Resource Summary Report

Generated by NIF on May 13, 2025

L1000 Characteristic Direction Signature Search Engine

RRID:SCR_016177
Type: Tool

Proper Citation

L1000 Characteristic Direction Signature Search Engine (RRID:SCR_016177)

Resource Information

URL: http://amp.pharm.mssm.edu/L1000CDS2

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Description: LINCS L1000 characteristic direction signatures search engine. Software tool to find consensus signatures that match user’s input gene lists or input signatures. Underlying dataset is LINCS L1000 small molecule expression profiles generated at Broad Institute by Connectivity Map team. Differentially expressed genes of these profiles were calculated using multivariate method called Characteristic Direction.

Abbreviations: L1000CDS2

Resource Type: web service, software resource, data set, data or information resource, data access protocol, service resource, database

Defining Citation: PMID:28413689

Keywords: signature, gene, dataset, ligand, characteristic, expression, benchmark

Funding: NHLBI U54 HL127624;
NCI U54 CA189201

Availability: Free, Freely available

Resource Name: L1000 Characteristic Direction Signature Search Engine

Resource ID: SCR_016177

Record Creation Time: 20220129T080329+0000

Record Last Update: 20250513T061734+0000

Ratings and Alerts

No rating or validation information has been found for L1000 Characteristic Direction Signature Search Engine.

No alerts have been found for L1000 Characteristic Direction Signature Search Engine.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Saez-Atienzar S, et al. (2024) Mechanism-free repurposing of drugs for C9orf72-related ALS/FTD using large-scale genomic data. Cell genomics, 4(11), 100679.

Adhikary U, et al. (2023) Targeting MCL-1 triggers DNA damage and an anti-proliferative response independent from apoptosis induction. Cell reports, 42(10), 113176.

Ghiasvand S, et al. (2021) Transcriptome analysis evinces anti-neoplastic mechanisms of hypericin: A study on U87 glioblastoma cell line. Life sciences, 266, 118874.

Lee JY, et al. (2020) Integrating Differential Gene Expression Analysis with Perturbagen-Response Signatures May Identify Novel Therapies for Thyroid-Associated Orbitopathy. Translational vision science & technology, 9(9), 39.

Ávalos-Moreno M, et al. (2020) Drug Repurposing for Triple-Negative Breast Cancer. Journal of personalized medicine, 10(4).

Koppelstaetter C, et al. (2019) Computational Drug Screening Identifies Compounds Targeting Renal Age-associated Molecular Profiles. Computational and structural biotechnology journal, 17, 843.

Keenan AB, et al. (2018) The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell systems, 6(1), 13.

Liu TP, et al. (2018) Systematic polypharmacology and drug repurposing via an integrated L1000-based Connectivity Map database mining. Royal Society open science, 5(11), 181321.