Resource Summary Report

Generated by RRID on Sep 10, 2026

LINCS Connectivity Map

RRID:SCR_002639
Type: Tool

Proper Citation

LINCS Connectivity Map (RRID:SCR_002639)

Resource Information

URL: http://lincscloud.org/

Proper Citation: LINCS Connectivity Map (RRID:SCR_002639)

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: 20260905T133118+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 650 mentions in open access literature.

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

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.

Projahn E, et al. (2026) Multicondition expression profiling reveals limitations of canonical housekeeping genes. BMC genomics, 27(1), 214.

Song L, et al. (2026) Identification of hypoxia-related gene signatures and molecular subtypes in chronic rhinosinusitis with nasal polyps. Brazilian journal of otorhinolaryngology, 92(3), 101788.

Daghar H, et al. (2026) CHK1 inhibition rescues abnormal glycogen buildup in a Caenorhabditis elegans model for glycogen storage disease III. Communications biology, 9(1), 257.

Li C, et al. (2026) Molecular decoupling of lineage identity and morphology in aggressive variant prostate cancer. medRxiv : the preprint server for health sciences.

Dammer EB, et al. (2026) Plasma Proteomic Analysis of APOE ?4 Homozygotes Identifies Preclinical Alzheimer's Disease Alterations Potentially Treatable with Semaglutide. medRxiv : the preprint server for health sciences.

Wang H, et al. (2026) Development of immune-derived molecular markers for coronary heart disease via multimachine learning. iScience, 29(3), 114853.

Zhang Q, et al. (2026) Genome-wide investigation highlights global and local pleiotropy linking neurodevelopmental disorders to acquired hearing problems. Psychological medicine, 56, e32.

Flouda S, et al. (2026) Peripheral blood transcriptomic analysis of patients with rheumatoid arthritis associated interstitial lung disease reveals: distinct molecular signature with evidence of humoral and myeloid immunity. Arthritis research & therapy, 28(1).

Gan L, et al. (2026) Integrated transcriptomic identification and validation reveal key autophagy-associated biomarkers in sleep deprivation. PeerJ, 14, e21426.

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.

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.

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.

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

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.

Cote AC, et al. (2025) A computational genetic- and transcriptomics-based study nominates drug repurposing candidates for the treatment of chronic pain. EBioMedicine, 122, 106022.

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.

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.

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.

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.