Resource Summary Report

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

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: 20250412T054803+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 FDI Lab - SciCrunch.org.

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.