Resource Summary Report

Generated by T1D on Jul 29, 2026

LINCS Project

RRID:SCR_016486
Type: Tool

Proper Citation

LINCS Project (RRID:SCR_016486)

Resource Information

URL: http://www.lincsproject.org/

Proper Citation: LINCS Project (RRID:SCR_016486)

Description: Project to create network based understanding of biology by cataloging changes in gene expression and other cellular processes when cells are exposed to genetic and environmental stressors. Program to develop therapies that might restore pathways and networks to their normal states. Has LINCS Data Coordination and Integration Center and six Data and Signature Generation Centers: Drug Toxicity Signature Generation Center, HMS LINCS Center, LINCS Center for Transcriptomics, LINCS Proteomic Characterization Center for Signaling and Epigenetics, MEP LINCS Center, and NeuroLINCS Center.

Abbreviations: LINCS

Synonyms: LINCS, Library of Integrated Network based Cellular Signatures, LINCS Program

Resource Type: data or information resource, organization portal, project portal, database, consortium, portal

Defining Citation: PMID:29199020

Keywords: data integration, network biology, gene expression, L1000, MCF10A, MEMA, P100, LINCS program, LINCS project, systems biology, systems pharmacology, FASEB list

Related Condition: cancer, heart disease, neurodegenerative disorder

Funding: NIH Common Fund ;
NHLBI U54 HL127624;
NHLBI U54 HL127366;
NHLBI U54 HL127365;

NHGRI U54 HG008100;
NHGRI U54 HG008097;
NHGRI U54 HG008098;
NINDS U54 NS091046

Availability: Free, Freely available

Resource Name: LINCS Project

Resource ID: SCR_016486

Alternate IDs: SCR_016487

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260729T044419+0000

Ratings and Alerts

No rating or validation information has been found for LINCS Project.

No alerts have been found for LINCS Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Yuan M, et al. (2025) HAPIR: a refined Hallmark gene set-based machine learning approach for predicting immunotherapy response in cancer patients. NPJ precision oncology, 9(1), 194.

Han Y, et al. (2025) Identifying an optimal perturbation to induce a desired cell state by generative deep learning. Cell systems, 101405.

Chaib S, et al. (2024) The efficacy of chemotherapy is limited by intratumoral senescent cells expressing PD-L2. Nature cancer, 5(3), 448.

Iida M, et al. (2024) A network-based trans-omics approach for predicting synergistic drug combinations. Communications medicine, 4(1), 154.

Liu D, et al. (2024) Predictive biomarkers for response to TGF- ? inhibition in resensitizing chemo(radiated) esophageal adenocarcinoma. Pharmacological research, 207, 107315.

Pognan F, et al. (2023) The evolving role of investigative toxicology in the pharmaceutical industry. Nature reviews. Drug discovery, 22(4), 317.

Parra-Rivas LA, et al. (2023) Serine-129 phosphorylation of ?-synuclein is an activity-dependent trigger for physiologic protein-protein interactions and synaptic function. Neuron, 111(24), 4006.

Iwata M, et al. (2022) Regulome-based characterization of drug activity across the human diseasome. NPJ systems biology and applications, 8(1), 44.

Namba S, et al. (2022) From drug repositioning to target repositioning: prediction of therapeutic targets using genetically perturbed transcriptomic signatures. Bioinformatics (Oxford, England), 38(Suppl 1), i68.

Iwata M, et al. (2022) Pathway trajectory analysis with tensor imputation reveals drug-induced single-cell transcriptomic landscape. Nature computational science, 2(11), 758.

Lu L, et al. (2022) Recent computational drug repositioning strategies against SARS-CoV-2. Computational and structural biotechnology journal, 20, 5713.

Fustero-Torre C, et al. (2021) Beyondcell: targeting cancer therapeutic heterogeneity in single-cell RNA-seq data. Genome medicine, 13(1), 187.

Sinkala M, et al. (2021) Integrated molecular characterisation of the MAPK pathways in human cancers reveals pharmacologically vulnerable mutations and gene dependencies. Communications biology, 4(1), 9.

Stanfill AG, et al. (2021) Enhancing Research Through the Use of the Genotype-Tissue Expression (GTEx) Database. Biological research for nursing, 23(3), 533.

He B, et al. (2021) A Review of Current In Silico Methods for Repositioning Drugs and Chemical Compounds. Frontiers in oncology, 11, 711225.

Han L, et al. (2021) Modeling drug response using network-based personalized treatment prediction (NetPTP) with applications to inflammatory bowel disease. PLoS computational biology, 17(2), e1008631.

Liu Z, et al. (2021) Unraveling Gene Fusions for Drug Repositioning in High-Risk Neuroblastoma. Frontiers in pharmacology, 12, 608778.

Mapelli SN, et al. (2020) A Novel Prostate Cell Type-Specific Gene Signature to Interrogate Prostate Tumor Differentiation Status and Monitor Therapeutic Response (Running Title: Phenotypic Classification of Prostate Tumors). Cancers, 12(1).

Kunc V, et al. (2020) On tower and checkerboard neural network architectures for gene expression inference. BMC genomics, 21(Suppl 5), 454.

Liu K, et al. (2020) Broad-Spectrum Profiling of Drug Safety via Learning Complex Network. Clinical pharmacology and therapeutics, 107(6), 1373.