# Resource Summary Report

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## 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:** database, data or information resource

**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

**Resource Name:** LINCS Connectivity Map

**Resource ID:** SCR_002639

**Alternate IDs:** nlx_156066

**Record Creation Time:** 20220129T080214+0000

**Record Last Update:** 20250519T204636+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 559 mentions in open access literature.

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

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.

Thaiparambil J, et al. (2023) Integrative metabolomics and transcriptomics analysis reveals novel therapeutic vulnerabilities in lung cancer. Cancer medicine, 12(1), 584.

Liang XZ, et al. (2023) IRF8 and its related molecules as potential diagnostic biomarkers or therapeutic candidates and immune cell infiltration characteristics in steroid-induced osteonecrosis of the femoral head. Journal of orthopaedic surgery and research, 18(1), 27.

Wang J, et al. (2023) Genomic, epigenomic, and transcriptomic signatures for telomerase complex components: a pan-cancer analysis. Molecular oncology, 17(1), 150.

Agrawal P, et al. (2023) Network-based approach elucidates critical genes in BRCA subtypes and chemotherapy response in Triple Negative Breast Cancer. bioRxiv : the preprint server for biology.

Gui CP, et al. (2023) Single-cell and spatial transcriptomics reveal 5-methylcytosine RNA methylation regulators immunologically reprograms tumor microenvironment

characterizations, immunotherapy response and precision treatment of clear cell renal cell carcinoma. Translational oncology, 35, 101726.

Wu C, et al. (2023) Comprehensive analysis of ferroptosis-related hub gene signatures as a potential pathogenesis and therapeutic target for systemic sclerosis: A bioinformatics analysis. International journal of immunopathology and pharmacology, 37, 3946320231187783.

Liu H, et al. (2023) Depiction of neuroendocrine features associated with immunotherapy response using a novel one-class predictor in lung adenocarcinoma. Discover. Oncology, 14(1), 71.

Khunsriraksakul C, et al. (2023) Multi-ancestry and multi-trait genome-wide association meta-analyses inform clinical risk prediction for systemic lupus erythematosus. Nature communications, 14(1), 668.

Chen Z, et al. (2023) Comprehensive analyses indicated the association between m6A related long non-coding RNAs and various pathways in glioma. Cancer medicine, 12(1), 760.

Fan K, et al. (2023) EZH2 as a prognostic-related biomarker in lung adenocarcinoma correlating with cell cycle and immune infiltrates. BMC bioinformatics, 24(1), 149.

Zhou Q, et al. (2023) Screening Key Pathogenic Genes and Small Molecule Compounds for PNET. Journal of pediatric hematology/oncology, 45(2), e180.

Zhou Y, et al. (2023) 5-methyladenosine regulators play a crucial role in development of chronic hypersensitivity pneumonitis and idiopathic pulmonary fibrosis. Scientific reports, 13(1), 5941.

Cao L, et al. (2023) Development and validation of an RBP gene signature for prognosis prediction in colorectal cancer based on WGCNA. Hereditas, 160(1), 10.

Jin L, et al. (2023) Osteoarthritis related epigenetic variations in miRNA expression and DNA methylation. BMC medical genomics, 16(1), 163.

Bakker MK, et al. (2023) Anti-Epileptic Drug Target Perturbation and Intracranial Aneurysm Risk: Mendelian Randomization and Colocalization Study. Stroke, 54(1), 208.

Tu Z, et al. (2023) The cell senescence regulator p16 is a promising cancer prognostic and immune check-point inhibitor (ICI) therapy biomarker. Aging, 15(6), 2136.

Zheng T, et al. (2023) The mechanism of the Nfe2l2/Hmox1 signaling pathway in ferroptosis regulation in acute compartment syndrome. Journal of biochemical and molecular toxicology, 37(1), e23228.

Yu J, et al. (2023) Single-cell transcriptome reveals Staphylococcus aureus modulating fibroblast differentiation in the bone-implant interface. Molecular medicine (Cambridge, Mass.), 29(1), 35.

Zhou Q, et al. (2023) Cancer functional states-based molecular subtypes of gastric cancer.

Journal of translational medicine, 21(1), 80.