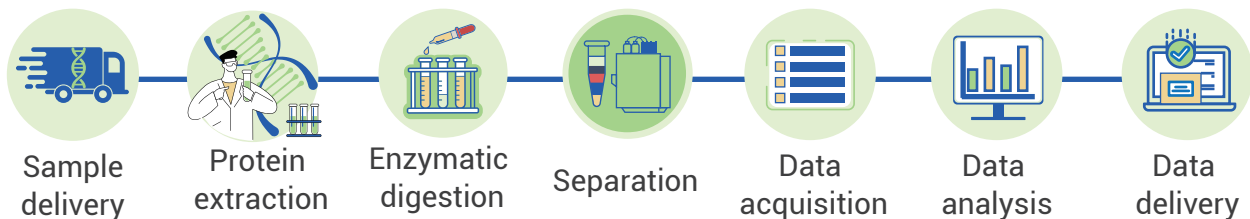


Proteomics

Proteomics is a field dedicated to unraveling the proteins expressed in organisms, cells, or tissues. It has broad applications in biology, medicine, agriculture, and biotechnology. Proteome sequencing and analysis enables the discovery of disease-specific biomarkers, the understanding of protein-protein interactions, and the exploration of essential biological pathways. The process involves protein extraction, separation, identification, and quantification, utilizing liquid chromatography (LC) and mass spectrometry (MS). BMKGENE possesses advanced instruments and substantial project experience, showcasing expertise in the field of proteomics.

Service Workflow



Proteomics Solutions

Qualitative Proteomics

(For SDS-PAGE/IP/Co-IP/Pull Down Samples)

- ▶ Protein-Protein Interactions
- ▶ Protein Identification

Quantitative Proteomics

- ▶ Non-targeted Quantification
 - Label-free
 - TMT (Tandem Mass Tag)
 - DIA (Data-Independent Acquisition)
- ▶ Targeted Quantification
 - PRM (Parallel Reaction Monitoring)

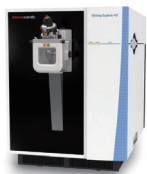
Service Advantages

- 1 Qualitative proteomics enables the identification of proteins in complex samples, such as protein mixtures or gel bands from eluates with advantages like short turn around time and high throughput.
- 2 Quantitative proteomics techniques facilitate the identification and quantification of proteins expressed in samples, allowing for the identification of differentially expressed proteins between samples or groups. Combined with bioinformatics analysis, the functions of differentially expressed proteins can be annotated, providing insights into biological questions.
- 3 PRM can be used for the validation of broad screening results, such as target proteins obtained from genomics/transcriptomics/quantitative proteomics. It enables relative/absolute quantitative analysis of these target proteins.

- ④ BMKGENE offers a range of proteomics solutions and can tailor them to specific research needs.
- ⑤ BMKGENE has extensive experience with cases over 300 species and 50,000 samples.

Service Specifications

Platform



Orbitrap Exploris 480



Q Exactive™ HF



Orbitrap Fusion™



Orbitrap Fusion™ Lumos



Orbitrap Eclipse

Comparison of Non-targeted Proteomics Techniques

	Label-free	DIA		TMT
Labeling	NO	NO		YES
Data Scanning Mode	DDA	DDA (Library Construction)	DIA	DDA
Reproducibility	Lower	High		High
Sensitivity	Lower	High		High
Multiplexing	NO	YES	NO	YES
Application	Comparing protein presence/absence	Large-scale samples	Analysis of different batches of samples	Comparing differential protein expression in the same species and tissue
Cost	★	★★		★★★

Sample Requirements

Sample Type	Lable-free	TMT/DIA/PRM
Animal tissue	20 mg	30 mg
Plant tissue	200 mg	300 mg
Microorganisms(Cellular precipitate)	50 µL	100 µL
Cells	5x10 ⁶	5x10 ⁶
Liquid samples	Depending on the specific type	
Protein	20 µg	200 µg
FFPE (Section thickness: 10 µm, area: 1.5x2 cm)	10	15-20

Featured Publications

Year	Journal	Title
2024	Int. J. Mol. Sci.	Multi-Omics Analysis Reveals the Distinct Features of Metabolism Pathways Supporting the Fruit Size and Color Variation of Giant Pumpkin
2024	Int. J. Mol. Sci.	Transcriptome and Metabolome Profiling Provide New Insights into Disuse Muscle Atrophy in Chicken: The Potential Role of Fast-Twitch Muscle Fibers
2024	Translational Oncology	Integrated multi-omics demonstrates enhanced antitumor efficacy of donafenib combined with FADS2 inhibition in hepatocellular carcinoma



Biomarker Technologies (BMKGENE)

✉ info@bmkgene.com 🌐 www.bmkgene.com

Global Locations

Germany United Kingdom United States China