

User-Friendly Web Apps for CPTAC Data Exploration

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Introduction

We built several intuitive web applications enabling access, to download, exploration, and visualization of CPTAC data without the need to code or learn complex programs.

I. iProFun allows users to explore the impact of DNA copy number alteration and methylation on the proteogenomic landscape of various tumor types

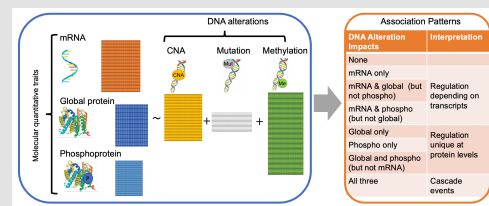
II. ProTrack enables users to visualize patterns across multiomic data types

III. ProNetView provides users with interactive 3D visualizations of gene and protein regulatory networks

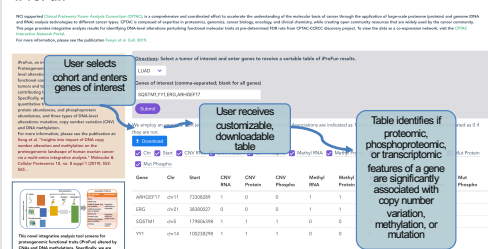
I. iProFun

cptac-iprofun.org

Identify genes whose proteogenomic functional traits are altered by CNAs and DNA methylations



iProFun



User selects cohort and enters genes of interest

User receives customizable, downloadable table

Table identifies if proteomic, phosphoproteomic, or transcriptomic features of a gene are significantly associated with copy number variation, methylation, or mutation

Gene	CNA	Met	Protein	Phospho	RNA	Protein	Phospho
ARHGAP27	1	0	0	1	1	1	1
SLC	1	0	0	0	1	1	1
SOST	1	1	1	0	0	0	0
Y11	1	1	1	0	0	0	0

Cohorts available:
Lung adenocarcinoma (LUAD)
clear cell Renal Cell Carcinoma (ccRCC)

[Song et al. Insights into Impact of DNA Copy Number Alteration and Methylation on the Proteogenomic Landscape in Human Ovarian Cancer via a Multi-Omics Integrative Analysis. Molecular & Cell Proteomics, June 2019](#)

II. ProTrack

ccrcc.cptac-data-view.org

Explore multi-omic heatmaps for genes of interest

Clear Cell Renal Cell Carcinoma (ccRCC) Discovery Cohort finding

110 treatment-naive RCC and 84 paired-matched NAT samples. We defined four tumor subtypes in this cohort, defined by unique genomic alterations and tumor microenvironment signatures:

CD8+ inflamed | **VEGF immune desert** |
CD8- inflamed | **Metabolic immune desert**

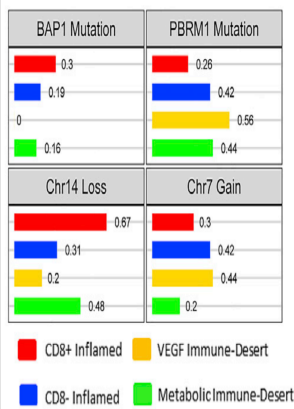
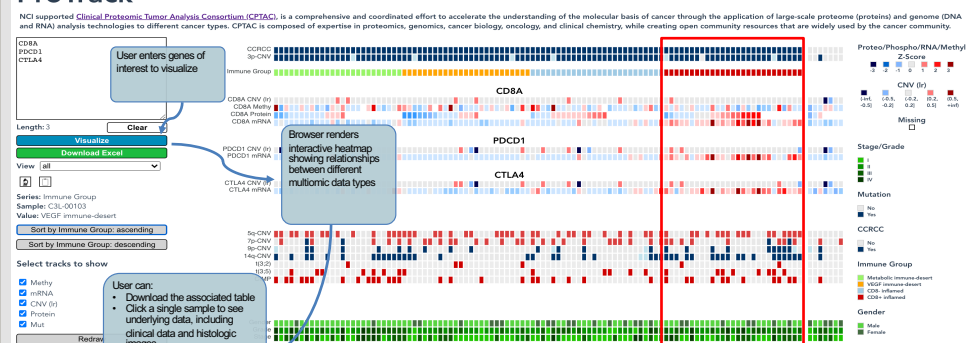
CD8+ inflamed tumors were characterized by:

- High degree of CD8+ T cell infiltration
- Increased expression of the immune evasion markers PD1, CTLA4
- High frequency of chromosome 14 loss [Fig. 6C, Clark et al]

To explore this cohort and visualize this finding with ProTrack:

Enter genes of interest (CD8, PD1, CTLA4) →
Sort by CD8+ ascending then by immune group

ProTrack



III. ProNetView

ccrcc.cptac-network-view.org

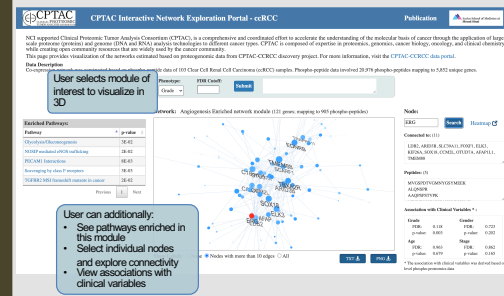
Explore co-expression networks in 3D

ccRCC Discovery Cohort Finding

We identified groups of highly connected genes as modules:

- Cell cycle and Angiogenesis enriched modules were captured only by phospho-proteomics data
- Angiogenesis enriched module is associated with lower grade and inversely correlated with BAP1 and chromosome 14 loss

ProNetView enables users to visualize and explore this and other important modules



[Kalayci et al. ProNetView-ccRCC: A Web-Based Portal to Interactively Explore Clear Cell Renal Cell Carcinoma Proteogenomics Networks. Proteomics, May 2020](#)

References

- [Clark et al. Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, Oct 2019.](#)
- [Gillette et al. Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, July 2020.](#)
- [Edwards et al. The CPTAC Data Portal: A Resource for Cancer Proteomics Research. J Proteome Res, June 2015.](#)

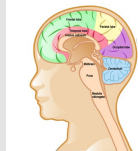
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Pediatric Brain Tumor pbt.cptac-data-view.org

Over 200 pediatric tumors across 7 subtypes from samples collected by the CBTTTC consortium

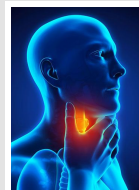


CPTAC
National Cancer Institute

[Calinawan et al. ProTrack: An Interactive Multi-Omics Data Browser for Proteogenomic Studies. Proteomics, June 2020](#)

Head and Neck Squamous Cell Carcinoma *Forthcoming*

108 HPV-negative cases, including treatment naive and normal adjacent tissue



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