

Resource Summary Report

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IsoformSwitchAnalyzeR

RRID:SCR_027320

Type: Tool

Proper Citation

IsoformSwitchAnalyzeR (RRID:SCR_027320)

Resource Information

URL:

<https://www.bioconductor.org/packages/release/bioc/html/IsoformSwitchAnalyzeR.html>

Proper Citation: IsoformSwitchAnalyzeR (RRID:SCR_027320)

Description: Software R package to identify, annotate and visualize isoform switches with functional consequences from both short- and long-read RNA-seq data. Analysis of alternative splicing and isoform switches with predicted functional consequences (e.g. gain/loss of protein domains etc.) from quantification of all types of RNASeq by tools such as Kallisto, Salmon, StringTie, Cufflinks/Cuffdiff etc.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:30989184](#)

Keywords: Identify, Annotate, Visualize, Isoform Switches with Functional Consequences, short- and long-read RNA-seq data,

Funding: Lundbeck Foundation ;
Independent Research Fund Denmark

Availability: Free, Available for download, Freely available

Resource Name: IsoformSwitchAnalyzeR

Resource ID: SCR_027320

Record Creation Time: 20250815T054452+0000

Record Last Update: 20260810T040925+0000

Ratings and Alerts

No rating or validation information has been found for IsoformSwitchAnalyzeR.

No alerts have been found for IsoformSwitchAnalyzeR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Vendramin R, et al. (2026) Nonsense-mediated mRNA decay inhibition reshapes the cancer immunopeptidome. *Immunity*, 59(5), 1398.

Xu J, et al. (2025) Long-read RNA-sequencing reveals transcript-specific regulation in human-derived cortical neurons. *Open biology*, 15(7), 250200.

Bernardi S, et al. (2025) CircCDYL Association With hnRNPL Modulates CDYL Isoform Switching in Breast Cancer Cells. *Cancer science*, 116(10), 2750.

Lu P, et al. (2025) Systematic characterization of full-length RNA isoforms in human colorectal cancer at single-cell resolution. *Protein & cell*, 16(10), 873.

Nakagawa S, et al. (2025) Early regulation and alternative splicing dynamics in glucocorticoid muscle atrophy revealed by temporal omics in C2C12 myotubes. *American journal of physiology. Cell physiology*, 329(4), C1300.

Song KJ, et al. (2024) Proteogenomic analysis reveals non-small cell lung cancer subtypes predicting chromosome instability, and tumor microenvironment. *Nature communications*, 15(1), 10164.

Guisasola-Serrano A, et al. (2024) Identifying transcriptomic profiles in ovine spleen after repetitive vaccination. *Frontiers in immunology*, 15, 1386590.

Salz R, et al. (2024) Multi-omic profiling of pathogen-stimulated primary immune cells. *iScience*, 27(8), 110471.

Jones EF, et al. (2024) Long-read RNA sequencing identifies region- and sex-specific C57BL/6J mouse brain mRNA isoform expression and usage. *bioRxiv : the preprint server for biology*.

Abbassi-Daloui T, et al. (2023) A transcriptome atlas of leg muscles from healthy human volunteers reveals molecular and cellular signatures associated with muscle location. *eLife*, 12.

Bergant V, et al. (2023) mRNA 3'UTR lengthening by alternative polyadenylation attenuates inflammatory responses and correlates with virulence of Influenza A virus.

Nature communications, 14(1), 4906.

Genov N, et al. (2019) Temporal Splicing Switches in Elements of the TNF-Pathway Identified by Computational Analysis of Transcriptome Data for Human Cell Lines. International journal of molecular sciences, 20(5).