

# Resource Summary Report

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## Multivariate Analysis of Transcript Splicing

RRID:SCR\_013049

Type: Tool

### Proper Citation

Multivariate Analysis of Transcript Splicing (RRID:SCR\_013049)

### Resource Information

**URL:** <http://rnaseq-mats.sourceforge.net/>

**Proper Citation:** Multivariate Analysis of Transcript Splicing (RRID:SCR\_013049)

**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. 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.

**Abbreviations:** MATS

**Synonyms:** RNAseq MATS, RMATS, rMATS, MATS, RNA MATS

**Resource Type:** software application, software resource, data analysis software, data processing software

**Keywords:** Differential alternative splicing events, splicing events calculation, RNA-Seq data, gene isoform ratio, alternative splicing patterns, patterns detection, patterns analysis, replicate RNA-Seq data

**Availability:** Free, Available for download, Freely available

**Resource Name:** Multivariate Analysis of Transcript Splicing

**Resource ID:** SCR\_013049

**Alternate IDs:** OMICS\_01336, SCR\_020941

**License:** 2-Clause BSD License

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20260729T044310+0000

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## Ratings and Alerts

No rating or validation information has been found for Multivariate Analysis of Transcript Splicing.

No alerts have been found for Multivariate Analysis of Transcript Splicing.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 192 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

Zhang B, et al. (2026) Human papillomavirus E7 inhibits immune responses in keratinocytes by activating HTRA1-mediated mitophagy. International journal of molecular medicine, 57(1).

Ciftci E, et al. (2025) Current methods in the diagnosis of invasive meningococcal disease. Frontiers in pediatrics, 13, 1511086.

Zhang P, et al. (2025) DAZAP1 maintains gastric cancer stemness by inducing mitophagy. JCI insight, 10(10).

González-Almela E, et al. (2025) Herpes simplex virus type 1 reshapes host chromatin architecture via transcription machinery hijacking. Nature communications, 16(1), 5313.

Borrow R, et al. (2025) Methods to evaluate the performance of a multicomponent meningococcal serogroup B vaccine. mSphere, 10(4), e0089824.

Memon AA, et al. (2025) Fibrinogen genotypes and their impact on recurrence of venous thromboembolism and family history: A prospective population-based study. British journal of haematology, 206(2), 657.

Alvarez NS, et al. (2025) Dysregulation of alternative splicing patterns in the ovaries of reproductively aged mice. bioRxiv : the preprint server for biology.

Ben X, et al. (2025) Transcriptome profiling reveals major structural genes, transcription factors and biosynthetic pathways in refractory epilepsy in tropical region of China. BMC neurology, 25(1), 288.

Falguières M, et al. (2025) Fluctuations in serogroup B meningococcal vaccine antigens prior to routine MenB vaccination in France. Communications medicine, 5(1), 87.

An MJ, et al. (2024) Reorganization of H3K9me heterochromatin leads to neuronal impairment via the cascading destruction of the KDM3B-centered epigenomic network. iScience, 27(8), 110380.

Jürgens M, et al. (2024) Chronic stimulation desensitizes  $\alpha$ 2-adrenergic receptor responses in natural killer cells. *European journal of immunology*, 54(12), e2451299.

Gan J, et al. (2024) RNA-seq analysis reveals transcriptome reprogramming and alternative splicing during early response to salt stress in tomato root. *Frontiers in plant science*, 15, 1394223.

Efron A, et al. (2024) Genetic characterization and estimated 4CMenB vaccine strain coverage of 284 *Neisseria meningitidis* isolates causing invasive meningococcal disease in Argentina in 2010-2014. *Human vaccines & immunotherapeutics*, 20(1), 2378537.

Lee E, et al. (2024) H3.3-G34W in giant cell tumor of bone functionally aligns with the exon choice repressor hnRNPA1L2. *Cancer gene therapy*, 31(8), 1177.

Calvert A, et al. (2024) Risk of Invasive Meningococcal Disease in Preterm Infants. *Open forum infectious diseases*, 11(4), ofae164.

Zhang ZY, et al. (2024) Increased global posterior tibial slope is significantly associated with higher ACL graft signal intensity on 2-Year postoperative MRI after primary ACL reconstruction using hamstring tendon autografts. *BMC musculoskeletal disorders*, 25(1), 905.

Howard GC, et al. (2024) Ribosome subunit attrition and activation of the p53-MDM4 axis dominate the response of MLL-rearranged cancer cells to WDR5 WIN site inhibition. *eLife*, 12.

Zhang ZY, et al. (2023) Chronic ACL-injured patients show increased medial and global anterior tibial subluxation measured on 1-year postoperative MR images after primary single-bundle ACL reconstruction. *Journal of orthopaedic surgery and research*, 18(1), 565.

Sklenarova B, et al. (2023) Entropy in scalp EEG can be used as a preimplantation marker for VNS efficacy. *Scientific reports*, 13(1), 18849.

Wang C, et al. (2023) The KLF7/PFKFB3/ACADL axis modulates cardiac metabolic remodelling during cardiac hypertrophy in male mice. *Nature communications*, 14(1), 959.