

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

LINCS Data Portal

RRID:SCR_014939

Type: Tool

Proper Citation

LINCS Data Portal (RRID:SCR_014939)

Resource Information

URL: <http://lincsportal.ccs.miami.edu/dcic-portal/>

Proper Citation: LINCS Data Portal (RRID:SCR_014939)

Description: Portal which provides a unified interface for searching LINCS dataset packages and reagents. Users can use the portal to access datasets, small molecules, cells, genes, proteins and peptides, and antibodies.

Resource Type: data or information resource, portal

Keywords: portal, assay, lincs, kinome, dataset, small molecule, cell, gene, protein, peptide, and antibodies.

Funding: NIH Common Fund ;
NHLBI 1U01HL111561;
NHLBI 3U01HL111561-01S1;
NHLBI 3U01HL111561-02S1;
NHGRI U54HG006097;
NHGRI U54 HG006093

Availability: Freely available

Resource Name: LINCS Data Portal

Resource ID: SCR_014939

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260905T133050+0000

Ratings and Alerts

No rating or validation information has been found for LINCS Data Portal.

No alerts have been found for LINCS Data Portal.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Zhang M, et al. (2026) A self-adaptive and versatile tool for eliminating multiple undesirable variations from large-scale transcriptomes. *Nature biomedical engineering*, 10(3), 413.

Thorman AW, et al. (2024) Accelerating drug discovery and repurposing by combining transcriptional signature connectivity with docking. *Science advances*, 10(35), eadj3010.

Xiong Y, et al. (2022) Proteomic cellular signatures of kinase inhibitor-induced cardiotoxicity. *Scientific data*, 9(1), 18.

Wang LB, et al. (2021) Proteogenomic and metabolomic characterization of human glioblastoma. *Cancer cell*, 39(4), 509.

, et al. (2021) An integrated multi-omic analysis of iPSC-derived motor neurons from C9ORF72 ALS patients. *iScience*, 24(11), 103221.

van Hasselt JGC, et al. (2020) Transcriptomic profiling of human cardiac cells predicts protein kinase inhibitor-associated cardiotoxicity. *Nature communications*, 11(1), 4809.

Finkelstein J, et al. (2020) Informatics Approaches for Harmonized Intelligent Integration of Stem Cell Research. *Stem cells and cloning : advances and applications*, 13, 1.

Dhruba SR, et al. (2019) Recursive model for dose-time responses in pharmacological studies. *BMC bioinformatics*, 20(Suppl 12), 317.

Lee H, et al. (2019) Comparison of Target Features for Predicting Drug-Target Interactions by Deep Neural Network Based on Large-Scale Drug-Induced Transcriptome Data. *Pharmaceutics*, 11(8).

Rigden DJ, et al. (2018) The 2018 Nucleic Acids Research database issue and the online molecular biology database collection. *Nucleic acids research*, 46(D1), D1.

Stathias V, et al. (2018) Sustainable data and metadata management at the BD2K-LINCS Data Coordination and Integration Center. *Scientific data*, 5, 180117.

Koleti A, et al. (2018) Data Portal for the Library of Integrated Network-based Cellular Signatures (LINCS) program: integrated access to diverse large-scale cellular perturbation response data. *Nucleic acids research*, 46(D1), D558.

Ong E, et al. (2017) Ontological representation, integration, and analysis of LINCS cell line cells and their cellular responses. *BMC bioinformatics*, 18(Suppl 17), 556.

Xiong Y, et al. (2017) A Comparison of mRNA Sequencing with Random Primed and 3'-Directed Libraries. *Scientific reports*, 7(1), 14626.