

The New-In Orbitrap Astral-Based DIA Quantification Proteomics Service

Accelerate Your Life Science Research

🤣 Deeper Coverage 🛛 🥑 Higher Sensitivity 🔗 Higher Throughput

DIA (Data-Independent Acquisition) protein quantification is a comprehensive mass spectrometry-based approach in proteomics. It enables simultaneous quantification of thousands of proteins in complex biological samples, making it ideal for large-scale studies, such as biomarker discovery, drug development, and functional proteomics.

### BGI Genomics: Leading the Way in High-Quality DIA Proteomics Services

BGI Genomics, with over 20 years of expertise in proteomics, provides DIA services for approximately 10,000 projects annually. Supported by a professional team and state-of-the-art instruments, BGI Genomics has developed a comprehensive SOP system and standardized project workflows. The entire process includes over 50 quality control points, ensuring the delivery of high-quality data with exceptional accuracy, reproducibility, and coverage to our clients. We are committed to providing end-to-end premium services.

BGI Genomics has also participated in some global research on quantitative performance assessment, as well as the standardization and harmonization of multinational DIA proteomics analysis. Our DIA data consistently demonstrates high accuracy and reproducibility.



Figure 1. The number of proteins identified (with a 1% FDR) from the HRMS1-DIA analyses of QC sample. Lab7 refers to BGI Genomics. As shown, both the identification number and reproducibility are outstanding<sup>[1]</sup>.



Figure 2. Reproducibility of SWATH-MS (DIA) measurements. Site10 refers to BGI Genomics. As demonstrated, the CV (coefficient of variation) values are below 20%, indicating higher reproducibility<sup>[2]</sup>.

#### **Reference:**

[1] Xuan, Yue et al. "Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies." Nature communications vol. 11,1 5248. 16 Oct. 2020, doi:10.1038/s41467-020 -18904-9

[2] Collins, Ben C et al. "Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry." *Nature communications vol.* 8,1 291. 21 Aug. 2017, doi:10.1038/s41467-017-00249-5

With the adoption of the Orbitrap<sup>™</sup> Astral<sup>™</sup> mass spectrometer, BGI Genomics now offers a more competitive and higher-quality DIA service. This advanced technology provides deeper coverage, higher sensitivity, and increased throughput, accelerating your life science research programs.

### **Deeper Coverage**

See more in less time or spend more time and go even deeper 45



Figure 3. Unlock near whole-proteome depth of coverage with the identification of 12,000 proteins in 1 hour from a single-shot experiment

# **Higher Sensitivity**



Figure 4. Increase throughput and depth of coverage with higher sensitivity by identifying over 5,000 proteins from 250 pg of HeLa at a rate of 80 samples per day

# **Higher Throughput**

#### Analyze one sample in only 8 minutes



Figure 5. Identify over 8,000 proteins with an 8-minute injection-to-injection cycle

Figures 3-5 source: Thermo Fisher Scientific

(https://www.thermofisher.cn/cn/en/home/industrial/mass-spectro metry/liquid-chromatography-mass-spectrometry-lc-ms/lc-ms-sy stems/orbitrap-lc-ms/orbitrap-astral-mass-spectrometer.html)

# **Request for Information or Quotation**

Contact a BGI Genomics representative to discuss how we can meet your specific needs or for expert advice on experiment design, from sample to bioinformatics.

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