

Multiplexing Protein Analysis Core Services

Targeted Quantitative Proteomics

We use LC-tandem mass spectrometry techniques of parallel reaction monitoring (PRM) and data independent acquisition (DIA) to measure protein abundance. The instruments used are a ThermoScientific Stellar quadrupole-linear ion trap and a ThermoScientific Exploris 480 quadrupole-orbitrap. The combination of experiments can quantify 500 to 5000 proteins in a single run. The targeted PRM assays are designed to target specific proteins based on their amino acid sequence, giving the assays high sensitivity in complex samples. Importantly, new software tools streamline the conversion of DIA results from the Exploris 480 into PRM methods on the Stellar.

Our workflow accommodates sufficient sample numbers to design experiments with good statistical power as well as a wide range of sample types and preparation methods. Users are asked to submit tissue or cell homogenates, made using tested methods from their lab, with precisely measured protein concentrations. We do the rest of the processing.

Synthesis & Turnover

Impaired protein homeostasis (proteostasis) is a hallmark of aging and is associated with several chronic diseases. Protein turnover, a primary proteostatic mechanism, is a dynamic process that consists of protein synthesis and protein degradation. To assess protein turnover as a proteostatic mechanism, the Core helps in the design and analysis of studies using deuterium oxide (D₂O).

Services

Service	Cost per Unit
Targeted analysis for single target	\$25/sample
Simple DIA	\$55/sample
Panel Development	\$1,100/each
Targeted analysis for large panel	\$130/panel
Deuterium incorporation into protein, including proteomic analysis and water enrichment (required)	\$260/panel
Deuterium incorporation into nucleotides (DNA and RNA), including water enrichment (required)	\$80/panel