

Resource Summary Report

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[rMATS](#)

RRID:SCR_023485

Type: Tool

Proper Citation

rMATS (RRID:SCR_023485)

Resource Information

URL: <https://rmats.sourceforge.io>

Proper Citation: rMATS (RRID:SCR_023485)

Description: Software tool to detect differential alternative splicing events from RNA-Seq data. Calculates P-value and false discovery rate that difference in isoform ratio of gene between two conditions exceeds given user-defined threshold. From RNA-Seq data can automatically detect and analyze alternative splicing events corresponding to all major types of alternative splicing patterns. Handles replicate RNA-Seq data from both paired and unpaired study design.

Resource Type: software resource

Defining Citation: [PMID:25480548](#)

Keywords: detection of differential alternative splicing, replicate RNA-Seq data, analysis of paired and unpaired replicates, clinical RNA-Seq datasets, genome studies,

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Availability: Free, Available to download, Freely available

Resource Name: rMATS

Resource ID: SCR_023485

Record Creation Time: 20230421T050214+0000

Ratings and Alerts

No rating or validation information has been found for rMATS.

No alerts have been found for rMATS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Corr BR, et al. (2025) SM08502-Mediated β -Catenin Repression Synergizes with Olaparib to Inhibit Tumor Progression. Cancer research communications, 5(12), 2112.

Tseng PL, et al. (2025) Mechanical control of the alternative splicing factor PTBP1 regulates extracellular matrix stiffness induced proliferation and cell spreading. iScience, 28(4), 112273.

Herbert A, et al. (2025) Precursor RNA structural patterns at SF3B1 mutation sensitive cryptic 3' splice sites. RNA biology, 22(1), 1.

Ning G, et al. (2025) BCAS2 promotes primitive hematopoiesis by sequestering β -catenin within the nucleus. eLife, 13.

Liu M, et al. (2025) INO80/SWR remodelers regulate Pol II transcription through BRD2 and chromatin landscape. Nucleic acids research, 53(17).

Li T, et al. (2024) Blocker-SELEX: a structure-guided strategy for developing inhibitory aptamers disrupting undruggable transcription factor interactions. Nature communications, 15(1), 6751.

Wong CH, et al. (2024) Genome-scale requirements for dynein-based transport revealed by a high-content arrayed CRISPR screen. The Journal of cell biology, 223(5).

Yu Z, et al. (2024) A delayed and unsynchronized ovary development as revealed by transcriptome of brain and pituitary of *Coilia nasus*. Frontiers in molecular biosciences, 11, 1361386.

Zhang Y, et al. (2024) CWF19L1 promotes T-cell cytotoxicity through the regulation of alternative splicing. The Journal of biological chemistry, 300(12), 107982.

Wu R, et al. (2024) Disruption of nuclear speckle integrity dysregulates RNA splicing in C9ORF72-FTD/ALS. Neuron, 112(20), 3434.

Ayers KL, et al. (2023) Variants in SART3 cause a spliceosomopathy characterised by failure of testis development and neuronal defects. *Nature communications*, 14(1), 3403.

Nabavizadeh N, et al. (2023) A progeroid syndrome caused by a deep intronic variant in TAPT1 is revealed by RNA/SI-NET sequencing. *EMBO molecular medicine*, 15(2), e16478.

Zhang F, et al. (2023) Mapping splice QTLs reveals distinct transcriptional and post-transcriptional regulatory variation of gene expression and identifies putative alternative splicing variation mediating complex trait variation in pigs. *BMC genomics*, 24(1), 240.

Martinez-Lozada Z, et al. (2023) Cooperative and competitive regulation of the astrocytic transcriptome by neurons and endothelial cells: Impact on astrocyte maturation. *Journal of neurochemistry*, 167(1), 52.

Tsitsikov EN, et al. (2023) TRAF7 is an essential regulator of blood vessel integrity during mouse embryonic and neonatal development. *iScience*, 26(8), 107474.

Kim S, et al. (2022) Brain Region-Dependent Alternative Splicing of Alzheimer Disease (AD)-Risk Genes Is Associated With Neuropathological Features in AD. *International neurourology journal*, 26(Suppl 2), S126.

Byun S, et al. (2020) The landscape of alternative splicing in HIV-1 infected CD4 T-cells. *BMC medical genomics*, 13(Suppl 5), 38.

Jin YJ, et al. (2020) Differential alternative splicing between hepatocellular carcinoma with normal and elevated serum alpha-fetoprotein. *BMC medical genomics*, 13(Suppl 11), 194.