Resource Summary Report

Generated by NIF on Apr 18, 2025

MISO

RRID:SCR_003124
Type: Tool

Proper Citation

MISO (RRID:SCR_003124)

Resource Information

URL: http://genes.mit.edu/burgelab/miso/

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Description: Probabilistic framework that quantitates the expression level of alternatively spliced genes from RNA-Seq and identifies differentially regulated isoforms or exons across samples.

Synonyms: Mixture of Isoforms (MISO), Mixture of Isoforms

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

Defining Citation: DOI:10.1038/nmeth.1528

Keywords: probabilistic framework, framework, bayesian inference, isoform

Funding:

Availability: Available for download

Resource Name: MISO

Resource ID: SCR_003124

Alternate IDs: OMICS_01337

Alternate URLs: https://github.com/yarden/MISO

License: GPL 2+ license

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250418T055012+0000

Ratings and Alerts

No rating or validation information has been found for MISO.

No alerts have been found for MISO.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 171 mentions in open access literature.

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

Zhao J, et al. (2024) Effect of thermal treatment on microcracking characteristics of granite under tensile condition based on bonded-particle model and moment tensor. Scientific reports, 14(1), 8806.

Samuel RM, et al. (2023) Generation of Schwann cell derived melanocytes from hPSCs identifies pro-metastatic factors in melanoma. bioRxiv : the preprint server for biology.

Pineda JMB, et al. (2023) DUX4 is a common driver of immune evasion and immunotherapy failure in metastatic cancers. bioRxiv : the preprint server for biology.

Jalloh B, et al. (2023) The Drosophila Nab2 RNA binding protein inhibits m6A methylation and male-specific splicing of Sex lethal transcript in female neuronal tissue. eLife, 12.

Tao Y, et al. (2023) Cell-free multi-omics analysis reveals potential biomarkers in gastrointestinal cancer patients' blood. Cell reports. Medicine, 4(11), 101281.

Dunker W, et al. (2023) The proto-oncogene SRC phosphorylates cGAS to inhibit an antitumor immune response. JCI insight, 8(12).

Wang F, et al. (2022) Single-cell architecture and functional requirement of alternative splicing during hematopoietic stem cell formation. Science advances, 8(1), eabg5369.

Lee K, et al. (2022) ASpediaFI: Functional Interaction Analysis of Alternative Splicing Events. Genomics, proteomics & bioinformatics, 20(3), 466.

Li S, et al. (2022) Nuclear Aurora kinase A switches m6A reader YTHDC1 to enhance an

oncogenic RNA splicing of tumor suppressor RBM4. Signal transduction and targeted therapy, 7(1), 97.

Ma XR, et al. (2022) TDP-43 represses cryptic exon inclusion in the FTD-ALS gene UNC13A. Nature, 603(7899), 124.

Zhu GQ, et al. (2022) Targeting HNRNPM Inhibits Cancer Stemness and Enhances Antitumor Immunity in Wnt-activated Hepatocellular Carcinoma. Cellular and molecular gastroenterology and hepatology, 13(5), 1413.

Gañez-Zapater A, et al. (2022) The SWI/SNF subunit BRG1 affects alternative splicing by changing RNA binding factor interactions with nascent RNA. Molecular genetics and genomics : MGG, 297(2), 463.

Jones A, et al. (2022) Multiomics analysis of the NAD+-PARP1 axis reveals a role for site-specific ADP-ribosylation in splicing in embryonic stem cells. Genes & development, 36(9-10), 601.

Xu T, et al. (2022) Alternative splicing downstream of EMT enhances phenotypic plasticity and malignant behavior in colon cancer. eLife, 11.

North K, et al. (2022) Synthetic introns enable splicing factor mutation-dependent targeting of cancer cells. Nature biotechnology, 40(7), 1103.

She X, et al. (2022) Accelerating input-output model estimation with parallel computing for testing hippocampal memory prostheses in human. Journal of neuroscience methods, 370, 109492.

Hauser D, et al. (2022) Targeted proteoform mapping uncovers specific Neurexin-3 variants required for dendritic inhibition. Neuron, 110(13), 2094.

Han BY, et al. (2022) HNRNPU promotes the progression of triple-negative breast cancer via RNA transcription and alternative splicing mechanisms. Cell death & disease, 13(11), 940.

Kitamura Y, et al. (2021) Identification of germ cell-specific Mga variant mRNA that promotes meiosis via impediment of a non-canonical PRC1. Scientific reports, 11(1), 9737.

Cha HJ, et al. (2021) Inner nuclear protein Matrin-3 coordinates cell differentiation by stabilizing chromatin architecture. Nature communications, 12(1), 6241.