

Resource Summary Report

Generated by [dkNET](#) on Aug 11, 2026

DSigDB

RRID:SCR_026202

Type: Tool

Proper Citation

DSigDB (RRID:SCR_026202)

Resource Information

URL: <https://dsigdb.tanlab.org/DSigDBv1.0/>

Proper Citation: DSigDB (RRID:SCR_026202)

Description: Online database provides collection of gene sets based on quantitative inhibition and/or drug-induced gene expression changes data of drugs and compounds. Allows users to search, view and download drugs/compounds and gene sets.

Synonyms: , Drug Signatures Database, drug SIGnatures DataBase

Resource Type: data or information resource, database

Defining Citation: [PMID:25990557](#)

Keywords: gene sets, quantitative inhibition, drug induced, gene expression changes, data, drugs, compounds,

Funding: NCI P30CA046934;
NCI P50CA058187

Availability: Free, Freely available,

Resource Name: DSigDB

Resource ID: SCR_026202

Record Creation Time: 20241220T053316+0000

Record Last Update: 20260811T043804+0000

Ratings and Alerts

No rating or validation information has been found for DSigDB.

No alerts have been found for DSigDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 165 mentions in open access literature.

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

Wu T, et al. (2026) Integrated WGCNA of lncRNA-mRNA Networks Identifies Novel Hub Genes and Potential Therapeutic Agents for Liver Cirrhosis via Molecular Docking Validation. International journal of molecular sciences, 27(3).

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

Zhang Y, et al. (2026) Biomarkers associated with Hashimoto's thyroiditis induced by viral infection: An integrative bioinformatics and machine learning. Journal of translational autoimmunity, 12, 100302.

Cui Z, et al. (2026) Expression profile of GSDMB in oral squamous cell carcinoma and its impact on tumor immune microenvironment and prognosis. BMC oral health, 26(1).

Shan B, et al. (2026) Identification of the biomarkers associated with lipid metabolism and endoplasmic reticulum stress in pediatric sepsis through bioinformatics analysis and quantitative reverse transcriptase PCR (qRT-PCR) assay. European journal of medical research, 31(1).

Peng X, et al. (2026) Integrating bulk and single-cell RNA sequencing identifies and validates lactylation-related signatures in diabetic foot ulcers. Scientific reports, 16(1).

Lou S, et al. (2026) Integrated Genome-wide Association and Single-cell Transcriptomic Analysis Identifies OAT as Therapeutic Targets for Periodontitis. Inflammation, 49(1).

Zhang X, et al. (2026) From Single-Cell Clusters to Causality: ITCH Engagement for CKD Uncovered by Integrative Analysis of MR and MAGMA. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(6), e71469.

Chen J, et al. (2026) Identification of potential biomarkers related to mannose metabolism in keloids: analysis of integrated bulk RNA-seq and scRNA-seq. Frontiers in immunology, 17, 1711588.

Li X, et al. (2026) F2R and MXRA5: the metabolic obesity-derived biomarkers for immunosuppression and poor survival in triple-negative breast cancer. Discover oncology, 17(1).

Li X, et al. (2026) Identification and Validation of FOXP1-Related Biomarkers in Diabetic Retinopathy. International journal of general medicine, 19, 581708.

Li J, et al. (2026) Macrophage Polarization-Related Biomarkers in Epilepsy: Integrated Bioinformatics Analysis and Clinical Validation. *Journal of inflammation research*, 19, 581430.

Guo QH, et al. (2026) Identification of biomarkers related to amino acid metabolism in nonobstructive azoospermia by bioinformatics. *Medicine*, 105(18), e48183.

Hu Y, et al. (2026) Integrative multi-omics analyses identify key genes and elucidate bidirectional regulatory mechanisms in thyroid dysfunction. *PloS one*, 21(1), e0338805.

Li N, et al. (2026) Exploration of m7G-related immune genes and construction of a prognostic risk model in gastric cancer. *Scientific reports*, 16(1).

Luo T, et al. (2026) The Mechanism of Gut Microbiota in Breast Cancer Based on the Bulk Transcriptome, Mendelian Randomization Analysis and Single Cell RNA Sequencing. *MicrobiologyOpen*, 15(2), e70284.

Liu H, et al. (2026) Development and validation of a prognosis model for low-grade gliomas based on metabolic gene risk scoring and immune microenvironment interaction. *Discover oncology*, 17(1).

Chen Y, et al. (2026) Identification of DHX58 as a potential therapeutic target for ovarian cancer through multi-omics Mendelian randomization and transcriptomic data analysis. *Journal of ovarian research*, 19(1).

Weng X, et al. (2026) Identification of COL5A1 and TGFBI as key basement membrane genes and their molecular mechanisms in gestational diabetes mellitus. *Medicine*, 105(18), e48610.

Wang W, et al. (2026) Ubiquitination-driven fibroblast dysfunction: a multi-omics blueprint for precision diagnosis and therapy in diabetic foot ulcer. *Scientific reports*, 16(1).