Resource Summary Report

Generated by ASWG on Aug 4, 2026

LINCS Connectivity Map

RRID:SCR_002639
Type: Tool

Proper Citation

LINCS Connectivity Map (RRID:SCR_002639)

Resource Information

URL: http://lincscloud.org/

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Description: A catalog of gene-expression data collected from human cells treated with chemical compounds and genetic reagents. Computational methods to reduce the number of necessary genomic measurements along with streamlined methodologies enable the current effort to significantly increase the size of the CMap database and along with it, our potential to connect human diseases with the genes that underlie them and the drugs that treat them. The NIH has funded a large expansion of the Connectivity Map dataset through the Library of Integrated Network-based Cellular Signatures (LINCS). The Broad Institute's LINCS center aims to create a first installment of data generation and analysis for the LINCS program. Through these data LINCS intends to accelerate the discovery process by systematically revealing connections between genes/compounds discovered in screens and molecular pathways that underlie disease states.

Abbreviations: CMap

Synonyms: Connectivity Map

Resource Type: data or information resource, database

Defining Citation: PMID:28069634

Keywords: functional genomics, gene, cell, gene expression, compound, molecule, pathway, disease, perturbagen, gene expression profile, genetic, cellular, chemical reagent, FASEB list

Funding: NIH Common Fund

Availability: Free, Freely available

Resource Name: LINCS Connectivity Map

Resource ID: SCR_002639

Alternate IDs: nlx_156066

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260804T043156+0000

Ratings and Alerts

No rating or validation information has been found for LINCS Connectivity Map.

No alerts have been found for LINCS Connectivity Map.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 637 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Zhu Y, et al. (2025) NIPAL1 as a prognostic biomarker associated with pancreatic adenocarcinoma progression and immune infiltration. BMC cancer, 25(1), 165.

Lindell E, et al. (2025) Identification of a small molecule targeting EPLIN as a novel strategy for the treatment of pediatric neuroblastoma and medulloblastoma. Cell death & disease, 16(1), 554.

Liu YY, et al. (2025) Elevated KIF2C Expression Drives Osteosarcoma Progression by Modulating the Wnt/?-Catenin Signaling Pathway and Contributing to an Immunosuppressive Tumor Microenvironment. Cancer medicine, 14(9), e70915.

Yin H, et al. (2025) Improved VPS4B O-GlcNAc modification triggers lipid droplets transferring from adipocytes to nasopharyngeal carcinoma cells. Cancer & metabolism, 13(1), 24.

Tang X, et al. (2025) Single-cell multi-omics analysis reveals cancer regulatory elements of transcriptional programs and clinical implications. Cell death & disease, 16(1), 746.

Zheng X, et al. (2025) Integrative analyses of mendelian randomization and bioinformatics reveal casual relationship and genetic links between COVID-19 and knee osteoarthritis. BMC medical genomics, 18(1), 2.

Xia J, et al. (2025) BDNF is a prognostic biomarker involved in the immune infiltration of lung adenocarcinoma and associated with programmed cell death. Oncology letters, 29(4), 191.

Shen G, et al. (2025) HSP90 co-regulates the formation and nuclear distribution of the glycolytic output complex to promote resistance and poor prognosis in gastric cancer patients. Journal of translational medicine, 23(1), 172.

López-Tejada A, et al. (2025) Signature-based repurposed drugs resemble the inhibition of TGF?-induced NDRG1 as potential therapeutics for triple-negative breast cancer. International journal of biological sciences, 21(9), 3949.

Suleiman M, et al. (2025) Functional recovery of islet ? cells in human type 2 diabetes: Transcriptome signatures unveil therapeutic approaches. Science advances, 11(41), eads2905.

Yin T, et al. (2025) A Novel Immune-Related Three-Gene Signature and Immune Infiltration Insights in Psoriasis and Chronic Kidney Disease. Clinical, cosmetic and investigational dermatology, 18, 267.

Yin T, et al. (2025) Immune-related hub genes and their role in psoriasis pathogenesis. Scientific reports, 15(1), 17765.

Tyler AL, et al. (2025) Transcripts with high distal heritability mediate genetic effects on complex metabolic traits. Nature communications, 16(1), 5507.

He W, et al. (2025) Comprehensive analysis of the leukocyte immunoglobulin-like receptor family in clear cell renal cell carcinoma. Annals of medicine, 57(1), 2546684.

Wang Z, et al. (2025) Development of immune-derived molecular markers for preeclampsia based on multiple machine learning algorithms. Scientific reports, 15(1), 1767.

Zhao J, et al. (2025) Identification of gene signatures associated with lactation for predicting prognosis and treatment response in breast cancer patients through machine learning. Scientific reports, 15(1), 13575.

Zatorski N, et al. (2024) Structural analysis of genomic and proteomic signatures reveal dynamic expression of intrinsically disordered regions in breast cancer. iScience, 27(9), 110640.

Zhou J, et al. (2024) Identification and validation of a glycosyltransferase gene signature as a novel prognostic model for lung adenocarcinoma. Heliyon, 10(8), e29383.

Zhang C, et al. (2024) Ferroptosis-related gene signature for predicting prognosis and identifying potential therapeutic drug in EGFR wild-type lung adenocarcinoma. Communications biology, 7(1), 1416.

Howard JN, et al. (2024) Isotretinoin promotes elimination of translation-competent HIV latent reservoirs in CD4T cells. PLoS pathogens, 20(10), e1012601.