

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: data or information resource, database

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: 20260912T200449+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 208 mentions in open access literature.

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

Wang Q, et al. (2026) Construction of taurine metabolism-related risk model and subtype identification in colorectal cancer to predict prognosis and immunological features. *Journal of gastrointestinal oncology*, 17(1), 7.

Lin J, et al. (2026) Exosomal P4HA3: a promising biomarker for diagnosis and prognosis in gastric cancer. *Translational cancer research*, 15(4), 320.

Mao C, et al. (2026) Integrating bulk and single-cell transcriptomic data to construct a risk model for histidine metabolism-related epithelial cell features in lung adenocarcinoma, predicting prognosis and immune landscape. *RNA biology*, 23(1), 1.

Wang R, et al. (2026) SLC26A2 as a key regulator and therapeutic target in hepatocellular carcinoma: evidence from pan-cancer and mechanistic studies. *Human genomics*, 20(1).

Liu C, et al. (2026) Integrating bulk RNA-seq and ScRNA-seq to identify manganese metabolism-related subtypes and immunoregulatory mechanisms in liver hepatocellular carcinoma. *Open life sciences*, 21(1), 20251298.

Ma P, et al. (2026) Multi-omics integration reveals pan-cancer roles of ZIC family genes in prognosis, immune microenvironment remodeling, and therapeutic vulnerability. *Discover oncology*, 17(1).

Liu Q, et al. (2026) Identification of RNA processing-related gene-based bladder cancer subtypes for prognosis and immune landscape assessment. *Translational andrology and urology*, 15(3), 74.

Pei Y, et al. (2026) Machine learning identifies disulfidptosis-related gene signature for pancreatic cancer prognosis and immune infiltration. *Discover oncology*, 17(1), 335.

Wei D, et al. (2026) Calcium-related genes predict prognosis, immune characteristics, and response to immunotherapy in LUAD patients. *Clinical proteomics*, 23(1).

Yao QQ, et al. (2026) Pan-Cancer Analysis of WRN: From Multi-Omics Biomarker Discovery to Therapy-Guiding Functional Evidence. *OncoTargets and therapy*, 19, 564441.

Zhao M, et al. (2026) Integrated analysis of scRNA-seq and bulk RNA-seq identifies matrisome-related biomarkers for prognostic stratification and immune landscape in lung adenocarcinoma. *The Korean journal of physiology & pharmacology : official journal of the Korean Physiological Society and the Korean Society of Pharmacology*, 30(3), 199.

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).

Ma R, et al. (2026) CLK1 is a potential tumor suppressor for NSCLC by regulating cell proliferation and immune infiltration. *Frontiers in cell and developmental biology*, 14, 1758135.

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 M, et al. (2025) Integrative analysis identifies TEAD4 as a universal prognostic biomarker in human cancers. *Frontiers in immunology*, 16, 1688563.

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

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.

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.

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.