

# Resource Summary Report

Generated by [NIF](#) on Sep 4, 2026

## SigCom LINCS

RRID:SCR\_022275

Type: Tool

---

### Proper Citation

SigCom LINCS (RRID:SCR\_022275)

---

### Resource Information

**URL:** <https://maayanlab.cloud/sigcom-lincs>

**Proper Citation:** SigCom LINCS (RRID:SCR\_022275)

**Description:** Web server that serves over million gene expression signatures processed, analyzed, and visualized from LINCS, GTEx, and GEO. Data and metadata search engine for gene expression signatures.

**Synonyms:** SigCom Library of Integrated Network-based Cellular Signatures

**Resource Type:** data access protocol, software resource, web service

**Defining Citation:** [PMID:35524556](#)

**Keywords:** FAIR data, data and metadata search engine, gene expression signatures, gene expression signature processed, analyzed, and visualized, LINCS, GTEx, GEO, gene expression signatures,

**Funding:** NHLBI U54HL127624;  
NIDDK R01DK131525;  
NIH Office of the Director OT2OD030160

**Availability:** Free, Freely available

**Resource Name:** SigCom LINCS

**Resource ID:** SCR\_022275

**Alternate URLs:** <https://github.com/MaayanLab/sigcom-lincs>

**Record Creation Time:** 20220511T050132+0000

**Record Last Update:** 20260903T235822+0000

---

### Ratings and Alerts

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

No alerts have been found for SigCom LINCS.

---

## 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](#) .

Mersich I, et al. (2026) Multi-omic integration identifies broad drug resistance mechanisms and strategies to therapeutically reprogram cancer cells. *iScience*, 29(1), 114293.

Marino GB, et al. (2025) GeneSetCart: assembling, augmenting, combining, visualizing, and analyzing gene sets. *GigaScience*, 14.

Wu Q, et al. (2025) The reprogramming impact of SMAC-mimetic on glioblastoma stem cells and the immune tumor microenvironment evolution. *Journal of experimental & clinical cancer research : CR*, 44(1), 191.

Thu VTA, et al. (2025) Deciphering linezolid-induced hematologic toxicity: Targeting TOP2A and TOP2B via its primary metabolite PNU142586. *Science advances*, 11(22), eadt5833.

Tang T, et al. (2025) Epigenetic Profiling of Curcumin on Histone Signatures in Breast Cancer using 3D Network. *bioRxiv : the preprint server for biology*.

Oka I, et al. (2025) A feasibility of computational drug screening for Fuchs endothelial corneal dystrophy. *Scientific reports*, 15(1), 14665.

Lemay SE, et al. (2025) Unraveling AURKB as a potential therapeutic target in pulmonary hypertension using integrated transcriptomic analysis and pre-clinical studies. *Cell reports. Medicine*, 6(2), 101964.

Yang W, et al. (2024) Aging-related biomarkers for the diagnosis of Parkinson's disease based on bioinformatics analysis and machine learning. *Aging*, 16(17), 12191.