Crown Bioscience Proteomics Services

Deep Protein Insights to Power Drug Discovery

Crown Bioscience offers a mass spectrometry-based proteomics platform, delivering deep protein insights to accelerate your drug discovery programs. Our services are designed to work seamlessly with our preclinical oncology models or as a standalone solution.
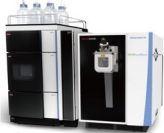
Proteomics Service Capabilities

We offer a comprehensive range of proteomics services to support various stages of drug discovery, from target identification to biomarker validation:

Service Type	Key Techniques	Applications
Global Proteomics (Discovery)	DIA, DDA, TMT, label-free quantification, bottom-up, top-down	Biomarker discovery, target identification, pharmacodynamics, patient stratification
Phosphoproteomics and PTM Analysis	Phosphoproteomics, ubiquitination, acetylation	Mechanism of action (MoA) studies, biomarker discovery
Targeted Proteomics	PRM, SRM/MRM, absolute quantification	Biomarker validation, target engagement, pharmacodynamic markers
Customized Proteomics Assays	Chemoproteomics, Immunopeptidomics, fit-for-purpose assay development	Tailored design around your research needs for customized biomarker and mechanistic studies

Our global proteomics services ensure deep coverage, with **10,000+ protein groups**.
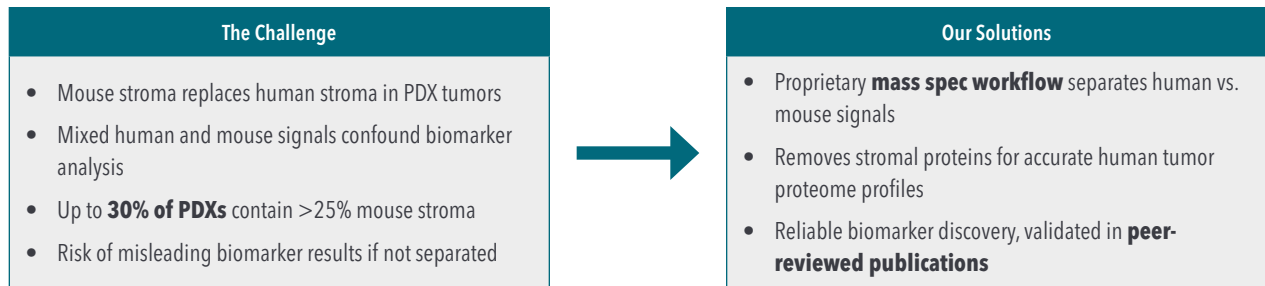
State-of-the-Art Proteomics Facility

Our facility utilizes cutting-edge mass spectrometry (LC-MS/MS) instruments to deliver the highest quality data.

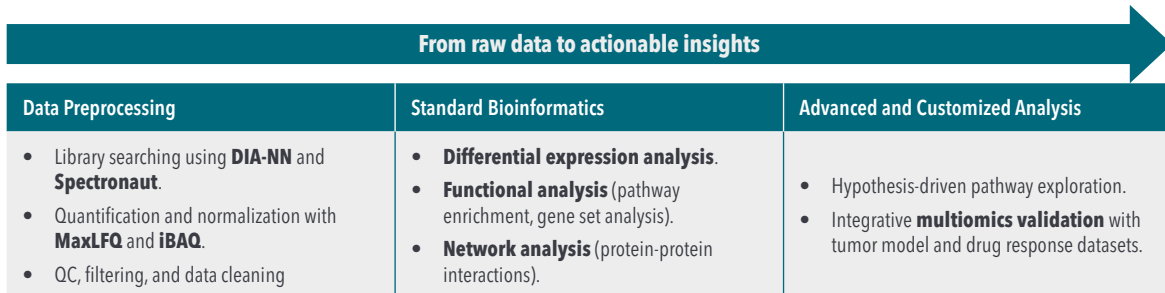|	Thermo Fisher Orbitrap™ Exploris™ 480	Thermo Fisher Orbitrap™ Astral™	BRUKER timsTOF™
Instrument	ThermoFisher SCIENTIFIC	ThermoFisher SCIENTIFIC	BRUKER
Key Benefits	• High-resolution quantification for discovery and targeted proteomics • Flexible workflows (DIA, DDA, TMT, PRM) • Reliable performance for biomarker discovery and targeted validation	• Next-gen sensitivity and speed • Deeper proteome coverage (10,000+ protein groups) • Lower sample input for precious samples	• Trapped ion mobility (TIMS) for 4D proteomics • Fast duty cycle for higher throughput • High sensitivity for PTM and low-abundance proteins

PDX Proteomics Workflow: Optimized for Human Tumor Signal

The Challenge	Our Solutions
• Mouse stroma replaces human stroma in PDX tumors • Mixed human and mouse signals confound biomarker analysis • Up to **30% of PDXs** contain >25% mouse stroma • Risk of misleading biomarker results if not separated	• Proprietary **mass spec workflow** separates human vs. mouse signals • Removes stromal proteins for accurate human tumor proteome profiles • Reliable biomarker discovery, validated in **peer-reviewed publications**

**Patient-derived xenograft** → Proteomics → **Data**

Comprehensive Data Analysis Pipeline

We provide a validated, full-spectrum proteomics analysis, transforming raw data into actionable biological insights.

From raw data to actionable insights

Data Preprocessing	Standard Bioinformatics	Advanced and Customized Analysis
• Library searching using **DIA-NN** and **Spectronaut**. • Quantification and normalization with **MaxLFQ** and **iBAQ**. • QC, filtering, and data cleaning	• **Differential expression analysis**. • **Functional analysis** (pathway enrichment, gene set analysis). • **Network analysis** (protein-protein interactions).	• Hypothesis-driven pathway exploration. • Integrative **multiomics validation** with tumor model and drug response datasets.

Standardized Analytical Service

We deliver interactive, web-based reports that are easy to navigate and share. The report includes:

- Project basic information.
- Quality check analysis.
- Bioinformatics analysis (including differential expression and functional enrichment).
- Methodology and References.
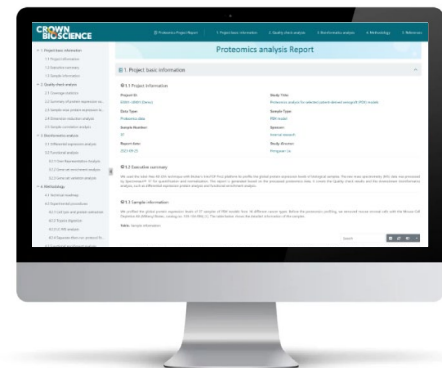
Your Partner in Advanced Proteomics Expertise

Deep oncology know-how and peer-reviewed workflows you can trust for translational impact.

- Expert in advanced proteomics workflows – TMT, DDA, DIA, optimized for oncology research.
- Validated by publications.