CPTAC is a national effort to accelerate the understanding of the molecular basis of cancer through the application of large-scale proteome and genome analysis, or proteogenomics.

Data, assays, and reagents are made available to the public to accelerate cancer research and advance patient care. All CPTAC investigators collaborate, share data and expertise across the consortium.

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For inquiries, contact cancer.proteomics@mail.nih.gov, or visit proteomics.cancer.gov

U.S. Department of Health & Human Services | National Institutes of Health

**WHY PROTEOGENOMICS**

Genomics is improving cancer prevention, detection, diagnosis and treatment, and is the foundation of precision oncology. Although the cancer research community has gathered a wealth of information on the genome, the current challenge is deciphering the proteome, including protein formations, quantification, modifications, and biological signaling to other molecules. Proteomic findings are integrated with genomics to better understand the molecular mechanisms of cancer. This is important because proteins carry out all the cell’s functions, and most cancer therapies target proteins. Integration of proteomics into precision oncology, or proteogenomics, provides a more complete picture of the molecular basis of cancer that is not possible through genomics alone.

The CPTAC program transforms tissue samples into rich, publicly available proteomic datasets, assays, and antibodies for the cancer research community. These efforts will expedite the development of individualized patient care.

To see a video about proteogenomics, visit: proteomics.cancer.gov
The CPTAC Pipeline builds on The Cancer Genome Atlas (TCGA) by comprehensively studying proteins, DNA, and RNA in cancer cells, and generates shareable genomic, proteomic and imaging data. The Biospecimen Core Resource turns tissue samples into molecular analytes, with TCGA characterizing the genome and Proteome Characterization Centers characterizing the proteome. Proteogenomic Data Analysis Centers analyze data. Proteogenomic Translational Research Centers use the data to address questions of drug responses and resistance in NCI-sponsored clinical trials. The CPTAC Data Coordinating Center collects, stores, and makes data available to researchers worldwide. CPTAC also makes antibodies, assays, and corresponding protocols available to the cancer research community through the CPTAC Antibody and Assay Portals.

PROTEOGENOMIC TRANSLATIONAL RESEARCH CENTERS

Primary and uniform genomic and proteomic data

PROTEOMIC TARGETED ASSAYS

CPTAC DATA COORDINATING CENTER

Primary genomic and proteomic data

CPTAC makes the following resources freely available

DATA
- Proteome sequence data
- Genome sequence data
- Histopathology, PET, and MRI images

ASSAYS
- "Fit-for-purpose" proteomic targeted assays

REAGENTS
- Antibodies

CPTAC RESOURCES

Accelerate the clinical application of molecular findings

SYSTEMATICALLY CHARACTERIZE PROTEINS AND GENES TO BETTER UNDERSTAND THE MOLECULAR BASIS OF CANCER

Provide resources to the cancer research community

GOALS OF CPTAC