

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>

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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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NIEHS R01ES024995;
NIGMS R01GM088342;
NIGMS R01GM105431;
NINDS R01NS076631;
NSF DMS1055286;
NSF DMS1310391

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 22 mentions in open access literature.

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

Tankka AT, et al. (2026) Integrative CRISPR Screening and RNA Analyses Discover an Essential Role for PUF60 Interactions with 3' Splice Sites in Cancer Progression. *Cancer research*, 86(7), 1586.

Yuan L, et al. (2026) The missense mutation Y65C in PQBP1 causes microcephaly and cognitive deficits through a combination of partial loss-of-function and gain-of-function effects. *Nature communications*, 17(1), 1463.

Ye Y, et al. (2026) DCPS modulates TDP-43-linked neurodegeneration through P-body-mediated RNA decay. *Neuron*, 114(11), 1970.

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

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

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.

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

Emerson J, et al. (2025) Early transcriptomic perturbations highlight the spinal cord as a key pathogenic region in spinocerebellar ataxia type 3. *Frontiers in cellular neuroscience*, 19, 1735225.

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).

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.

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.