Resource Summary Report

Generated by NIF on Apr 17, 2025

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 set, database, data or information resource, software resource, web application

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

Funding:

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

Record Creation Time: 20220129T080329+0000

Record Last Update: 20250417T065542+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 323 mentions in open access literature.

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

Gao K, et al. (2025) HERB 2.0: an updated database integrating clinical and experimental evidence for traditional Chinese medicine. Nucleic acids research, 53(D1), D1404.

Yin T, et al. (2025) A Novel Immune-Related Three-Gene Signature and Immune Infiltration Insights in Psoriasis and Chronic Kidney Disease. Clinical, cosmetic and investigational dermatology, 18, 267.

Tseng YH, et al. (2025) Utilizing TP53 hotspot mutations as effective predictors of gemcitabine treatment outcome in non-small-cell lung cancer. Cell death discovery, 11(1), 26.

Aldakheel FM, et al. (2025) Comprehensive computational analysis of differentially expressed miRNAs and their influence on transcriptomic signatures in prostate cancer. Scientific reports, 15(1), 3646.

Zhao N, et al. (2025) Identification of critical endoplasmic reticulum stress-related genes in advanced atherosclerotic plaque. Scientific reports, 15(1), 2107.

Wang Z, et al. (2025) Development of immune-derived molecular markers for preeclampsia based on multiple machine learning algorithms. Scientific reports, 15(1), 1767.

Wang S, et al. (2025) Ferroptosis-related genes participate in the microglia-induced

neuroinflammation of spinal cord injury via NF-?B signaling: evidence from integrated single-cell and spatial transcriptomic analysis. Journal of translational medicine, 23(1), 43.

Zhao Y, et al. (2025) Aurora kinase B inhibitor AZD1152: repurposing for treatment of lupus nephritis driven by the results of clinical trials. EBioMedicine, 112, 105553.

Shi Y, et al. (2024) Mining key circadian biomarkers for major depressive disorder by integrating bioinformatics and machine learning. Aging, 16(12), 10299.

Li B, et al. (2024) Identification of co-expressed central genes and transcription factors in acute myocardial infarction and diabetic nephropathy. BMC medical genomics, 17(1), 134.

Gao L, et al. (2024) The Construction of a Multi-Gene Risk Model for Colon Cancer Prognosis and Drug Treatments Prediction. International journal of molecular sciences, 25(7).

Chen W, et al. (2024) Exploring the immune escape mechanisms in gastric cancer patients based on the deep AI algorithms and single-cell sequencing analysis. Journal of cellular and molecular medicine, 28(10), e18379.

Gouveia Roque C, et al. (2024) The broken Alzheimer's disease genome. Cell genomics, 4(5), 100555.

Cartas-Cejudo P, et al. (2024) Neuropathological stage-dependent proteome mapping of the olfactory tract in Alzheimer's disease: From early olfactory-related omics signatures to computational repurposing of drug candidates. Brain pathology (Zurich, Switzerland), 34(4), e13252.

Jeong SY, et al. (2024) Hyaluronic acid stimulation of stem cells for cardiac repair: a cell-free strategy for myocardial infarct. Journal of nanobiotechnology, 22(1), 149.

Cao M, et al. (2024) Characterization of hypoxia-responsive states in ovarian cancer to identify hot tumors and aid adjuvant therapy. Discover. Oncology, 15(1), 23.

Chen Y, et al. (2024) Targeting FBXO22 enhances radiosensitivity in non-small cell lung cancer by inhibiting the FOXM1/Rad51 axis. Cell death & disease, 15(1), 104.

Pan Y, et al. (2024) ATP6V1C1, associated with the tumor microenvironment and mTORC1 signaling pathway, is a potential diagnostic, prognostic, and therapeutic biomarker for hepatocellular carcinoma. Discover oncology, 15(1), 673.

Zhou M, et al. (2024) Identification of immune-related genes and small-molecule drugs in hypertension-induced left ventricular hypertrophy based on machine learning algorithms and molecular docking. Frontiers in immunology, 15, 1351945.

Jia Z, et al. (2024) Comprehensive pan-cancer analysis of FUTs family as prognostic and immunity markers based on multi-omics data. Discover oncology, 15(1), 567.