Private Meeting Email

The National Cancer Institute's Office of Cancer Clinical Proteomics Research (OCCPR) and Clinical Proteomic Tumor Analysis Consortium (CPTAC) are pleased to announce the **2021 CPTAC Virtual Scientific Symposium**. Join us on **October 13-14, 2021** to learn about the most current advances in the field of cancer proteogenomics and cancer research by our CPTAC investigators.

The CPTAC program is a national effort to accelerate the understanding of cancer biology through the marriage of large-scale proteome and genome analysis, or proteogenomics. This comprehensive approach allows CPTAC researchers to broaden our understanding of cancer by not only distinguishing tumor types through genomics, but by also examining the downstream mechanisms of the resultant proteins and post-translational modifications.

Most cancer therapeutics use proteins and their modifications as the direct site of action, but genomic analysis alone does not always translate to therapeutic success. With the addition of proteomics, proteogenomics allows CPTAC researchers to paint a clearer picture of tumor carcinogenesis and progression, micro-environments, and immune landscapes. This information may then be exploited therapeutically to improve patient care.

CPTAC pushes the boundaries of proteogenomic research by the characterization of cancer phenotypes, through developing and applying open-source community resources, and accelerating precision oncology by applying proteogenomics to questions of toxicity and resistance in association with clinical trials.

If you are presenting a poster, please email your virtual poster in a PDF format, not exceeding 20 MB in size, directly to me at mesrim@mail.nih.gov no later than Friday, October 1st, 2021.

We are excited to share our findings with you! We hope you can join us! Please register here.

Public Meeting Email

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CPTAC has pioneered the integrated proteogenomic analysis of colorectal, breast, ovarian, endometrial and lung cancer to reveal new insights into these cancer types, such as: identification of proteomic-centric subtypes, prioritization of driver mutations by correlative analysis of copy number alterations and protein abundance and understanding cancer-relevant pathways through posttranslational modifications.

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