

Resource Summary Report

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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, DRKB

Funding: NCI CA295532;
NIGMS ;
NIH

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

Resource Name: Molecular Signatures Database

Resource ID: SCR_016863

Alternate URLs: <https://www.gsea-msigdb.org/gsea/msigdb/>

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Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T200217+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 1702 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Chen X, et al. (2026) Biomimetic bone niche reconstructs proliferation-inhibited and therapy-resistant bone-metastatic prostate cancer. *Bioactive materials*, 56, 15.

Szpotkowska J, et al. (2026) Oxidative stress and GPX2 control pancreatic vs. non-pancreatic cell fate in human endoderm. *Nature communications*, 17(1), 1407.

Lu Z, et al. (2026) [Construction of a prognosis forecasting model for breast cancer based on lipid metabolism-related genes and functional verification of ALDH2]. *Zhejiang da xue xue bao. Yi xue ban = Journal of Zhejiang University. Medical sciences*, 55(1), 77.

Ling S, et al. (2026) Integrative omics and experimental validation reveal METTL17 and SLC27A1 as biomarkers and potential therapeutic targets in chronic kidney disease. *Frontiers in immunology*, 17, 1724740.

Zhu L, et al. (2026) Integrated analysis and validation of metabolism-related genes in lung transplantation-induced cold ischemia/ reperfusion injury. *PeerJ*, 14, e20857.

Zhang L, et al. (2026) Prognostic significance of calcium signaling-related genes in bladder cancer and the role of ATP2B4 in regulating mitochondrial calcium ion levels via the VDAC1/MCU pathway. *Frontiers in immunology*, 17, 1561666.

Liu XZ, et al. (2026) Targeting the Lipid Metabolism Proteins FASN and GPAM in Alveolar Type II Cells Decreases Lung Metastasis. *Cancer discovery*, 16(7), 1412.

Chen B, et al. (2026) Charting cell-type-specific positive genetic interaction at single-cell resolution for lung adenocarcinoma. *NPJ precision oncology*, 10(1).

Liao X, et al. (2026) Transcriptomic analysis reveals synaptic dysregulation and mitochondrial dysfunction in autism spectrum disorder. *Brain, behavior, & immunity - health*, 53, 101197.

Ofuchi T, et al. (2026) Intratumoral *Fusobacterium nucleatum* Drives Cancer-Associated Fibroblasts Enrichment and Immune Exclusion in Esophageal Squamous Cell Carcinoma. *Annals of gastroenterological surgery*, 10(2), 611.

Lin B, et al. (2026) Transcriptome and experimental validation identify prognostic genes associated with lipotoxicity in thyroid carcinoma. *BMC cancer*, 26(1).

Li Y, et al. (2026) Revealing key genes and molecular mechanisms associated with dietary restriction in ulcerative colitis. *Frontiers in molecular biosciences*, 13, 1786138.

Han S, et al. (2026) RUNX1-deficiency drives immune-active ER+ mammary tumorigenesis through activation of interferon signaling. *bioRxiv : the preprint server for biology*.

Wang Y, et al. (2026) A pyroptosis-related gene signature for the diagnosis of acute pancreatitis. *PloS one*, 21(4), e0347204.

Heintz MM, et al. (2026) Hepatic transcriptomic responses in gravid and non-gravid rats exposed to HFPO-DA: Analyses to inform the role of maternal effects in neonatal toxicity. *PloS one*, 21(4), e0345643.

Dong X, et al. (2026) Identification of glycometabolism-related genes for predicting the prognosis of patients with glioblastoma and its correlation with immune infiltration. *Discover oncology*, 17(1).

Zhong Y, et al. (2026) Nicotine-induced immune escape mechanisms in lung adenocarcinoma: ceRNA network toxicology, and molecular dynamics simulations. *PeerJ*, 14, e21103.

Huang R, et al. (2026) The role of R-loop aberrations in lower-grade gliomas: prognostic, immune, and metabolic implications from multi-omics and machine learning analysis. *Frontiers in immunology*, 17, 1758954.

Zhao Y, et al. (2026) Single-Cell and Multi-Omics-Based Characterization of Gastric Cancer Identifies TPP1 as a Potential Target for Gastric Cancer Progression and Treatment. *Oncology research*, 34(4), 27.

Cao G, et al. (2026) Cross-species scRNA-seq finds ideal mouse models for aortic dissection mechanisms. *iScience*, 29(3), 115147.