

Resource Summary Report

Generated by [ASWG](#) on Aug 26, 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: consortium, data or information resource, database, organization portal, portal, project 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: NHGRI U54 HG008097;
NHGRI U54 HG008098;
NHGRI U54 HG008100;
NHLBI U54 HL127365;

NHLBI U54 HL127366;
NHLBI U54 HL127624;
NIH Common Fund ;
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: 20260821T194105+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 56 mentions in open access literature.

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

Chen R, et al. (2026) Pathogenomic analysis reveals clinically relevant epithelial-mesenchymal plasticity in esophageal squamous cell carcinoma. Theranostics, 16(7), 3870.

Baxter LL, et al. (2026) Anti-inflammatory and pro-proliferative effects of fasudil in human trisomy 21 neural progenitor cells. bioRxiv : the preprint server for biology.

Liu H, et al. (2026) Single-Cell Computational Frameworks for Quantifying BET Bromodomain Inhibitor Resistance and Screening Re-Sensitizer Drugs in Triple-Negative Breast Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(29), e13246.

Sanchez-Michael LA, et al. (2025) Functional Characterization of VS-186B, a Novel HDAC Inhibitor with Anticancer Activity. International journal of molecular sciences, 26(23).

Zhou Q, et al. (2025) Vorapaxar enhanced mitochondria-associated ferroptosis primes cancer immunotherapy via targeting FOXO1/HMOX1 axis. Cell reports. Medicine, 102371.

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.

Costa MC, et al. (2024) Identification of therapeutic targets in osteoarthritis by combining heterogeneous transcriptional datasets, drug-induced expression profiles, and known drug-target interactions. Journal of translational medicine, 22(1), 281.

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

Cioce M, et al. (2023) Interrogating colorectal cancer metastasis to liver: a search for clinically viable compounds and mechanistic insights in colorectal cancer Patient Derived Organoids. Journal of experimental & clinical cancer research : CR, 42(1), 170.

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 α -synuclein is an activity-dependent trigger for physiologic protein-protein interactions and synaptic function. Neuron, 111(24), 4006.

Chakraborty R, et al. (2022) In-silico screening and in-vitro assay show the antiviral effect of Indomethacin against SARS-CoV-2. Computers in biology and medicine, 147, 105788.

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.

Abdelsayed M, et al. (2022) Repurposing drugs to treat cardiovascular disease in the era of precision medicine. Nature reviews. Cardiology, 19(11), 751.

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

Zauner R, et al. (2022) Transcriptome-Guided Drug Repurposing for Aggressive SCCs. International journal of molecular sciences, 23(2).