

Resource Summary Report

Generated by [dkNET](#) on Aug 31, 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: data or information resource, database, software resource, web application

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: 20260829T182503+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 [dkNET](#) .

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.

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.

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.

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 meclofenoxate 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.