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,

Funding: NIGMS R01GM088342;
NINDS R01NS076631;
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Availability: Free, Available to download, Freely available

Resource Name: rMATS

Resource ID: SCR_023485

Record Creation Time: 20230421T050214+0000

Record Last Update: 20260808T190245+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 nidm-terms .

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 ?-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 ?-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).

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.