# Resource Summary Report

Generated by RRID on Apr 9, 2025

# CMAP

RRID:SCR_009034
Type: Tool

## Proper Citation

CMAP (RRID:SCR_009034)

## Resource Information

**URL:** http://gmod.org/wiki/Cmap

**Proper Citation:** CMAP (RRID:SCR_009034)

**Description:** Web-based tool that allows users to view comparisons of genetic and physical maps. The package also includes tools for curating map data. (entry from Genetic Analysis Software)

**Abbreviations:** CMap

**Synonyms:** genetic and comparative maps

**Resource Type:** data analysis software, software resource, software application, data processing software

**Defining Citation:** PMID:19648141

**Keywords:** gene, genetic, genomic, perl, unix, solaris, freebsd, linux, sequence, FASEB list

**Funding:**

**Availability:** GNU General Public License

**Resource Name:** CMAP

**Resource ID:** SCR_009034

**Alternate IDs:** nlx_153998, OMICS_00933

**Alternate URLs:** https://sourceforge.net/projects/gmod/files/cmap/

**Old URLs:** http://www.gmod.org/cmap/

**Record Creation Time:** 20220129T080250+0000

**Record Last Update:** 20250409T060808+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 391 mentions in open access literature.

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

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.

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.

Xu Y, et al. (2025) ScDrugAct: a comprehensive database to dissect tumor microenvironment cell heterogeneity contributing to drug action and resistance across human cancers. Nucleic acids research, 53(D1), D1536.

Chen J, et al. (2025) Computational frameworks transform antagonism to synergy in optimizing combination therapies. NPJ digital medicine, 8(1), 44.

Guo X, et al. (2025) Shared genetic architecture and bidirectional clinical risks within the psycho-metabolic nexus. EBioMedicine, 111, 105530.

Yang X, et al. (2025) CHST3, PGBD5, and SLIT2 can be identified as potential genes for the diagnosis and treatment of osteoporosis and sarcopenia. Scientific reports, 15(1), 374.

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.

Xu J, et al. (2025) Single-microglia transcriptomic transition network-based prediction and real-world patient data validation identifies ketorolac as a repurposable drug for Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14373.

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.

Zhang M, et al. (2025) Biological characteristics, immune infiltration and drug prediction of PANoptosis related genes and possible regulatory mechanisms in inflammatory bowel disease. Scientific reports, 15(1), 2033.

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

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

Yang H, et al. (2025) Prognostic signature and therapeutic drug identification for dilated cardiomyopathy based on necroptosis via bioinformatics and experimental validation. Scientific reports, 15(1), 319.

Wang Y, et al. (2024) A novel anoikis-related gene signature predicts prognosis in patients with sepsis and reveals immune infiltration. Scientific reports, 14(1), 2313.

He Y, et al. (2024) Pyroptosis-related signatures predict immune characteristics and prognosis in IPF. Heliyon, 10(1), e23683.

Wang S, et al. (2024) Integrating PANoptosis insights to enhance breast cancer prognosis and therapeutic decision-making. Frontiers in immunology, 15, 1359204.

Stemmer E, et al. (2024) Exploring potential biomarkers and therapeutic targets in inflammatory bowel disease: insights from a mega-analysis approach. Frontiers in immunology, 15, 1353402.

Wang D, et al. (2024) Identification of ferroptosis-associated genes and potential pharmacological targets in sepsis-induced myopathy. Heliyon, 10(7), e29062.

Chen D, et al. (2024) IGF2BP2-related modification patterns in pancreatic cancer: A machine learning-driven approach towards personalized treatment. Heliyon, 10(6), e28243.