

Resource Summary Report

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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, database, web application, data set, software resource

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: 20260801T190741+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 483 mentions in open access literature.

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

Liu D, et al. (2026) Age-Dependent KLK8 Upregulation Contributes to Elevated Susceptibility to Ventilator-Induced Lung Injury in the Elderly Mice. *Aging cell*, 25(1), e70304.

Wang R, et al. (2026) Apolipoprotein C1 functions as a target of thyroid carcinoma and synergistic effects with promising candidate-cyclopamine. *Translational oncology*, 63, 102617.

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.

Yan Z, et al. (2025) Constructing a Novel Amino Acid Metabolism Signature: A New Perspective on Pheochromocytoma Diagnosis, Immune Landscape, and Immunotherapy. *Biochemical genetics*, 63(1), 850.

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.

Hong Z, et al. (2025) Identification of the immune infiltration and biomarkers in ulcerative colitis based on liquid-liquid phase separation-related genes. *Scientific reports*, 15(1), 4484.

Hu L, et al. (2025) Targeting TCMR-associated cytokine genes for drug screening identifies PPAR γ agonists as novel immunomodulatory agents in transplantation. *Frontiers in immunology*, 16, 1539645.

Du Q, et al. (2025) Investigating the efficacy of immune checkpoint inhibitors in clear cell renal cell carcinoma based on methylation cross talk scoring. *Medicine*, 104(11), e41795.

Zhang Y, et al. (2025) Comprehensive Analysis Based on Genes Associated With Cuproptosis, Ferroptosis, and Pyroptosis for the Prediction of Diagnosis and Therapies in Coronary Artery Disease. *Cardiovascular therapeutics*, 2025, 9106621.

Gao K, et al. (2025) Machine learning analysis of FOSL2 and RHoBTB1 as central immunological regulators in knee osteoarthritis synovium. *The Journal of international medical research*, 53(4), 3000605251333646.

Yin T, et al. (2025) Immune-related hub genes and their role in psoriasis pathogenesis. *Scientific reports*, 15(1), 17765.

Hou Y, et al. (2025) Integrated multi-omics data and machine learning reveal CD151 as a key biomarker inducing chemoresistance in metabolic syndrome-related early-onset left-sided colorectal cancer. *Functional & integrative genomics*, 25(1), 122.

Shang J, et al. (2025) Identification of compounds to promote diabetic wound healing based on transcriptome signature. *Frontiers in pharmacology*, 16, 1576056.

Guan G, et al. (2025) Cell lineage-resolved embryonic morphological map reveals signaling associated with cell fate and size asymmetry. *Nature communications*, 16(1), 3700.

Xiong J, et al. (2025) Exploring hypoxia driven subtypes of pulmonary arterial hypertension through transcriptomics single cell sequencing and machine learning. *Scientific reports*, 15(1), 14251.

Zhang Z, et al. (2025) Targeting MCM10 disrupts cancer stemness and counteracts sorafenib resistance in hepatocellular carcinoma. *Cancer gene therapy*.

Liu J, et al. (2025) Leveraging machine learning models to evaluate immune infiltration in the ovarian cancer microenvironment: a single-cell analysis approach. *Discover oncology*, 16(1), 1291.

Tang H, et al. (2025) Identification and validation of epithelial-mesenchymal transition-related genes for diabetic nephropathy by WGCNA and machine learning. *Molecular medicine reports*, 32(3).

Ye Z, et al. (2025) Multimodal diagnostic models and subtype analysis for neoadjuvant therapy in breast cancer. *Frontiers in immunology*, 16, 1559200.