

Proteome Sciences plc: Mass Spectrometry Based Proteomics

Proteome Sciences has been dedicated to developing and advancing proteomic technologies and novel biomarkers for over two decades

Proteome Sciences plc is a specialist CRO providing mass spectrometry-based proteomic services to support our global clients with their drug discovery, development, and biomarker programs. We have been developing proteomics technologies and novel biomarkers for over 20 years and developed the Tandem Mass Tag® (TMT®) technology. We work across all preclinical and clinical phases and can provide targeted biomarker measurements under GCLP conditions.

Whether you are looking to explore new targets, consolidate mechanisms of action, or obtain pharmacodynamic biomarkers, we have a range of proteomics workflows that deliver deep biological insights. We work largely with human/rodent based fluid and tissue samples, in-gel band sequencing and mass spectrometry-based immunoprecipitation proteomics. Handling everything from sample preparation through to bioinformatics and biological interpretation, we are your perfect partner for proteomics.

Innovative Technologies for Biomarker Discovery:

- **SysQuant®** is a combined phosphoproteomic and LC-MS2 proteomic workflow quantifying >20,000 unique phosphorylation sites and >8,000 proteins in typical cell or tissue-based studies
- **TMTcalibrator™** uses the power and flexibility of TMT to mix peripheral fluids – CSF, plasma, urine – with an excess of disease tissue that acts as a trigger for lower abundance biomarkers

- **Plasma Super Depletion** is designed for ultimate sensitivity in blood biomarker discovery. On its own it allows >4,000 medium and low abundant plasma proteins to be quantified with TMT. When combined with TMTcalibrator, we can quantify over 8,500 plasma proteins per sample

The Power of Purpose-built Bioinformatics:

- Proteomics involves a number of sample processing steps and in-process interferences that can lead to high technical variance. Understanding this, we have developed a suite of the most advanced statistical analysis tools to model data variance and select the most valid biomarker candidates
- Each bioinformatic package is data-driven for selection of normalisation, integration, and modelling modules, reducing the risk of user bias. Outputs are provided at peptide, phosphopeptide and protein levels, dependent on the study design
- A detailed package of interim analysis tables and visualisations are provided to allow clients complete transparency on the bioinformatics process
- Functional analysis is also provided as standard in discovery experiments offering enrichments based on the significantly regulated features for various gene ontology terms and other biological references such as pathways

Staying on Target:

- Selected Reaction Monitoring (**SRM/ MRM assays**) and parallel reaction monitoring (**PRM**) – validation of multiple biomarkers and preparation for use in clinical trials requires a switch to targeted methods
- PRM assays for measurement of >60 unique phosphorylation events in up to seven samples in a single 3h analysis with quantification against an internal calibration curve
- A PRM method with sensitivity in the low pg/ml range
- Two SRM assays for proprietary biomarkers in neurodegeneration and oncology will be launched later this year

Working with Us:

- Close client interactions to design the optimum experiments based on available budget and samples
- Clients are updated regularly on progress and receive a detailed written report with accompanying data files
- Extensive bioinformatics to aid interpretation of the experimental findings
- Post-project follow-up includes a dedicated data orientation meeting

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