

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: 20260821T194058+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 [dkNET](#) .

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

Raschdorf A, et al. (2026) Colonic spatial single-cell proteomics and murine models link mitochondrial dysfunction to dimeric IgA-secreting plasma cell deficiency in Crohn's disease. Nature communications, 17(1), 1590.

Zhen S, et al. (2026) Unraveling heterogeneity in LUAD via multi-omics integration: molecular classification and therapeutic implications. Discover oncology, 17(1).

Yang L, et al. (2026) TEAD4 and RXRA Regulate the Function of Nucleus Pulposus Cells in Intervertebral Disc Degeneration Via the TNF- α /NF- κ B Pathway: An Integrated Analysis of Single-Cell RNA-Seq, Bulk RNA-Seq, and In Vitro Validation. Applied biochemistry and biotechnology, 198(3), 1939.

Moore N, et al. (2026) Biological Mechanisms of Strength Preservation During Calorie Restriction-Induced Weight Loss Among Young- to Middle-Aged Adults without Obesity. bioRxiv : the preprint server for biology.

Zhu Q, et al. (2026) STING synergizes with TOX suppressing HO-1 expression to trigger ferroptosis in tumor-infiltrating CD8⁺ T cell and immunotherapy resistance. Nature communications, 17(1).

Zhang P, et al. (2026) Integrative machine learning identifies a TEAD4-driven endothelial program shaping drug sensitivity and microvascular invasion in HCC. Journal of translational medicine, 24(1).

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.

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

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

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).

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.

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

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.

Xiao T, et al. (2026) Lactylation-related genes signature panel in hepatocellular carcinoma reveals the prognostic and therapeutic optimization. *Molecular & cellular oncology*, 13(1), 2621475.

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.

Chen W, et al. (2026) Identification of an age-related monocyte-derived macrophages characteristic genes-based signature for high-grade diffuse glioma. *Scientific reports*, 16(1).

Jin J, et al. (2026) Identification and histological validation of autophagy-related core genes ADRB2 and PLK2 in keloids, with integrated immune infiltration analysis. *Frontiers in immunology*, 17, 1724230.

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.