

Overview of Mass Spectrometry Service Quantitative Proteomics

An Overview of The Service

We provide proteome and biologics characterization services to help you go forward with your life science research program. Our comprehensive LC-MS service portfolio capitalizes on our expertise in administering large-scale computing infrastructure and developing innovative bioinformatics technologies.

The experts at our mass spectrometry service laboratory have substantial experience in the fields of liquid chromatography and mass spectrometry-based analytical methods. This cutting-edge facility is outfitted to accommodate a wide range of research applications for our clients.

We can assist you in simplifying your research project. To meet the specific needs of a given project, we can provide workflow customization and advisory services.

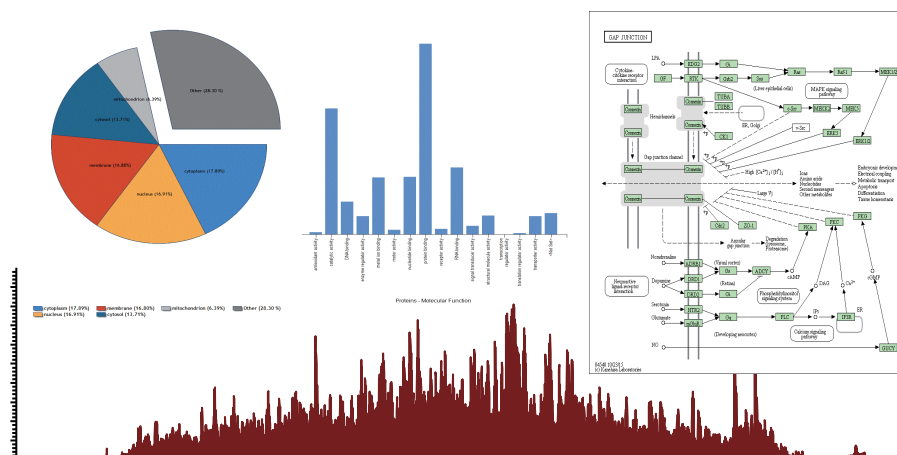
Our services have a turnaround time of around 4 weeks.



Mass Spectrometry Services for Quantitative Proteomics

Multi-omics research increasingly utilize proteomics and metabolomics data with genomics data to improve fundamental research and drug development endeavors. We provide cutting-edge proteomics and bioinformatics services to back up our clients' research 1, 2.

Mass spectrometry has advanced rapidly in recent years, providing scientists with potent new tools to analyze proteins in all sorts of organisms and cell types. We use cutting-edge mass spectrometry-based methods for the purpose of protein identification, protein characterization, relative and absolute quantitation, and the study of post-translational modifications (PTMs) and protein-protein interactions.



Cutting Edge Solutions for Quantitative Proteomics

Our state-of-the-art Mass Spec Service Center provides proteomic services for customers in North America. Our laboratory, based in San Jose, California, will deliver complete solutions for a broad range of proteomic profiling and protein identification projects. All of our proteomic services can be customized to meet your drug discovery project needs.

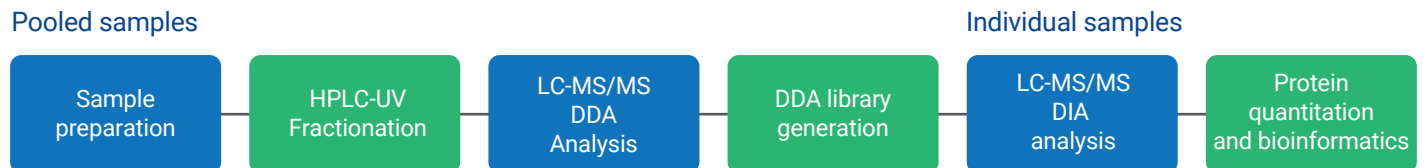
Quantitative Proteomic Services

We support multiple quantitative proteomics workflows. To facilitate the precise quantification of proteins in biological matrices and other complex mixtures, we have devised innovative solutions to optimize the process. We provide quantitative services including Targeted Quantitation, Isobaric Label (TMT tag), and Label-Free Data-Independent Acquisition (DIA). We will gladly collaborate with you to determine which quantitative proteomics service is ideal for your project.

Parameter	Label-Free DIA	Isobaric Label TMT	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 that offers extensive proteome coverage and highly accurate quantitation. Your particular sample is used to build a customized spectral library, which is then used to analyze individual samples utilizing nano-flow LC-MS/MS with DIA scanning and quantitation. The Label-Free DIA Quantitative Proteomics service is appropriate for long-term or large sample set projects that require precise and reproducible quantitation⁴.



Isobaric Label TMT Quantitative Proteomics

Isobaric Label services incorporate sample multiplexing to provide comprehensive proteome coverage and highly accurate quantification of small or moderate sample sets. We offer an Isobaric Label Quantitative Proteomics service utilizing Tandem Mass Tagging (TMT) technology that was developed by Proteome Sciences plc and licensed by Thermo Fisher Scientific⁵.



Targeted PRM Quantitation

The most sensitive and selective peptide quantitation approach is targeted PRM. This service is appropriate for screening massive quantities of samples or absolute peptide quantitation for biomarker proteins and post-translational modification sites. In comparison to Selected/Multiple Reaction Monitoring (SRM/MRM), Parallel Reaction Monitoring (PRM) technology is more cost-effective and high-bandwidth⁶.



Mass Spectrometry Service Specification

We provide quantitative proteomics services employing high resolution Orbitrap mass spectrometry and nano-flow liquid chromatography. Sample digestion is carried out using sequencing-grade trypsin or an alternative proteolytic method. We can deliver Targeted PRM Peptide Quantitation employing 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
- Nano-flow LC-MS/MS using a Thermo Q Exactive™ HF-X, Thermo Orbitrap Eclipse™ Tribrid™ , or Bruker TimsTOF Pro 2 mass spectrometer

Isobaric Label Quantitative Proteomics Sample Preparation and Services

- Increase proteome depth of coverage using UHPLC-UV sample fractionation
- Each fraction analyzed using nano-flow LC-MS/MS with a Thermo Q Exactive™ HF-X, Thermo Orbitrap Eclipse™ Tribrid™ , or Bruker TimsTOF Pro 2 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 Quantitative Proteomics	Recommended	400 µg with fractionation; 2 µg/µl	200 µl
	Minimum Required	100 µg with fractionation; 1 µg/µl	100 µl
Isobaric Label Quantitative Proteomics	Recommended	At least 500 µg; 2 µg/µl	250 µl
	Minimum Required	50 µg; 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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- [3] Wong, J. W. H., & Cagney, G. (2009). An Overview of Label-Free Quantitation Methods in Proteomics by Mass Spectrometry. *Proteome Bioinformatics*, 273–283. doi:10.1007/978-1-60761-444-9_18.
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To learn more

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

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