, 131.

Fang J, et al. (2017) Ubiquitination of hnRNPA1 by TRAF6 links chronic innate immune signaling with myelodysplasia. *Nature immunology*, 18(2), 236.

Tan JH, et al. (2017) The combinatorial control of alternative splicing in C. elegans. *PLoS genetics*, 13(11), e1007033.

Arun G, et al. (2016) Differentiation of mammary tumors and reduction in metastasis upon Malat1 lncRNA loss. *Genes & development*, 30(1), 34.

de Bruin RG, et al. (2016) Quaking promotes monocyte differentiation into pro-atherogenic macrophages by controlling pre-mRNA splicing and gene expression. *Nature communications*, 7, 10846.

Giudice J, et al. (2016) Neonatal cardiac dysfunction and transcriptome changes caused by the absence of Celf1. *Scientific reports*, 6, 35550.

Ragle JM, et al. (2015) Coordinated tissue-specific regulation of adjacent alternative 3' splice sites in *C. elegans*. *Genome research*, 25(7), 982.

Linares AJ, et al. (2015) The splicing regulator PTBP1 controls the activity of the transcription factor Pbx1 during neuronal differentiation. *eLife*, 4, e09268.

Viner C, et al. (2014) Validation of predicted mRNA splicing mutations using high-throughput transcriptome data. *F1000Research*, 3, 8.

Gelfman S, et al. (2013) DNA-methylation effect on cotranscriptional splicing is dependent on GC architecture of the exon-intron structure. *Genome research*, 23(5), 789.