

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, software resource, data analysis software, data processing software, software application

Defining Citation: [DOI:10.1038/nmeth.1528](https://doi.org/10.1038/nmeth.1528)

Keywords: probabilistic framework, framework, bayesian inference, isoform

Availability: Free, Available for download, Freely available

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: 20260807T042548+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 181 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Zhang F, et al. (2026) Spatially multimodal and multiscale network for representation learning from spatial multi-omics. BMC genomics, 27(1).

Yan X, et al. (2026) AKAP95 condensates regulate transcription and can be targeted in MLL-fusion driven oncogenesis. Nature communications, 17(1), 1457.

Chen SC, et al. (2025) Microbial iron oxide respiration coupled to sulfide oxidation. Nature, 646(8086), 925.

Chen Y, et al. (2025) iPSCs derived sEVs ameliorate NK cell senescence by targeting CISH-STAT3. Stem cell research & therapy, 16(1), 634.

Gabel AM, et al. (2025) Muscleblind-like proteins are novel modulators of the tumor-immune microenvironment. PloS one, 20(4), e0321148.

Han C, et al. (2025) An Isoform-Specific RUNX1C-BTG2 Axis Governs AML Quiescence and Chemoresistance. Blood cancer discovery, 6(5), 464.

Schmauch B, et al. (2025) A deep learning-based multiscale integration of spatial omics with tumor morphology. Nature communications, 16(1), 11674.

McKellar SA, et al. (2025) Chorionic Gonadotropin Beta 7 is a marker of immune evasion in cancer. bioRxiv : the preprint server for biology.

Zhu D, et al. (2025) DDX1 methylation mediated MATR3 splicing regulates intervertebral disc degeneration by initiating chromatin reprogramming. Nature communications, 16(1), 6153.

Eldfors S, et al. (2025) Sensitivity to ATR-CHK1 pathway inhibition in AML/MDS is enhanced by SRSF2 mutations and reduced by RUNX1 loss. bioRxiv : the preprint server for biology.

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).

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.

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.

Ga??ez-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.