Resource Summary Report

Generated by dkNET on Apr 29, 2025

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;
NIEHS R01ES024995;
NIGMS R01GM105431;
NSF DMS1055286;
NSF DMS1310391;
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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: 20250420T015248+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 13 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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

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.

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.

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.

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.

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

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.

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.