

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

DGIdb

RRID:SCR_006608

Type: Tool

Proper Citation

DGIdb (RRID:SCR_006608)

Resource Information

URL: <http://dgidb.genome.wustl.edu/>

Proper Citation: DGIdb (RRID:SCR_006608)

Description: A database of drug-gene relationships that provides drug-gene interactions and potential druggability data given list of genes. There are about 15 data sources that are being aggregated by DGIdb, with update date and these data sources are listed on this page: <http://dgidb.genome.wustl.edu/sources>, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: DGIdb

Synonyms: Drug-Gene Interaction database, Drug Gene Interaction Database

Resource Type: data or information resource, data access protocol, database, software resource, application programming interface

Defining Citation: [PMID:24122041](#)

Keywords: drug, gene, interaction, bio.tools, FASEB list

Related Condition: Cancer

Funding: NHGRI U54 HG003079

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DGIdb

Resource ID: SCR_006608

Alternate IDs: nlx_155686, biotools:DGIdb, OMICS_01579

Alternate URLs: <https://bio.tools/DGIdb>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260801T190313+0000

Ratings and Alerts

No rating or validation information has been found for DGIdb.

No alerts have been found for DGIdb.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 353 mentions in open access literature.

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

Cao Z, et al. (2026) Study on the mechanism of PSENEN in modulating cisplatin resistance in NSCLC through stromal cell interactions. International immunopharmacology, 169, 116037.

Müller D, et al. (2025) EpigenPlot: An interactive web platform for DNA methylation-based biomarker and drug target discovery in colorectal cancer. British journal of pharmacology, 182(7), 1452.

Alfaro-García JP, et al. (2025) Characterization of the Temporal Dynamics of the Endothelial-Mesenchymal-like Transition Induced by Soluble Factors from Dengue Virus Infection in Microvascular Endothelial Cells. International journal of molecular sciences, 26(5).

Chen Y, et al. (2025) A Machine Learning-Based Strategy Predicts Selective and Synergistic Drug Combinations for Relapsed Acute Myeloid Leukemia. Cancer research, 85(14), 2753.

Zhang J, et al. (2025) Integrated bioinformatics analysis of the effects of chronic pain on patients with spinal cord injury. Frontiers in cellular neuroscience, 19, 1457740.

Ma Y, et al. (2025) Systematic dissection of pleiotropic loci and critical regulons in excitatory neurons and microglia relevant to neuropsychiatric and ocular diseases. Translational psychiatry, 15(1), 24.

Fang Q, et al. (2025) Identification of differentially expressed immune-related genes in patients with systemic lupus erythematosus and the development of a hub gene-based diagnostic model. European journal of medical research, 30(1), 689.

Zhao C, et al. (2025) Identification of cell adhesion related signature for molecular subtyping and prognostic prediction in acute myeloid leukemia. Discover oncology, 16(1),

Li N, et al. (2025) Analyses of the mechanism and therapeutic targets of senescence related genes in ischemic stroke with multi-omics approach. *Scientific reports*, 15(1), 26178.

Li J, et al. (2025) Identification of four key genes related to the diagnosis of chronic obstructive pulmonary disease using bioinformatics analysis. *Frontiers in genetics*, 16, 1499996.

Wang S, et al. (2025) Bioinformatics analysis of genes associated with disulfidptosis in spinal cord injury. *PloS one*, 20(2), e0318016.

Xu S, et al. (2025) Identification of telomere-related diagnostic markers in osteoarthritis based on bioinformatics analysis and machine learning. *The Korean journal of physiology & pharmacology : official journal of the Korean Physiological Society and the Korean Society of Pharmacology*, 29(3), 359.

Zhang T, et al. (2025) Copper Metabolism-Related Genes as Biomarkers in Colon Adenoma and Cancer. *International journal of general medicine*, 18, 3021.

Zhou X, et al. (2025) The working mechanism of biomarkers related to sumoylation modification in coronary artery disease. *Scientific reports*, 15(1), 17055.

Vasquez YA, et al. (2025) Comparative analysis of RNA expression identifies effective targeted drug in myoepithelial carcinoma. *NPJ precision oncology*, 9(1), 145.

Liu Y, et al. (2025) Development and validation of a multiple myeloma diagnostic model based on systemic lupus erythematosus-associated genes and identification of specific genes. *Discover oncology*, 16(1), 803.

Lyu G, et al. (2025) Integrative Analysis of Cuproptosis-Related Mitochondrial Depolarisation Genes for Prognostic Prediction in Non-Small Cell Lung Cancer. *Journal of cellular and molecular medicine*, 29(4), e70438.

Zhang G, et al. (2025) Uncovering Candidate Genes Associated with Cardiovascular Disease in Patients with Arteriovenous Fistula and End-Stage Renal Disease. *Cardiorenal medicine*, 15(1), 386.

Teixeira LCR, et al. (2025) Common miRNAs, Genes, and Regulatory Pathways in Alzheimer's Disease and Type 2 Diabetes Mellitus: An Integrative Analysis of Systematic Reviews, Bioinformatics and Data Mining. *Journal of neurochemistry*, 169(8), e70196.

Yukui T, et al. (2025) Utilising bioinformatics and molecular docking technology to explore the underlying mechanisms of intervertebral disc degeneration with potential therapeutic drugs and formulas. *Journal of global health*, 15, 04298.