

From Volcanoes to the Bench

Advantages of Novel Hyperthermoacidic Archaeal Proteases for Proteomics Workflows

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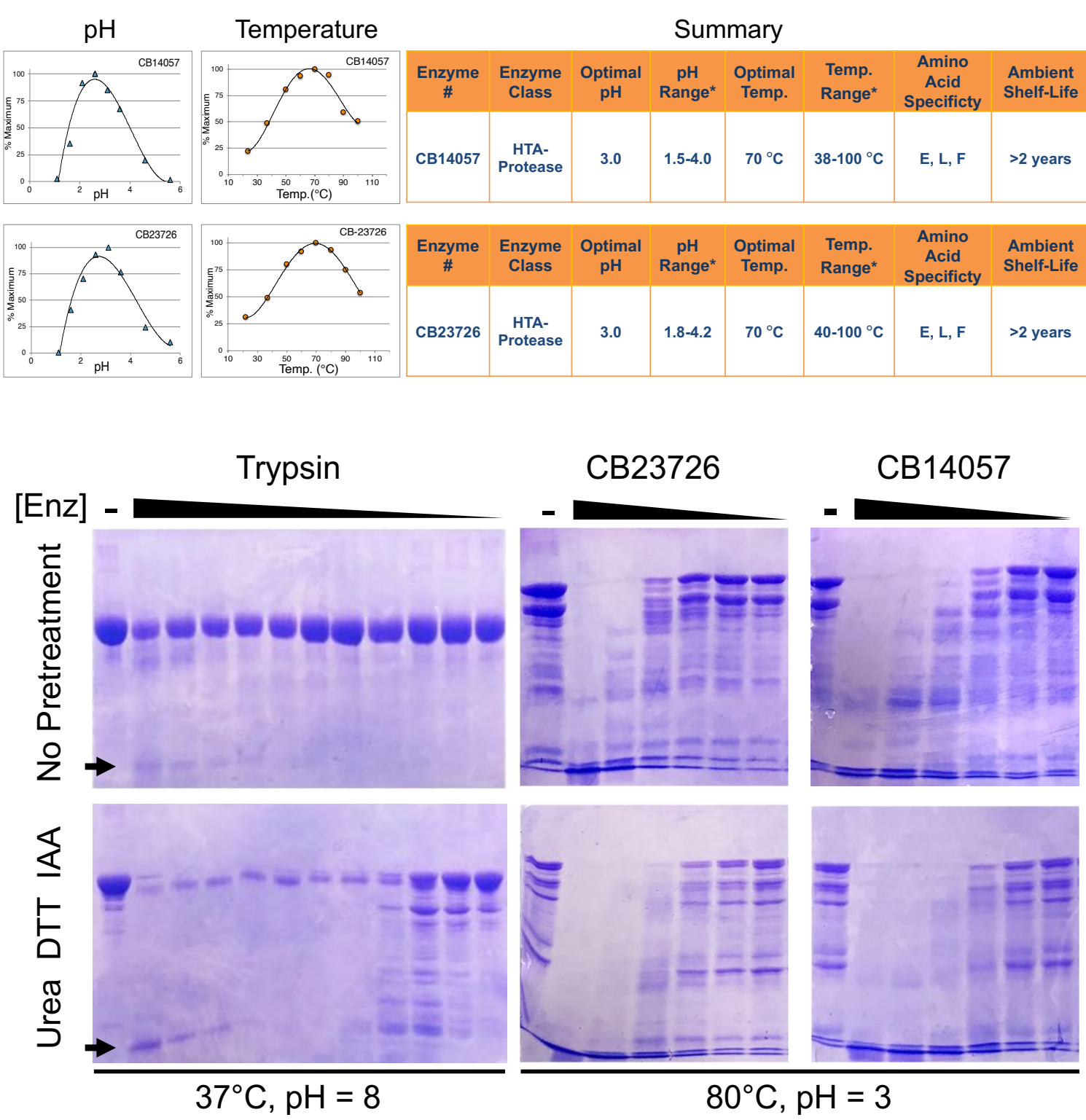
One-Step 30-Minute Sample Preparation

Add Sample and Heat 30 min

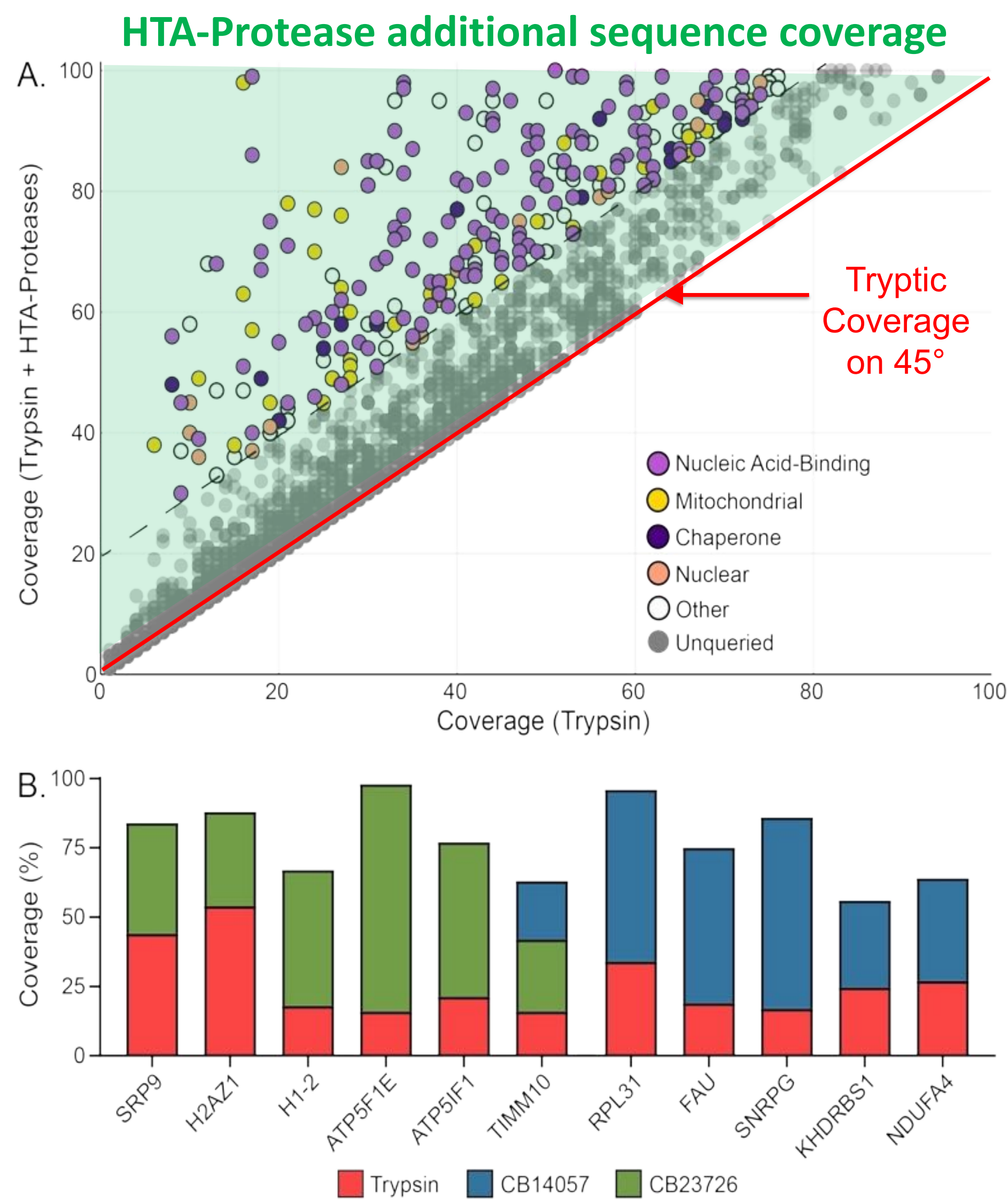
Reconstitute sample in reducing acidic buffer with **HTA-Protease**
Incubate 80°C, 5-60 min

No Sample Loss/No Manipulation

HTA-Proteases function optimally in hot acid that denatures sample proteins and blocks disulfide reformation. No Chaotropes or IAA needed for rapid sample preparation.

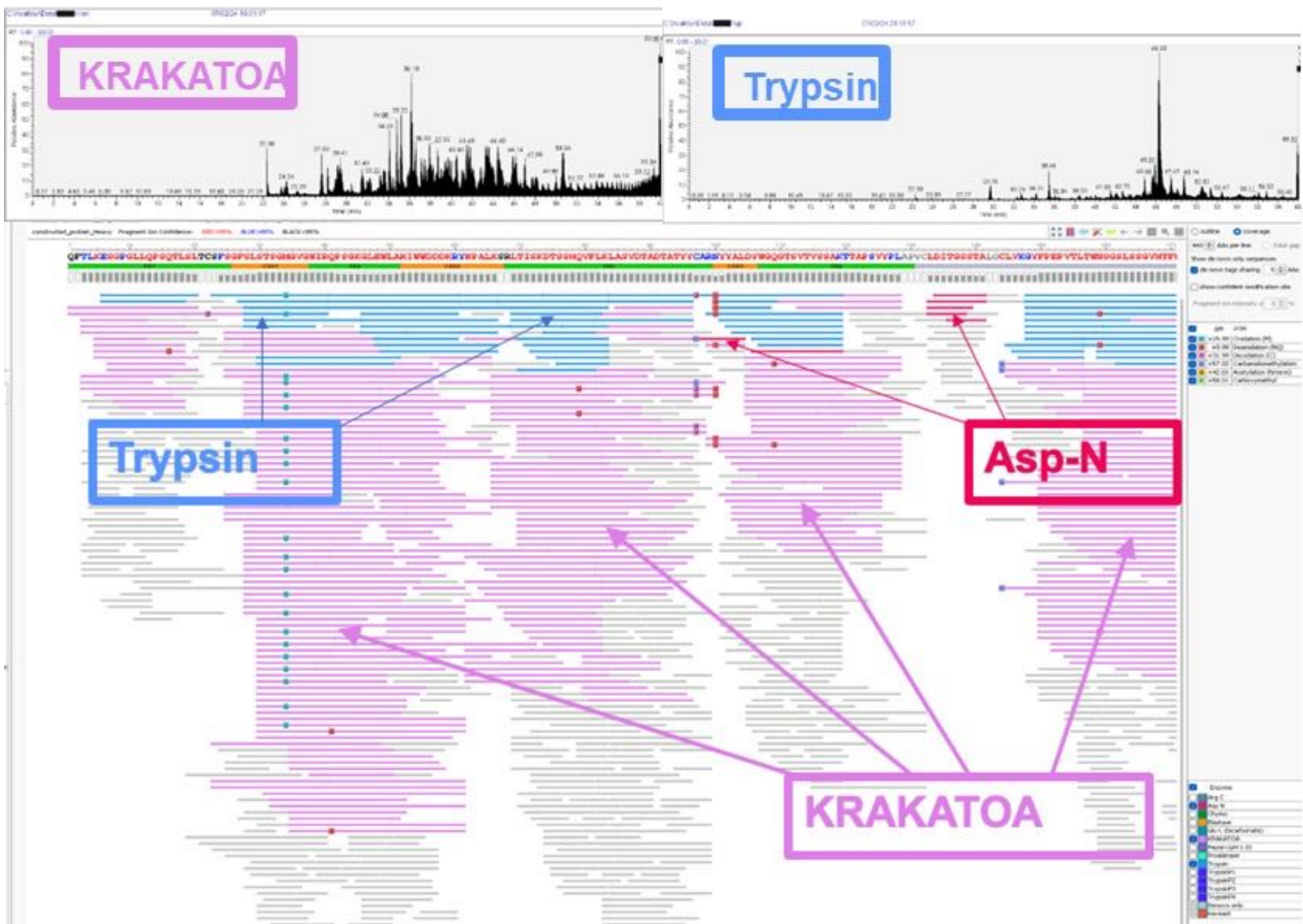


Novel ID's and New Sequence and PTM's

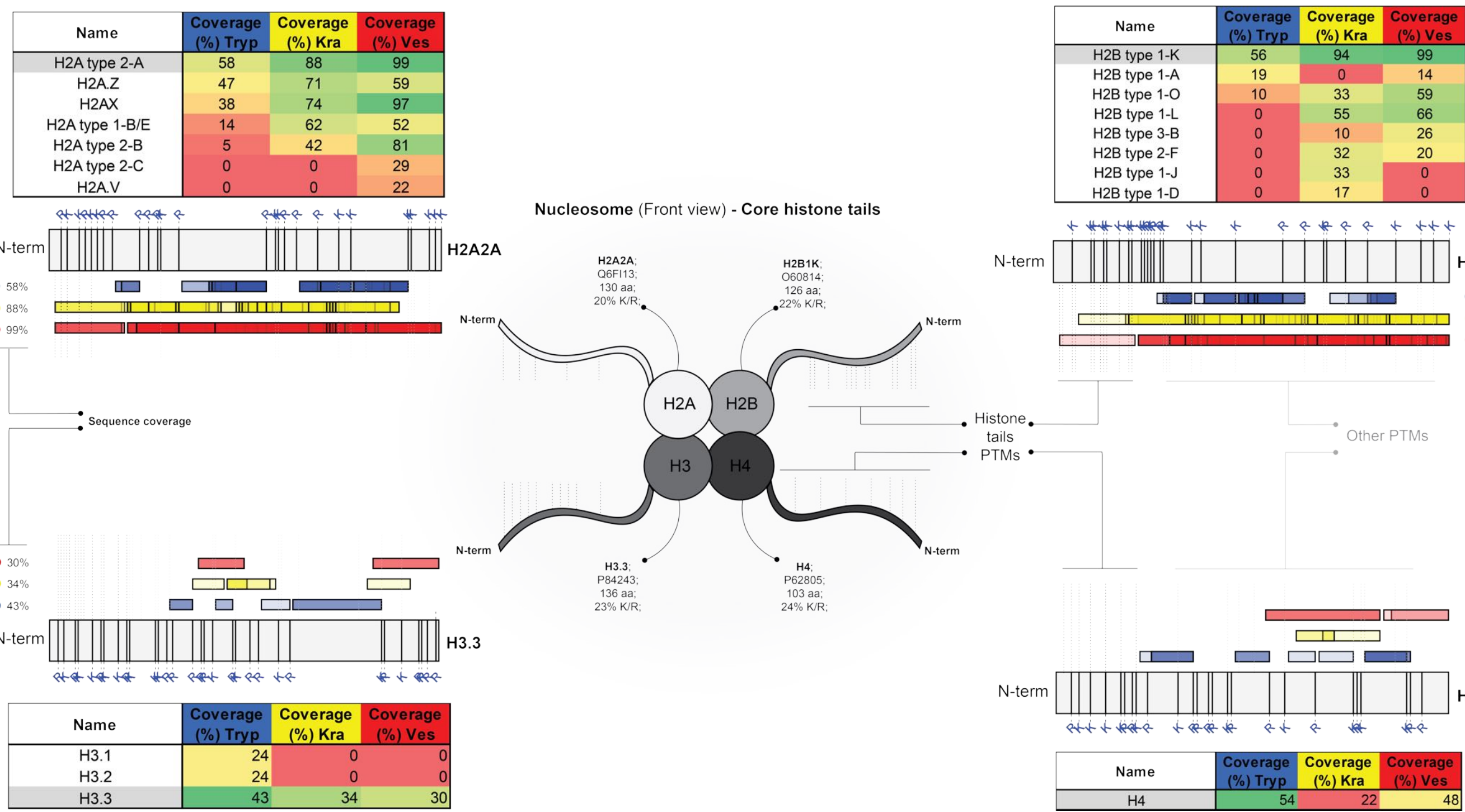


HTA-Proteases provide improved coverage for specific protein classes when combined with trypsin digest data. (A) Scatter plot of protein coverage with trypsin alone vs. trypsin in combination with HTA-Protease data. Proteins with <20% coverage improvement are in grey, proteins with >20% coverage improvement are colored by class. The dashed line indicates the 20% improvement boundary. (B) Bar plots showing coverage contributions by trypsin (red), CB14057 (blue), and CB23726 (green) for representative proteins from each listed class.

Deep De Novo IgG Sequence Coverage



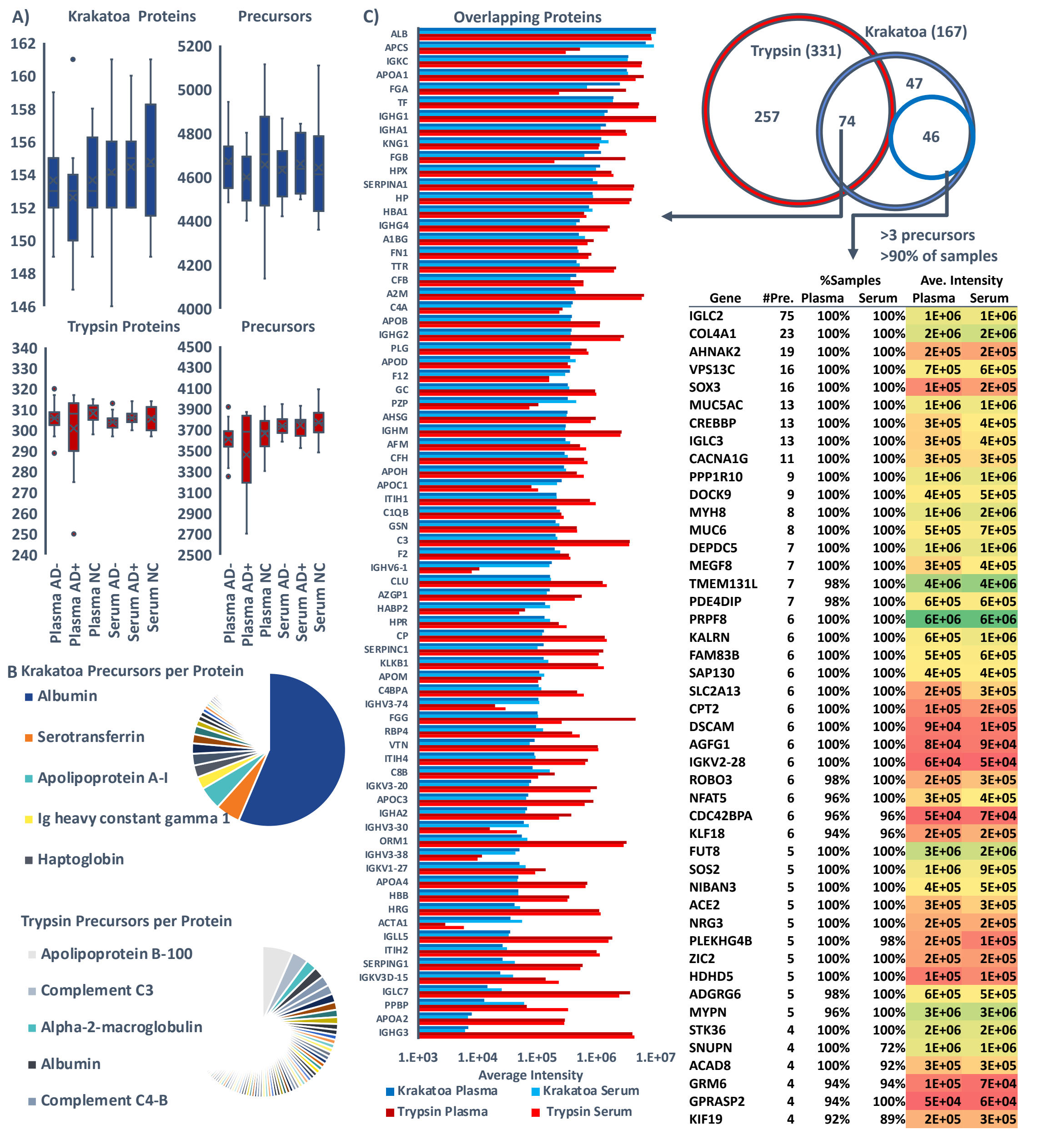
Simple Histone Coverage from Lysates



Commercially available K562 whole-cell lysate HTA-protease digestion with no chemistry or manipulation. Data publicly available on PRIDE.

Coverage for ‘Difficult’ Target Proteins

New ID's, Hormones, & PTM's in Blood



Yannone SM, Tuteja V, Goleva O, Leung DYM, Stotland A, Keoseyan AJ, Hendricks NG, Van Eyk JE, Kreimer S. **Blood to Biomarker Quantitation in Under One Hour** with Rapid Proteomics using a Hyperthermoacidic Protease. bioRxiv [Preprint]. 2024 Jun

CinderBio HTA-Proteases Available



HTA-Proteases HTA-Protocol

[1] M.C. McCabe, V. Gejji, A. Barnebey, G. Suizdak, L.T. Hoang, T. Pham, K.Y. Larson, A.J. Saviola, S.M. Yannone, K.C. Hansen, From volcanoes to the bench: Advantages of novel hyperthermoacidic archaeal proteases for proteomics workflows, J Proteomics (2023) 104992.
[2] S.M. Yannone, J.O. Fuss, A. Barnebey, Methods for rapidly digesting biopolymers with ultrastable enzymes for mass spectrometry-based analyses, in: USPTO (Ed.) Cinder Biological, Inc., US, 2017.