

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

CMap

RRID:SCR_016204

Type: Tool

Proper Citation

CMap (RRID:SCR_016204)

Resource Information

URL: <https://clue.io>

Proper Citation: CMap (RRID:SCR_016204)

Description: Dataset of cellular signatures that catalogs transcriptional responses of human cells to chemical and genetic perturbation. CMap contains perturbagens, expression signatures, and small molecules from cell lines.

Synonyms: LINCS CMap L1000, LINCS L1000, LINCS CMap, ConnectivityMap, Connectivity Map

Resource Type: data or information resource, data set, database, software resource, web application

Keywords: data, set, connectivity, gene, expression, database, heat map, drug, tool, perturbational, perturbagen, signature, bio.tools, FASEB list

Availability: Free for academic use, Subscription for commercial use, Available for download, Acknowledgement requested

Resource Name: CMap

Resource ID: SCR_016204

Alternate IDs: biotools:CMap

Alternate URLs: <https://bio.tools/CMap>

License: BSD 3-Clause License

License URLs: <https://clue.io/connectopedia/category/terms>

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260912T200018+0000

Ratings and Alerts

No rating or validation information has been found for CMap.

No alerts have been found for CMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 789 mentions in open access literature.

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

Chen Z, et al. (2026) Targeting TPX2-dependent lineage plasticity by CDK4/6 inhibition reverses therapy resistance in neuroendocrine bladder carcinoma. *Cell reports. Medicine*, 7(4), 102712.

Eriksson J, et al. (2026) Single-Cell Lineage Tracing Uncovers Resistance Signatures and Sensitizing Strategies to FLT3 Inhibitors in Acute Myeloid Leukemia. *Cancer research*, 86(7), 1724.

Zhang M, et al. (2026) Integrated transcriptomics and molecular docking identify hub genes and statin regulators in *Helicobacter pylori*-associated gastric mucosal pathogenesis. *Frontiers in cellular and infection microbiology*, 16, 1688009.

Zhang L, et al. (2026) Prognostic significance of calcium signaling-related genes in bladder cancer and the role of ATP2B4 in regulating mitochondrial calcium ion levels via the VDAC1/MCU pathway. *Frontiers in immunology*, 17, 1561666.

Lee EY, et al. (2026) Computational discovery of precision therapeutics for hidradenitis suppurativa. *bioRxiv : the preprint server for biology*.

Deisseroth CA, et al. (2026) Transcriptomic data and biomedical literature synergize in finding pharmacologic gene regulators. *bioRxiv : the preprint server for biology*.

Kim DW, et al. (2026) Defective autophagy in GNE myopathy is rescued by inhibition of noncanonical Akt-mTORC1 activation across multiple isogenic models. *Experimental & molecular medicine*, 58(4), 1187.

Zhou L, et al. (2026) WSTF-associated regulation of GLYCTK and metabolic adaptation in colorectal cancer. *Frontiers in immunology*, 17, 1819148.

Sun X, et al. (2026) Multi-Omics and network-based exploration of potential molecular pathways in heart failure relevant to left bundle branch pacing response heterogeneity: Immune remodeling, hub gene identification, and drug repurposing hypotheses. *PloS one*, 21(5), e0348601.

Qiao L, et al. (2026) Advances in high-throughput drug screening based on pharmacotranscriptomics. *Journal of advanced research*, 84, 1073.

Gutierrez DA, et al. (2026) Discovery of Two Novel Pyrazole Derivatives as Anticancer Agents Targeting Tubulin Polymerization and MAPK Signaling Pathways. *Oncology research*, 34(4), 14.

Curiel-Gomez E, et al. (2026) Pancreatic Cancer Stem Cells Co-Expressing SOX2, OCT4, and TERT High Represent an Aggressive Subpopulation. *Cells*, 15(2).

Liang S, et al. (2026) An integrated drug repositioning analysis identifies rosiglitazone as a treatment for sarcopenia. *Communications biology*, 9(1).

Xiao T, et al. (2026) Lactylation-related genes signature panel in hepatocellular carcinoma reveals the prognostic and therapeutic optimization. *Molecular & cellular oncology*, 13(1), 2621475.

He Z, et al. (2026) SCMO: a deep learning model integrating the single-cell resolution TME ecosystem and multi-omics for survival prediction in CRC patients. *Journal of translational medicine*, 24(1), 281.

Vryza P, et al. (2026) Predicting skin melanoma progression via LAG-3, TIGIT and HAVCR2. *Functional & integrative genomics*, 26(1).

Han Y, et al. (2026) Mitophagy-related molecular signatures in ulcerative colitis revealed by machine learning and molecular dynamics. *Frontiers in genetics*, 17, 1760869.

Kumar S, et al. (2026) Unlocking the potential of computational phenotypic drug discovery: methods, challenges, and future directions. *NPJ systems biology and applications*, 12(1).

Shi YX, et al. (2026) Exploring the molecular function of LYPD3 from pan-cancer to lung cancer: based on bioinformatics and cellular experiments. *Mammalian genome : official journal of the International Mammalian Genome Society*, 37(1), 26.

Feng Y, et al. (2026) Unraveling the genetic interplay and therapeutic potentials between major depressive disorder and metabolic syndrome: multi-ancestry and multi-trait genome-wide association analyses. *BMC psychiatry*, 26(1), 153.