

Resource Summary Report

Generated by T1D on Aug 1, 2026

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: NIH ;
NIGMS ;
NCI CA295532

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: 20260729T044428+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 762 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Herbrich S, et al. (2026) TET2-mutant clonal hematopoiesis enhances macrophage antigen presentation and improves immune checkpoint therapy in solid tumors. *Cancer cell*, 44(1), 187.

Lorenz SM, et al. (2026) A fin-loop-like structure in GPX4 underlies neuroprotection from ferroptosis. *Cell*, 189(1), 287.

Mogi M, et al. (2026) Pan-cancer analysis of RNA expression signatures associated with cancer tissue architecture. *British journal of cancer*, 134(1), 141.

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. *Cancer discovery*, 15(6), 1203.

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.

Westermann S, et al. (2025) Activation of STAT6 in Intestinal Epithelial Cells Predisposes to Gut Inflammation. *European journal of immunology*, 55(2), e202451394.

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.

Timilsina S, et al. (2025) Epigenetic silencing of DNA sensing pathway by FOXM1 blocks stress ligand-dependent antitumor immunity and immune memory. *Nature communications*, 16(1), 3967.

Kogai H, et al. (2025) Broad-Spectrum Efficacy of CEACAM6-Targeted Antibody-Drug Conjugate with BET Protein Degradator in Colorectal, Lung, and Breast Cancer Mouse Models. *Molecular cancer therapeutics*, 24(3), 392.

Cai D, et al. (2025) Personalized risk stratification in colorectal cancer via PIANOS system. *Nature communications*, 16(1), 6561.

Gregory RC, et al. (2025) In Situ Proinflammatory Effects of Dazostinag Alone or with Chemotherapy on the Tumor Microenvironment of Patients with Head and Neck Squamous Cell Carcinoma. *Cancer research communications*, 5(7), 1243.

Sun M, et al. (2025) Transcriptome combined with Mendelian randomization to identify key genes related to polyamine metabolism in childhood obesity and elucidate their molecular regulatory mechanisms. *Scientific reports*, 15(1), 17799.

Lee LH, et al. (2025) Defining Non-small Cell Lung Cancer Tumor Microenvironment Changes at Primary and Acquired Immune Checkpoint Inhibitor Resistance Using Clinical and Real-World Data. *Cancer research communications*, 5(6), 1049.

Liu XF, et al. (2025) Tumor-infiltrated double-negative regulatory T cells predict outcome of T cell-based immunotherapy in nasopharyngeal carcinoma. *Cell reports. Medicine*, 6(5), 102096.

Yuan Y, et al. (2025) Stemness-associated WNT3A and EDN3 as key regulators of tumor progression and immunotherapy efficacy in LUAD. *International journal of surgery (London, England)*, 111(11), 7886.

Zhao Q, et al. (2025) Feasibility of machine learning-based modeling and prediction to assess osteosarcoma outcomes. *Scientific reports*, 15(1), 17386.

Gaertner Z, et al. (2025) Molecular and spatial transcriptomic classification of midbrain dopamine neurons and their alterations in a LRRK2G2019S model of Parkinson's disease. *eLife*, 13.

Rask GC, et al. (2025) Seclidemstat (SP-2577) Induces Transcriptomic Reprogramming and Cytotoxicity in Multiple Fusion-Positive Sarcomas. *Cancer research communications*, 5(9), 1584.

Wang T, et al. (2025) Prognostic value of a circadian rhythm-related gene signature in breast cancer patients: A retrospective cohort study. *Medicine*, 104(33), e43882.

Wu P, et al. (2025) Machine learning derived development and validation of extracellular matrix related signature for predicting prognosis in adolescents and young adults glioma. *Scientific reports*, 15(1), 28926.