

Mass Spectrometry Service Overview

Quantitative Proteomics



Service Description

BGI America now offers proteomic and biologics characterization services to accelerate your life science research program. Our new portfolio of end-to-end LC-MS services leverages BGI's strengths in managing large scale computing infrastructure and pioneering innovative bioinformatics technologies.

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

We can help simplify your research challenge. BGI can provide workflow customization and consultation services to address unique project requirements.

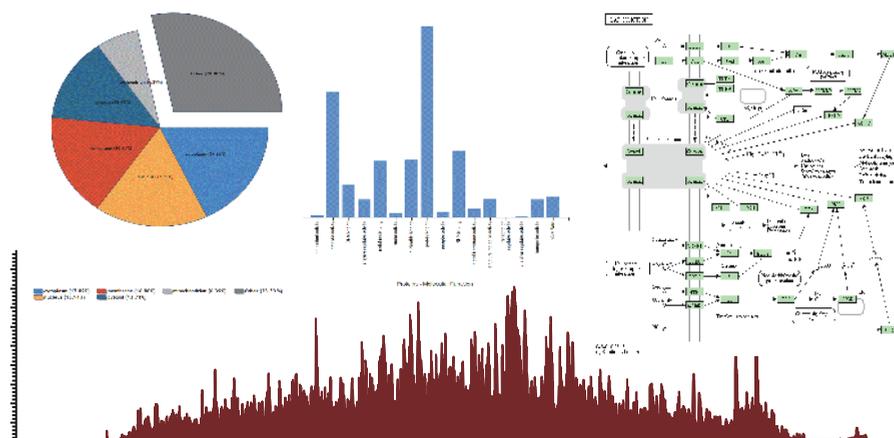
Turnaround time is approximately 4 weeks for our services.



Mass Spectrometry Services for Quantitative Proteomics

Proteomics and metabolomics 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}.

Recent advances in mass spectrometry have provided powerful tools for the analysis of proteins from a variety of organisms and cell types. BGI applies state-of-the-art MS-based techniques for protein identification, protein characterization, relative and absolute quantitation, as well as for the study of post-translational modifications (PTMs) and protein-protein interactions.



Cutting Edge Solutions for Quantitative Proteomics

We are proud to announce the opening of BGI's new state-of-the-art Mass Spec Service Center to provide proteomic services for customers in North America. This new laboratory, based at BGI's Center of Excellence in San Jose, California, will deliver complete solutions for a broad range of proteomic profiling and protein identification projects³. All of our proteomic services can be customized to meet your drug discovery project needs.

Quantitative Proteomic Services

BGI supports multiple workflows for proteomic quantitation. We have developed innovative solutions for optimizing the process of accurately quantifying proteins in complex biological matrices and other complex mixtures. Our quantitative services include Label-Free Data-Independent Acquisition (DIA), Isobaric Label (TMT tag), or Targeted Quantitation. We are happy to work with you to determine the best quantitative proteomics service for your project³.

Parameter	Label-Free DIA	Isobaric Label	Targeted PRM
Proteome Coverage	●●	●●●	
Quantitative Accuracy	●●●	●●	●●●●
Dynamic Range	●●	●	●●●●
Overall Sensitivity	●●	●●	●●●●
Service Throughput	●●●	●●	●●●●

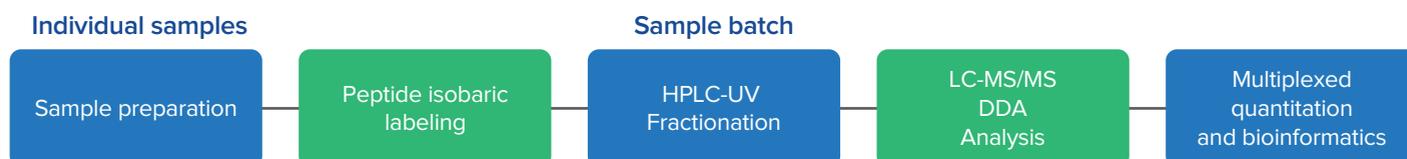
Label-Free DIA Quantitative Proteomics

Data-Independent Acquisition (DIA) is a label-free quantitative technique which provides highly consistent quantitation and broad proteome coverage. We create a customized spectral library with your specific sample and then analyze individual samples using nano-flow LC-MS/MS with DIA scanning and quantitation⁴. Label-Free DIA Quantitative Proteomics service is ideal for long-term projects or projects with large sample sets which require accurate and reproducible quantitation.



Isobaric Label Quantitative Proteomics

Isobaric Label services incorporate sample multiplexing to provide deep proteome coverage and highly precise quantitation of small or medium-sized sample sets. We provide Isobaric Label Quantitative Proteomics service using Tandem Mass Tagging (TMT) technology developed by Proteome Sciences plc and licensed by Thermo Fisher Scientific⁵.



Targeted PRM Quantitation

Targeted PRM is the most sensitive and specific method for peptide quantitation. This service is ideal for absolute quantitation of peptides or screening large numbers of samples for biomarker proteins and post-translational modification sites. Parallel Reaction Monitoring (PRM) technology is a cost-effective, high-bandwidth alternative to Selected/Multiple Reaction Monitoring (SRM/MRM)⁶.



Mass Spectrometry Service Specification

Our quantitative proteomics services are performed using nano-flow liquid chromatography and high resolution Orbitrap mass spectrometry. Sample digestion is performed using sequencing-grade trypsin or alternative proteolytic method. We can provide Targeted PRM Peptide Quantitation service using micro-flow or analytical flow rates for high sample throughput.

Label Free DIA Quantitative Proteomics Sample Preparation and Services

- DDA-Spectral Library generated using UHPLC-UV technology and sample fractionation
- 180 min nano-flow LC-MS/MS using a Q Exactive HF-X Orbitrap mass spectrometer

Isobaric Label Quantitative Proteomics Sample Preparation and Services

- Increase proteome depth of coverage using UHPLC-UV sample fractionation
- Each fraction analyzed using 180 min nano-flow LC-MS/MS using a Q Exactive HF-X Orbitrap mass spectrometer

Targeted PRM Quantitation Sample Preparation and Services

- Customized LC method and PRM-acquisition MS method

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

Mass Spec Services Quality Standard

Label-Free DIA Quantitative Proteomics, Isobaric Label Quantitative Proteomics and Targeted PRM Quantitation summary includes 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 for Label-Free DIA Quantitative Proteomics, Isobaric Label Quantitative Proteomics and Targeted PRM Quantitation.

Sample Requirements

We accept protein samples in a variety of formats. For attaining maximum proteome coverage we recommend utilizing our sample fractionation services, performed using our off-line UHPLC-UV platform.

Protein sample in liquid solution	Amount and Concentration		Minimum sample volume
Label-Free DIA	Recommended	400 ug with fractionation; 2 µg/µl	200 µl
Quantitative Proteomics	Minimum Required	100 ug with fractionation; 1 µg/µl	100 µl
Isobaric Label Quantitative Proteomics	Recommended	At least 500 ug; 2 µg/µl	250 µl
	Minimum Required	50 ug; 1 µg/µl	50 µl

Sample type	Minimum sample volume
Targeted PRM Quantitation: Protein sample in liquid solution	100 µl
	10 µl

Targeted PRM Quantitation Data Analysis

We can adapt our Targeted PRM peptide quantitation services to meet your requirements using multiple data analysis platforms, including Skyline, Chromeleon, or Qual Browser.

References

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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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