

Resource Summary Report

Generated by RRID on Sep 20, 2026

ICGC Data Portal

RRID:SCR_021722

Type: Tool

Proper Citation

ICGC Data Portal (RRID:SCR_021722)

Resource Information

URL: <https://dcc.icgc.org/>

Proper Citation: ICGC Data Portal (RRID:SCR_021722)

Description: Portal provides tools for visualizing, querying, and downloading cancer data, which is released on quarterly schedule.

Synonyms: International Cancer Genome Consortium Data Portal

Resource Type: data or information resource, data repository, disease-related portal, portal, service resource, storage service resource, topical portal

Keywords: Cancer data, visualizing cancer data, querying cancer data, downloading cancer data, cancer

Related Condition: Cancer

Availability: Restricted

Resource Name: ICGC Data Portal

Resource ID: SCR_021722

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260919T195457+0000

Ratings and Alerts

No rating or validation information has been found for ICGC Data Portal.

No alerts have been found for ICGC Data Portal.

Data and Source Information

Usage and Citation Metrics

We found 891 mentions in open access literature.

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

Huang C, et al. (2026) Survival Genie 2: a next-generation web server for targeted and single-cell-based survival analyses. *Genome medicine*, 18(1).

Shin KJ, et al. (2026) NSMF modulates replication stress to facilitate colorectal cancer progression. *Nucleic acids research*, 54(2).

Song Y, et al. (2026) A novel integrative machine learning-based prognostic model reveals lactylation regulation in hepatocellular carcinoma progression. *Cancer cell international*, 26(1).

Sun W, et al. (2026) TRIM47 Regulates Energy Metabolism via Glycolytic Reprogramming to Drive Hepatocellular Carcinoma Progression and Represents an Efficient Therapeutic Target. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(17), e16996.

Luo MR, et al. (2026) TONSL promotes hepatocellular carcinoma progression and radioresistance by orchestrating DNA damage repair and cell cycle dynamics. *Discover oncology*, 17(1).

Li D, et al. (2026) ASPDH inhibits the proliferation, migration, and invasion of liver cancer cells by regulating lactate metabolism and the NF- κ B/PD-L1 pathway. *Clinics (Sao Paulo, Brazil)*, 81, 100946.

Lv W, et al. (2026) Adverse Effects of Low Serum HDL-C Levels on Prognosis and Tumor Immune Microenvironment in Patients With Newly Diagnosed Chronic Lymphocytic Leukemia. *Cancer medicine*, 15(4), e71791.

Wu F, et al. (2026) Integrative immunogenomic profiling identifies CALU as a brown adipocyte-linked modulator of progression and treatment response in pancreatic cancer. *Discover oncology*, 17(1), 158.

Wen Q, et al. (2026) Identification and Validation of the Prognostic Value of PTTG1-Related Genes in Hepatocellular Carcinoma by Mendelian Randomization and Single-Cell Transcriptome Analysis. *Iranian journal of biotechnology*, 24(1), e4221.

Zhang S, et al. (2026) The critical role of GRP78/BiP MARYlation in ER stress of KRAS-mutant colorectal cancer. *JCI insight*, 11(2).

Zheng Z, et al. (2026) Machine Learning-Based Sialylation-Associated Gene Signature Predicts Prognosis and Immune Landscape in Hepatocellular Carcinoma: Validation via Multi-Omics Analysis and in vitro Assays. *Journal of hepatocellular carcinoma*, 13, 575986.

Qu X, et al. (2026) Construction of a prognostic model based on protein post-translational modification genes for prediction of immune characteristics and therapeutic response in hepatocellular carcinoma. *Discover oncology*, 17(1).

Xu B, et al. (2026) Palmitoylation remodeling dictates HCC heterogeneity: implications for subtype-specific prognostication and targeting the YAP-RhoA axis. *BMC medical genomics*, 19(1).

Chen S, et al. (2026) A novel gene signature based on Like-Smith family members-related genes for predicting the prognosis of hepatocellular carcinoma. *Translational cancer research*, 15(2), 113.

Zhou L, et al. (2026) Integrated multi-dataset screening to predict prognosis and identify immunotherapy gene targets in hepatocellular carcinoma patients. *Scientific reports*, 16(1), 7014.

Huang K, et al. (2026) Extrachromosomal DNA drives molecular and clinical heterogeneity in hepatocellular carcinoma: a multi-omics analysis and prognostic model development. *Human genomics*, 20(1).

Lv X, et al. (2026) Single-Cell RNA-seq Reveals Deubiquitination Genes as Prognostic Markers in Hepatocellular Carcinoma. *International journal of genomics*, 2026, 4893924.

Pan Y, et al. (2026) Targeting SPAK suppresses progression and averts an immune exhaustive microenvironment in hepatocellular carcinoma. *Nature communications*, 17(1), 1414.

Fu C, et al. (2026) Prognostic gene screening and experimental validation in renal clear cell carcinoma based on spatial transcriptomics and single-cell sequencing. *Frontiers in immunology*, 17, 1699883.

Li Y, et al. (2026) A novel signature of palmitoylation for predicting prognosis and therapeutic response of hepatocellular carcinoma. *Discover oncology*, 17(1).