Resource Summary Report

Generated by RRID on May 25, 2025

Connectivity Map 02

RRID:SCR_015674
Type: Tool

Proper Citation

Connectivity Map 02 (RRID:SCR_015674)

Resource Information

URL: https://portals.broadinstitute.org/cmap/

Proper Citation: Connectivity Map 02 (RRID:SCR_015674)

Description: Collection of genome-wide transcriptional expression data from cultured human cells treated with bioactive small molecules and simple pattern-matching algorithms. camp aims to enable the discovery of functional connections between drugs, genes and diseases through the transitory feature of common gene-expression changes.

Abbreviations: cmap

Synonyms: Broad Institute Connectivity Map 02 Build, cmap

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

Defining Citation: PMID:17008526

Keywords: transcription, expression, gene, drug, disease pattern-matching algorithm, FASEB list

Funding:

Availability: Freely available, Account required

Resource Name: Connectivity Map 02

Resource ID: SCR_015674

Old URLs: https://www.broadinstitute.org/cmap_build01

License URLs: https://portals.broadinstitute.org/cmap/terms_and_conditions.jsp

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250525T031419+0000

Ratings and Alerts

No rating or validation information has been found for Connectivity Map 02.

No alerts have been found for Connectivity Map 02.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 169 mentions in open access literature.

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

Zhu Y, et al. (2025) NIPAL1 as a prognostic biomarker associated with pancreatic adenocarcinoma progression and immune infiltration. BMC cancer, 25(1), 165.

Cai T, et al. (2024) Deciphering the prognostic features of bladder cancer through gemcitabine resistance and immune-related gene analysis and identifying potential small molecular drug PIK-75. Cancer cell international, 24(1), 125.

Sun H, et al. (2024) Multi-omics analysis-based macrophage differentiation-associated papillary thyroid cancer patient classifier. Translational oncology, 43, 101889.

Yan Q, et al. (2024) Bronchial epithelial transcriptomics and experimental validation reveal asthma severity-related neutrophilc signatures and potential treatments. Communications biology, 7(1), 181.

Huang Y, et al. (2024) DrugRepoBank: a comprehensive database and discovery platform for accelerating drug repositioning. Database : the journal of biological databases and curation, 2024.

Hong H, et al. (2024) Pyroptosis-related lncRNAs are potential biomarkers for predicting prognoses and immune landscapes in patients with gastric adenocarcinoma. Discover oncology, 15(1), 684.

Xiang L, et al. (2024) Oxyresveratrol as a novel ferroptosis inducer exhibits anticancer activity against breast cancer via the EGFR/PI3K/AKT/GPX4 signalling axis. Frontiers in

pharmacology, 15, 1527286.

You X, et al. (2024) Identification of key genes and immune infiltration in osteoarthritis through analysis of zinc metabolism-related genes. BMC musculoskeletal disorders, 25(1), 227.

April-Monn SL, et al. (2024) Patient derived tumoroids of high grade neuroendocrine neoplasms for more personalized therapies. NPJ precision oncology, 8(1), 59.

Zhao Y, et al. (2024) Identification of biomarkers related to angiogenesis in myocardial ischemia-reperfusion injury and prediction of potential drugs. PloS one, 19(6), e0300790.

Xia Y, et al. (2024) Drug repurposing for cancer therapy. Signal transduction and targeted therapy, 9(1), 92.

Cao W, et al. (2024) Pan?cancer analysis on the role of KMT2C expression in tumor progression and immunotherapy. Oncology letters, 28(3), 444.

Ge J, et al. (2024) New HCC Subtypes Based on CD8 Tex-Related lncRNA Signature Could Predict Prognosis, Immunological and Drug Sensitivity Characteristics of Hepatocellular Carcinoma. Journal of hepatocellular carcinoma, 11, 1331.

Yan F, et al. (2024) Exploring molecular mechanisms of postoperative delirium through multi-omics strategies in plasma exosomes. Scientific reports, 14(1), 29466.

Zheng S, et al. (2023) Dissecting the role of cancer-associated fibroblast-derived biglycan as a potential therapeutic target in immunotherapy resistance: A tumor bulk and single-cell transcriptomic study. Clinical and translational medicine, 13(2), e1189.

Wei H, et al. (2023) Comprehensive investigation of the prognostic values and molecular mechanisms of syntaxin binding protein 5 antisense RNA 1 in patients with colon adenocarcinoma based on RNA sequencing dataset. Journal of Cancer, 14(9), 1607.

Wang XK, et al. (2023) Comprehensive analysis of candidate signatures of long non-coding RNA LINC01116 and related protein-coding genes in patients with hepatocellular carcinoma. BMC gastroenterology, 23(1), 216.

Ding B, et al. (2023) Immune-Related Genes' Prognostic, Therapeutic and Diagnostic Value in Ovarian Cancer Immune-Related Gene Biomarker in Ovarian Cancer. Cancer control : journal of the Moffitt Cancer Center, 30, 10732748231168756.

Zhang Z, et al. (2023) Expression signature of ten small nuclear RNAs serves as novel biomarker for prognosis prediction of acute myeloid leukemia. Scientific reports, 13(1), 18489.

Zhang B, et al. (2023) An EMT-Related Gene Signature to Predict the Prognosis of Triple-Negative Breast Cancer. Advances in therapy, 40(10), 4339.