

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

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: 20260801T190546+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 131 mentions in open access literature.

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

Xiong X, et al. (2025) Bioinformatics exploration of the S1PR1 receptor in various human cancers and its clinical relevance. Discover oncology, 16(1), 449.

Zhao YM, et al. (2025) GPATCH4 functions as a regulator of nucleolar R-loops in hepatocellular carcinoma cells. Nucleic acids research, 53(10).

Zhuang S, et al. (2025) Integrated cytomembrane proteomics identifies EpCAM/MGST1 as therapeutic targets in metastatic laryngeal carcinoma. Frontiers in genetics, 16, 1615570.

Wang J, et al. (2025) Pan-cancer analysis identifies tRNA modification enzyme CTU2 as a novel tumor biomarker and its role in immune microenvironment. Frontiers in immunology, 16, 1547794.

Fujimoto M, et al. (2025) Plasma cell-free DNA methylation profile before afatinib treatment is associated with progression-free and overall survival of patients with epidermal growth factor receptor gene mutation-positive non-small cell lung cancer. Clinical epigenetics, 17(1), 63.

Song Y, et al. (2025) Molecules interacting with CasL-Like 2 enhances tumor angiogenesis and progression by activating mTOR/HIF1 α /VEGF pathway in kidney renal clear cell carcinoma. Scientific reports, 15(1), 36581.

Unger M, et al. (2025) Deep Learning for Biomarker Discovery in Cancer Genomes. bioRxiv : the preprint server for biology.

Shao T, et al. (2025) Prediction of pathological grade of oral squamous cell carcinoma and construction of prognostic model based on deep learning algorithm. Discover oncology, 16(1), 976.

Liu Y, et al. (2025) Rewired glycolysis by DTL accelerates oncometabolite L-lactate generation to promote breast cancer progression. Frontiers in oncology, 15, 1583752.

Wang Y, et al. (2025) Cytoplasmic TRIM24 promotes colorectal cancer cell proliferation by activating Wnt/ β -catenin signaling. Nature communications, 16(1), 8598.

Khan MN, et al. (2025) AKR1B10 as a novel prognostic biomarker linking methylation and immune escape in hepatocellular carcinoma. *Discover oncology*, 16(1), 1551.

Karthikeyan SK, et al. (2025) MammOnc-DB, an integrative breast cancer data analysis platform for target discovery. *NPJ breast cancer*, 11(1), 35.

Mills J, et al. (2025) Acute degradation of nucleolin reveals its novel functions in cell cycle progression and cell division in triple negative breast cancer. *Journal of experimental & clinical cancer research : CR*, 44(1), 204.

Yuan W, et al. (2025) Pancancer outcome prediction via a unified weakly supervised deep learning model. *Signal transduction and targeted therapy*, 10(1), 285.

Zhao Q, et al. (2025) A pan-cancer analysis of the oncogenic and immunological roles of THOC3 in human cancer. *Scientific reports*, 15(1), 36240.

Zhao C, et al. (2025) Identification of Tumor-Specific Surface Proteins Enables Quantification of Extracellular Vesicle Subtypes for Early Detection of Pancreatic Ductal Adenocarcinoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(21), e2414982.

Xiong N, et al. (2025) N-glycosylation Modification of CTSD Affects Liver Metastases in Colorectal Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(7), e2411740.

Bai C, et al. (2025) Machine Learning-Enabled Drug-Induced Toxicity Prediction. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(16), e2413405.

Zhou K, et al. (2025) THEMIS2 contributes to ovarian cancer metastasis via DOCK4-mediated activation of Rap1 signaling. *Cellular oncology (Dordrecht, Netherlands)*, 48(4), 961.

Li Y, et al. (2025) Analysis and identification of PTBP2 as an oncogene in hepatocellular carcinoma. *Discover oncology*, 16(1), 520.