

Resource Summary Report

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CellMiner

RRID:SCR_025648

Type: Tool

Proper Citation

CellMiner (RRID:SCR_025648)

Resource Information

URL: <https://discover.nci.nih.gov/cellminer/>

Proper Citation: CellMiner (RRID:SCR_025648)

Description: Database and query tool designed for cancer research community to facilitate integration and study of molecular and pharmacological data for the NCI-60 cancerous cell lines. The NCI-60, panel of 60 diverse human cancer cell lines used by the Developmental Therapeutics Program of the U.S. National Cancer Institute to screen over 100,000 chemical compounds and natural products since 1990.

Synonyms: Cell Miner, CellMiner

Resource Type: database, data or information resource

Defining Citation: [PMID:17339364](#)

Keywords: cancer research, integration and study of molecular and pharmacological data, NCI-60 cancerous cell lines,

Availability: Free, Freely available

Resource Name: CellMiner

Resource ID: SCR_025648

Record Creation Time: 20240823T053238+0000

Record Last Update: 20260803T040901+0000

Ratings and Alerts

No rating or validation information has been found for CellMiner.

No alerts have been found for CellMiner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Wang F, et al. (2026) Regulation and reversal of paclitaxel resistance via the STAT1? mediated apoptotic pathway in ovarian cancer. International journal of oncology, 68(2).

Teitel J, et al. (2025) Pan-cancer Myc modulator that targets Myc-?-tubulin interaction to drive selective mitotic catastrophe. Scientific reports, 15(1), 38188.

Yang L, et al. (2025) The construction of a prognostic nomogram model for colorectal cancer and the prediction of immune characteristics and immune treatment responses based on the bioinformatics analysis of soluble mediator-related genes. Human vaccines & immunotherapeutics, 21(1), 2555699.

Liu Y, et al. (2025) A Pan-Cancer Analysis of Natriuretic Peptide Receptor 3 (NPR3) with Clinical Cohort and in vitro Validation. Journal of inflammation research, 18, 9989.

Zhai J, et al. (2025) Prognosis, immunological features and potential mechanisms of HKR1 in prostate cancer via single-cell and bulk RNA-sequencing. BMC cancer, 25(1), 822.

Wang Z, et al. (2025) Development of a machine learning-based predictive risk model combining fatty acid metabolism and ferroptosis for immunotherapy response and prognosis in prostate cancer. Discover oncology, 16(1), 744.

Tang Q, et al. (2025) Comprehensive Analyses of Single-Cell and Bulk RNA Sequencing Data From M2 Macrophages to Elucidate the Immune Prognostic Signature in Patients with Gastric Cancer Peritoneal Metastasis. ImmunoTargets and therapy, 14, 383.

Du W, et al. (2025) Integrated bioinformatics and experimental analysis of CHAF1B as a novel biomarker and immunotherapy target in LUAD. Discover oncology, 16(1), 43.

Masood MBE, et al. (2025) Integrated pan-cancer analysis revealed therapeutic targets in the ABC transporter protein family. PloS one, 20(5), e0308585.

Qiao L, et al. (2025) YRDC is a Prognostic-Related Biomarker Correlated With Immune Infiltration and Drug Sensitivity in Pan-Cancer. Cancer reports (Hoboken, N.J.), 8(9), e70325.

Li G, et al. (2025) Lysosome-derived biomarkers for predicting survival outcome in acute myeloid leukemia. Discover oncology, 16(1), 1455.

Deng X, et al. (2025) Selection of tumor invasion-related genes to build a prognostic model and predict immune response and potential drugs for esophageal cancer patients

based on WGCNA. Discover oncology, 16(1), 1695.

You M, et al. (2025) Integrated bioinformatics analysis of biomarkers and pathways to explore the mechanisms and molecular targets related to allergic rhinitis and pyroptosis. Scientific reports, 15(1), 15241.

Fang HY, et al. (2025) An innovative glutamine metabolism-related gene signature for predicting prognosis and immune landscape in cervical cancer. Discover oncology, 16(1), 368.

Li R, et al. (2025) Revealing the prognostic potential of natural killer cell-related genes in hepatocellular carcinoma: the key role of NRAS. Discover oncology, 16(1), 807.

Yuan H, et al. (2025) Identification of critical biomarkers and immune landscape patterns in glioma based on multi-database. Discover oncology, 16(1), 35.

Shen C, et al. (2025) The effect of PDLIM7 on cell proliferation, migration, and drug sensitivity in clear cell renal cell carcinoma. Scientific reports, 15(1), 26111.

Zhang HJ, et al. (2025) SIRPA, BTN3A1, and TDO2 in osteosarcoma: a prognostic triad with therapeutic implications from integrated genomic and pharmacogenomic data. Journal of orthopaedic surgery and research, 20(1), 742.

Yin J, et al. (2025) Disulfidptosis: a novel gene-based signature predicts prognosis and immunotherapy efficacy of pancreatic adenocarcinoma. Discover oncology, 16(1), 308.

Yang C, et al. (2025) ERCC3 serves as a prognostic biomarker for hepatocellular carcinoma and positively regulates cell proliferation and migration. Discover oncology, 16(1), 419.