Resource Summary Report

Generated by RRID on May 25, 2025

Molecular Signatures Database

RRID:SCR_016863
Type: Tool

Proper Citation

Molecular Signatures Database (RRID:SCR_016863)

Resource Information

URL: http://software.broadinstitute.org/gsea/msigdb/index.jsp

Proper Citation: Molecular Signatures Database (RRID:SCR_016863)

Description: Collection of annotated gene sets for use with Gene Set Enrichment Analysis (GSEA) software.

Abbreviations: MSigDB

Synonyms: Molecular Signatures Database, The Molecular Signatures Database, MSigDB, MSigDB database v6.2

Resource Type: data or information resource, database

Keywords: collection, annotated, gene, set, GSEA, enrichment, analysis, genome, RNA, expression, data, FASEB list

Funding: NCI ;
NIH ;
NIGMS

Availability: Free, Freely available, Registration required to download GSEA software

Resource Name: Molecular Signatures Database

Resource ID: SCR_016863

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Record Creation Time: 20220129T080332+0000

Record Last Update: 20250525T032417+0000

Ratings and Alerts

No rating or validation information has been found for Molecular Signatures Database.

No alerts have been found for Molecular Signatures Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 638 mentions in open access literature.

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

Corinaldesi C, et al. (2025) Single-cell transcriptomics of pediatric Burkitt lymphoma reveals intra-tumor heterogeneity and markers of therapy resistance. Leukemia, 39(1), 189.

Ye L, et al. (2025) Multi?omics identification of a novel signature for serous ovarian carcinoma in the context of 3P medicine and based on twelve programmed cell death patterns: a multi-cohort machine learning study. Molecular medicine (Cambridge, Mass.), 31(1), 5.

Zou YP, et al. (2025) Systematic identification of pathological mechanisms, prognostic biomarkers and therapeutic targets by integrating lncRNA expression variation in salivary gland mucoepidermoid carcinoma. Scientific reports, 15(1), 1573.

Ohri N, et al. (2025) Gene expression dynamics in fibroblasts during early-stage murine pancreatic carcinogenesis. iScience, 28(1), 111572.

Pongma C, et al. (2025) Effect of mRNA formulated with lipid nanoparticles on the transcriptomic and epigenetic profiles of F4/80+?liver-associated macrophages. Scientific reports, 15(1), 1146.

Yu Z, et al. (2025) Accurate Spatial Heterogeneity Dissection and Gene Regulation Interpretation for Spatial Transcriptomics using Dual Graph Contrastive Learning. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(3), e2410081.

Chen Y, et al. (2025) Comparative transcriptomics and metabolomics provide insight into degeneration-related physiological mechanisms of Morchella importuna after long-term preservation. Microbial biotechnology, 18(1), e70045.

Yu R, et al. (2025) ATRX mutation modifies the DNA damage response in glioblastoma multiforme tumor cells and enhances patient prognosis. Medicine, 104(2), e41180.

da Silva Fernandes T, et al. (2025) Inosine monophosphate dehydrogenase 2 (IMPDH2) modulates response to therapy and chemo-resistance in triple negative breast cancer. Scientific reports, 15(1), 1061.

Torrance HD, et al. (2024) A Transcriptomic Approach to Understand Patient Susceptibility to Pneumonia After Abdominal Surgery. Annals of surgery, 279(3), 510.

Schott CR, et al. (2024) Osteosarcoma PDX-Derived Cell Line Models for Preclinical Drug Evaluation Demonstrate Metastasis Inhibition by Dinaciclib through a Genome-Targeted Approach. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 849.

Vu LT, et al. (2024) Single-cell transcriptomics of the immune system in ME/CFS at baseline and following symptom provocation. Cell reports. Medicine, 5(1), 101373.

Kink JA, et al. (2024) Large-scale bioreactor production of extracellular vesicles from mesenchymal stromal cells for treatment of acute radiation syndrome. Stem cell research & therapy, 15(1), 72.

Xiao Z, et al. (2024) Identification and immunological characterization of genes associated with ferroptosis in Alzheimer's disease and experimental demonstration. Molecular medicine reports, 30(3).

Tian X, et al. (2024) LINC01614 is a promising diagnostic and prognostic marker in HNSC linked to the tumor microenvironment and oncogenic function. Frontiers in genetics, 15, 1337525.

Eiken AP, et al. (2024) Novel Spirocyclic Dimer, SpiD3, Targets Chronic Lymphocytic Leukemia Survival Pathways with Potent Preclinical Effects. Cancer research communications, 4(5), 1328.

Cao C, et al. (2024) CXCR4 orchestrates the TOX-programmed exhausted phenotype of CD8+ T cells via JAK2/STAT3 pathway. Cell genomics, 4(10), 100659.

De Bellis C, et al. (2024) Genomic, epigenomic and transcriptomic inter- and intra-tumor heterogeneity in desmoid tumors. Clinical cancer research : an official journal of the American Association for Cancer Research.

Koganemaru S, et al. (2024) The tumor immune microenvironment and therapeutic efficacy of trastuzumab deruxtecan in gastric cancer. Cancer research communications.

Gong K, et al. (2024) Intestinal Nogo-B reduces GLP1 levels by binding to proglucagon on

the endoplasmic reticulum to inhibit PCSK1 cleavage. Nature communications, 15(1), 6845.