# Resource Summary Report

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## CPTAC

RRID:SCR_017135
Type: Tool

### Proper Citation

CPTAC (RRID:SCR_017135)

### Resource Information

**URL:** https://proteomics.cancer.gov/programs/cptac

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**Description:** Clinical proteomic tumor analysis consortium to systematically identify proteins that derive from alterations in cancer genomes and related biological processes, in order to understand molecular basis of cancer that is not possible through genomics and to accelerate translation of molecular findings into clinic. Operates through Proteome Characterization Centers, Proteogenomic Translational Research Centers, and Proteogenomic Data Analysis Centers. CPTAC investigators collaborate, share data and expertise across consortium, and participate in consortium activities like developing standardized workflows for reproducible studies.

**Synonyms:** Clinical Proteomic Tumor Analysis Consortium

**Resource Type:** organization portal, data or information resource, topical portal, portal, disease-related portal, consortium

**Keywords:** identify, protein, alteration, cancer, genome, clinical, study, proteome, proteogenomic, tumor, data, analysis, consortium, reproducibility

**Related Condition:** cancer

**Resource Name:** CPTAC

**Resource ID:** SCR_017135

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260810T040711+0000

### Ratings and Alerts

No rating or validation information has been found for CPTAC.

No alerts have been found for CPTAC.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 213 mentions in open access literature.

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


Ziman B, et al. (2026) ETS1 Orchestrates a Hybrid EMT Program Driving Metastasis and Immune Evasion. Cancer research.

Zhang Z, et al. (2026) Machine learning model on multi-omics data enables risk stratification and identifies molecular heterogeneity and therapeutic targets in glioblastoma. Molecular cancer, 25(1).

Mu N, et al. (2026) Pan-cancer analysis reveals the oncogenic and immunomodulatory roles of PTGFRN across human cancers. Scientific reports, 16(1).

Wang S, et al. (2026) Apolipoprotein D downregulation in OSCC: multi-database validation and clinical significance. BMC medical genomics, 19(1).

Zhang Z, et al. (2026) Multi-omics profiling-derived signature links cellular ecosystem to glioblastoma prognosis. iScience, 29(6), 115982.

Wang Y, et al. (2026) A 15-layer multi-omics analysis of gastric cancer ecotypes provides therapeutic insights. Cell reports. Medicine, 7(5), 102756.

Wu F, et al. (2026) Metabolic profiling defines glioblastoma subtypes with distinct prognoses and therapeutic vulnerabilities. Neuro-oncology, 28(4), 880.

Zhao Y, et al. (2026) Effect of TGF??-ITGB6 feedback loop on liver metastasis in SMAD4 wild-type pancreatic cancer. Chinese medical journal, 139(9), 1388.

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).

Zhou D, et al. (2026) AK3 as a Hypoxia-Angiogenesis-Related Prognostic Biomarker and Therapeutic Target in Clear Cell Renal Cell Carcinoma. International journal of general medicine, 19, 552108.

Maurencova D, et al. (2026) Cellular senescence escape and antiviral response discriminate glioblastoma from lower-grade gliomas. Neuro-oncology advances, 8(1), vdag122.

Khan UK, et al. (2026) DKC1 promotes colorectal cancer progression and therapy resistance by dysregulating sphingolipid biosynthesis. Nature communications, 17(1).

Yang D, et al. (2026) Assessment of susceptibility to mTOR rs2295080 gene polymorphism in Guangxi Zhuang lung cancer population. Journal of thoracic disease, 18(3), 189.

Guan B, et al. (2026) TRIM21-Mediated ubiquitination of FBL suppresses PI3K/AKT signaling and tumor progression in clear cell renal cell carcinoma. Cellular and molecular life sciences : CMLS, 83(1).

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

Zhang P, et al. (2026) Histone lactylation increases CXCL1 expression for neutrophil infiltration and immune escape in pancreatic cancer. Nature communications, 17(1).

Chen S, et al. (2026) Hypoxia-induced PRMT6 expression promotes temozolomide chemoresistance in glioblastoma via G3BP1. Journal of translational medicine, 24(1), 226.

Li J, et al. (2026) Multiomics analysis identifies the prognostic significance and biological roles of the HNRNP family in lung adenocarcinoma. Discover oncology, 17(1).

Qiu J, et al. (2026) Development and validation of a herb-related gene signature for prognosis prediction and therapeutic response assessment in breast cancer. Translational cancer research, 15(1), 48.

Murr J, et al. (2026) The Protein Phosphatase Inhibitor LB100 Targets the Mesenchymal Lineage of Pancreatic Ductal Adenocarcinoma. MedComm, 7(6), e70794.