Mass Spectrometry Service Overview
Protein Profiling

Service Description

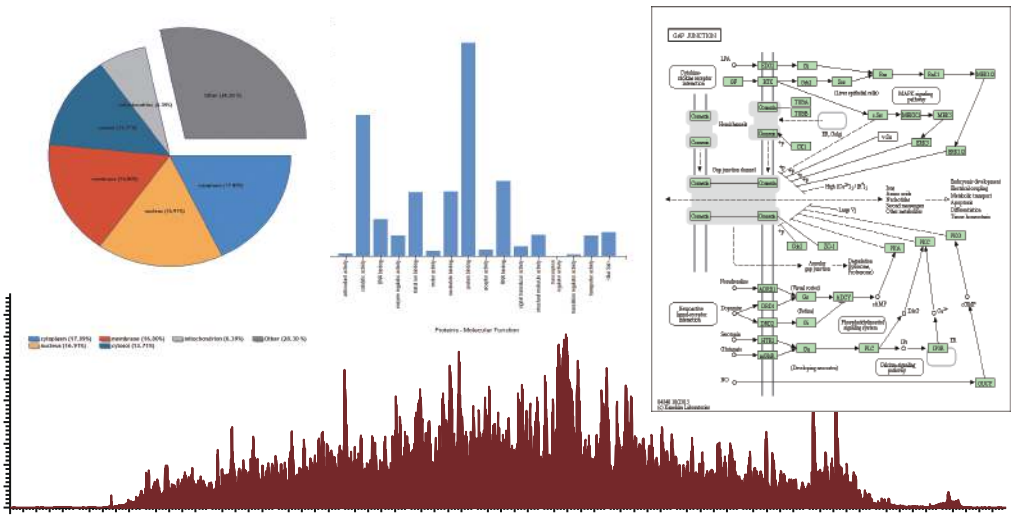
Proteomics data are increasingly combined with genomics information in multi-omics studies to enhance basic research and drug development projects. BGI is a pioneer in the field of multi-omics and offers advanced proteomics and bioinformatics solutions to support our client's research [1,2].

Our service laboratory in San Jose, CA is staffed by scientists with extensive experience in liquid chromatography and mass spectrometry-based analytical methods. Our state-of-the-art facility supports a broad range of protein research applications.

Profiling Global Protein Expression

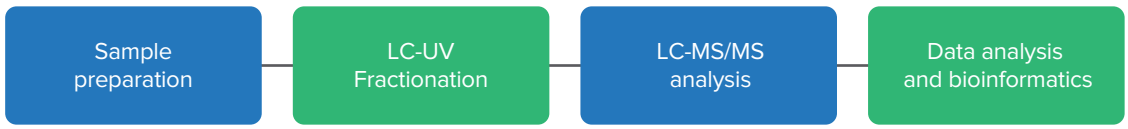
BGI provides innovative LC-MS-based services for profiling proteins and post-translational modifications (PTMs). We can accommodate a broad variety of sample types and experimental scale.

Our services are designed to simplify the challenge of measuring changes in protein expression and chemical modifications. BGI can provide workflow customization and consultation services to address unique project requirements. Turnaround time is approximately 4 weeks for our services.



Proteome Profiling

Proteome Profiling is a cost effective, high value solution for monitoring hundreds-to-thousands of proteins simultaneously. Our HPLC-UV sample fractionation services are highly recommended for complex sample types to maximize protein sequence coverage and detection dynamic range[3].
We perform sample digestion using sequencing-grade trypsin or alternative proteolytic method. Trypsin-digested peptide samples are analyzed using nano-flow LC-MS/MS[4].



PTM Profiling

Our PTM Profiling service utilizes multiple protease digests run independently to provide high sequence coverage of detected proteins which is critical for confident PTM site identifications[5].

Phospho Enrichment Profiling

Phosphorylated peptides are enriched using titanium dioxide. For deep phopho-proteome analysis, off-line fractionation is highly recommended[6]. We provide a full data report detailing detected protein IDs, peptide-localized PTM assignments, and Peptide Spectrum Match (PSM) counts.

Mass Spectrometry Service Specification

- Proteome and PTM Profiling services are performed using nano-flow liquid chromatography and high resolution Orbitrap mass spectrometry
- Customized services available

Sample Preparation and Services

- Digestion performed using sequencing-grade trypsin
- Off-line sample fractionation using UHPLC-UV technology
- Each fraction analyzed using 180 min nano-flow LC-MS/MS using a Q Exactive HF-X Orbitrap mass spectrometer
- Protein Peptide Spectral Match (PSM) data utilized for constructing proteomic profile

Mass Spec Services Quality Standard

- Summary including all methods and data analysis
- Reports provided in Excel or PDF format, RAW files available upon request

Turn Around Time

- Typical 20 working days from sample QC acceptance to data report delivery

Sample Requirements

We accept protein samples in a variety of formats. For maximum proteome coverage complex samples can be extensively fractionated off-line using our UHPLC-UV platform.

Sample type	Amount and Concentration		Minimum sample volume
Protein sample in liquid solution or in gel band/spot	Recommended	100 μg for each enzyme; 2 μg/μL	100 μL for each enzyme
	Minimum Required	10 μg for each enzyme; 1 μg/μL	10 μL for each enzyme

Data Analysis

- Data analysis and validation performed with SEQUEST or Mascot
- GO (Gene Ontology) category analysis
- COG (Cluster of Orthologous Groups of proteins) category analysis
- Pathway analysis
- DEPs (differentially expressed proteins) cluster analysis
- DEPs GO enrichment analysis
- DEPs pathway enrichment analysis

References

[1] Xun Z, Shangbo X et al. Tissue-specific Proteogenomics Analysis of Plutella xylostella Larval Midgut Using a Multialgorithm Pipeline. Mol Cell Proteomics. 2016; 15(6): 1791-1807. doi: 10.1074/mcp.M115.050989.

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[3] Chandramouli K, Qian PY. Proteomics: challenges, techniques and possibilities to overcome biological sample complexity. Hum Genomics Proteomics. 2009 Dec 8;2009. pii: 239204. doi: 10.4061/2009/239204.

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[5] Giansanti P, Tsiatsiani L, Low TY, Heck AJ. Six alternative proteases for mass spectrometry-based proteomics beyond trypsin. Nat Protoc. 2016 May;11(5):993-1006. doi: 10.1038/nprot.2016.057.

[6] Salter AI, Ivey RG, Kennedy JJ, Voillet V, Rajan A, Alderman EJ, Voytovich UJ, Lin C, Sommermeyer D, Liu L, Whiteaker JR, Gottardo R, Paulovich AG, Riddell SR. Phosphoproteomic analysis of chimeric antigen receptor signaling reveals kinetic and quantitative differences that affect cell function. Sci Signal. 2018 Aug 21;11(544). pii: eaat6753. doi: 10.1126/scisignal.aat6753.

[7] Baldwin MA. Protein identification by mass spectrometry: issues to be considered. Mol Cell Proteomics. 2004 Jan;3(1):1-9. Epub 2003 Nov 6. Review. PubMed PMID: 14608001

Request for Information or Quotation

Contact your BGI account representative for the most affordable rates in the industry and to discuss how we can meet your specific project requirements or for expert advice on experiment design, from sample to bioinformatics.

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