

Advancing Molecular Insights Into Cancer

Scientists built a dataset with genomic, proteomic, and clinical data from more than 1,000 tumors across 10 cancer types.

September 21, 2023 By Harrison Wein and National Institutes of Health

Cancer is caused by cells that grow and divide when they should not. This dangerous process can happen almost anywhere in the body. So, cancer is not one disease: there are hundreds of different kinds of cancers.

Some cancers have overlapping causes, but uncovering the complicated drivers of such varied cancers can be difficult. This complexity makes finding ideal treatments challenging. Tumors are also notoriously adaptable and often become resistant to treatment.

Genomics—the study of all the genes in the body—has opened new angles to explore. But many cancers are still resistant to treatments that rely on genomics to guide therapy. To develop more effective approaches, researchers have been expanding their scope to include proteomics—the study of proteins, the molecules encoded by genes. Proteins are responsible for carrying out most of the functions of a cell. But proteins add further levels of complexity. Different proteins can arise from one gene. Proteins can also be modified in a variety of ways that affect their function.

Finding effective cancer treatments will require approaches that use all this information. The attempt to link genomic mutations to their broader impact on function is called [proteogenomics](#). Examining all of these diverse data to find patterns across cancer types is a formidable challenge.

A research team funded by NIH's National Cancer Institute—the Clinical Proteomic Tumor Analysis Consortium (CPTAC)—set out to build an expansive tumor proteogenomic dataset based on studies of more than 1,000 tumors across 10 cancer types. They described their project and demonstrated its ability to give new insights in a series of papers published in *Cell* and *Cancer Cell* on August 14, 2023.

In the [first paper](#), the researchers examined cancer-driving mutations across the different cancer types. They were able to detect distinct patterns in how these mutations impact various aspects of cell function.

[Another paper](#) examined how protein modifications, called post-translational modifications, affect

cell function. The team identified shared patterns of protein regulation involved in cancer processes across different tumor types. These patterns affect DNA repair, metabolism, and immunity.

[A third paper](#) examined patterns of DNA methylation, a type of reversible modification that regulates gene activity. The team identified changes that altered how RNA and proteins were made from crucial cancer-associated genes. They also found methylation patterns associated with various tumor characteristics. These findings, taken together, included many new insights into how cancer develops and suggest potential novel targets for therapies.

“These articles demonstrate the impact of studying both the genetic and protein-related aspects of cancer, and they show how scientists from different fields can work together,” says Dr. Ana I. Robles, Program Director at NCI’s Office of Cancer Clinical Proteomics.

“Adding proteogenomics into clinical trials and patient care and improving data sharing could change how we treat patients and understand various diseases. This shift could impact not only cancer but also many other medical conditions,” adds Dr. Henry Rodriguez, Director of NCI’s Office of Cancer Clinical Proteomics Research.

These publicly available resources now can help researchers around the world to address unsolved questions about how cancers develop, progress, and evade treatments.

This [research summary](#) was published by the National Institutes of Health on September 12, 2023.