CHOP-Penn Proteomics Core Grant Boilerplate

The CHOP-Penn Proteomics Core provides a variety of protein and proteomics services for investigators at CHOP, University of Pennsylvania, and outside institutions. A wide range of state-of-the-art proteomics experiments are possible. These include, but are not limited to, comprehensive whole proteome and sub-proteome analysis, post-translational modification analysis, interactome analysis, protein identification, and targeted multiplexed quantification.

We offer a full array of services focused on meeting all of your proteomic needs. These services include but are not limited to:

- Proteomics: whole proteome, sub-proteome, interactome
- Post-translational modification analysis, omic scale: phosphoproteomics, ubiquitylomics, lysine acetylomics, and glycoproteomics
- Gel-purified protein identification
- HLA peptidomics
- Complete workflow for urine and plasma proteomics analysis
- Targeted proteomics: multiplexed parallel reaction monitoring
- Quantitative proteomics: label-free, DIA, SILAC, SILAM, AQUA peptide, and more
- Basic analysis of proteomics data using sequence database search algorithms and visualization software
- Advanced statistical and bioinformatic analyses including data processing and visualization, network and pathway analysis, and identification of statistically significant protein changes

In addition to the usual laboratory equipment found in a biochemical laboratory, the principal instrumentation used for proteomic analyses is:

- Thermo Q exactive HF mass spectrometer with Dionex nano ultimate 3000 UPLC
- Waters H-class Acquity UPLC standalone used for first dimension of multidimensional liquid chromatography to increase depth of analysis of complex proteome samples.

