

Resource Summary Report

Generated by T1D on Aug 7, 2026

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: cmap

Synonyms: Broad Institute Connectivity Map 02 Build, cmap

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

Defining Citation: [PMID:17008526](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260807T042843+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 243 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Zhang F, et al. (2026) A comprehensive study integrating bioinformatics analysis and experimental results on HROB as a potential biomarker for the prognosis of lung adenocarcinoma. Scientific reports, 16(1), 5056.

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.

Li J, et al. (2026) Single-cell RNA-seq reveals the piperlongumine is a potential drug for ischemic stroke. PloS one, 21(1), e0340725.

Pereira-Martins DA, et al. (2026) ??Np73 isoform defines a TP53-mutant-like poor-risk subgroup of acute myeloid leukemia. Cell reports. Medicine, 102540.

Yi X, et al. (2026) Use of Single-Cell Data and scPagwas Analysis to Identify T Cell Subsets and Construct a Prognostic Model for Clear Cell Renal Cell Carcinoma. Human mutation, 2026, 1916444.

Chen Z, et al. (2025) Molecular subtyping and prognostic evaluation in idiopathic pulmonary fibrosis: a focus on mechanical-related genes. Journal of translational medicine, 23(1), 1405.

Zhou W, et al. (2025) Unveiling a Novel Glioblastoma Deep Molecular Profiling: Insight into the Cancer Cell Differentiation-Related Mechanisms. ACS omega, 10(10), 10230.

He W, et al. (2025) Comprehensive analysis of the leukocyte immunoglobulin-like receptor family in clear cell renal cell carcinoma. Annals of medicine, 57(1), 2546684.

Ji G, et al. (2025) Single-cell RNA sequencing and multi-omics analysis of prognosis-related staging in papillary thyroid cancer. Cancer immunology, immunotherapy : CII, 74(8), 267.

Liang J, et al. (2025) Identification of isoliquiritigenin as a promising compound targeting lactate metabolism for heart failure alleviation. Scientific reports, 15(1), 35378.

Zhang H, et al. (2025) Repurposing the memory-promoting meclizine hydrochloride as a treatment for Parkinson's disease through integrative multi-omics analysis. NPJ Parkinson's disease, 11(1), 167.

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

Dey S, et al. (2025) Repurposing of CNS accumulating drugs Gemfibrozil and Doxylamine for enhanced sensitization of glioblastoma cells through modulation of autophagy. Scientific reports, 15(1), 20560.

Liu Y, et al. (2025) Comprehensive Multi-Omics Analysis Identifies FUT1 as a Prognostic and Therapeutic Biomarker Across Pan-Cancer. International journal of medical sciences, 22(6), 1313.

Zhang W, et al. (2025) Uncovering a fibroblast differentiation-based keloid classification by integration of single-cell and bulk RNA sequencing. Communications biology, 8(1), 1387.

Sun X, et al. (2025) Identification of plasma cell infiltration-related gene signatures as a novel prognostic model for clear cell renal cell carcinoma. Clinical and experimental medicine, 25(1), 365.

Amarilla-Quintana S, et al. (2025) CRISPR targeting of FOXL2 c.402C>G mutation reduces malignant phenotype in granulosa tumor cells and identifies anti-tumoral compounds. Molecular oncology, 19(4), 1092.

Yu Y, et al. (2025) Clinical significance and immune landscape analyses of the coagulation-related gene signatures in gastric cancer. Journal of Cancer, 16(6), 1971.

Liu Y, et al. (2025) Construction and validation of renal cell carcinoma tumor cell differentiation-related prognostic classification (RCC-TCDC): an integrated bioinformatic analysis and clinical study. Annals of medicine, 57(1), 2490830.

Lu B, et al. (2025) Construction of a prostate adenocarcinoma molecular classification: integrating spatial transcriptomics with retrospective cohort validation. Journal of translational medicine, 23(1), 717.