

Human Blood DIA Quantitative Proteomics Service Overview



Service Description

Data-independent acquisition (DIA) is a relatively new approach to acquisition in Mass Spectrometry (MS) but one which has already been applied in many National Precision Medical Projects, such as the "Cancer Moonshot", "Zurich Cancer Map" and "ProCan Project".

Protein DIA quantification, is a specific method used to perform quantitative analysis of enzymatic peptides by LC-MS/MS DIA analysis. Combining traditional DDA technology based spectral libraries and Spectronaut, the industry's leading commercial DIA analysis software, BGI participates in quantitative performance assessment as well as standardization and harmonization of Multi-National DIA proteomics analysis supporting precision medicine studies and therefore is able to accurately identify and quantify the proteome and provide customers with a range of information including:

- information on the source of peptides
- protein identification as well as their species
- changes in protein expression

Challenges with Blood Proteome Studies



Broad dynamic range
10 orders of magnitude

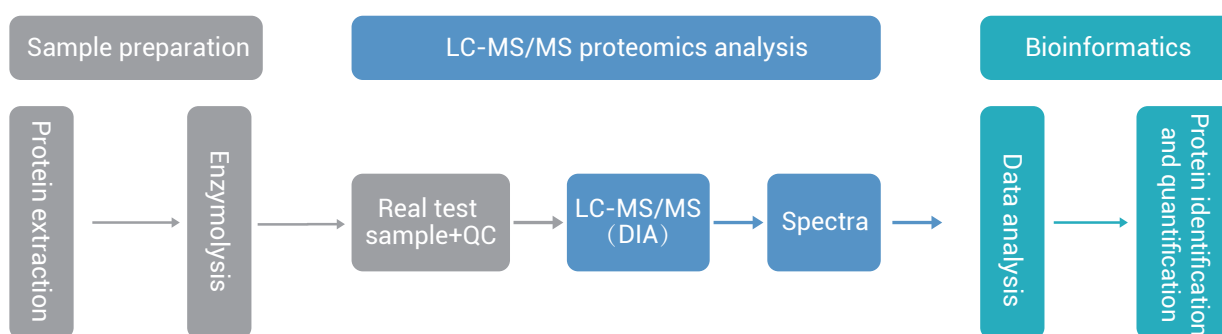


The 10 most abundant proteins
account for 90% of total content



Highly-diverse
proteins categories

Workflow



Service Features

01

Self-built blood spectrum library "BGI-BPSL" (Blood Proteome Spectral Library) avoids need to build extra libraries for the project.

02

Repeatability and stability of up to 90% enables reliable proteome research of large cohort blood samples.

03

Over 1,500 proteins identified, covering a wide range of low abundance and low molecular weight proteins

04

A complete set of Multi-Omic Correlation Analysis and Targeted Protein Quantitative Validation services provide customers with a one-stop service from clinical research to clinical application.

Applications



Discovery of disease protein markers



Establishment of health physiological reference baselines



Study of drug regulation, drug prediction and the mechanism of adverse drug effects



Research into the diagnosis and treatment of tumors



Accurate monitoring of big health data

Bioinformatics Analysis Workflow

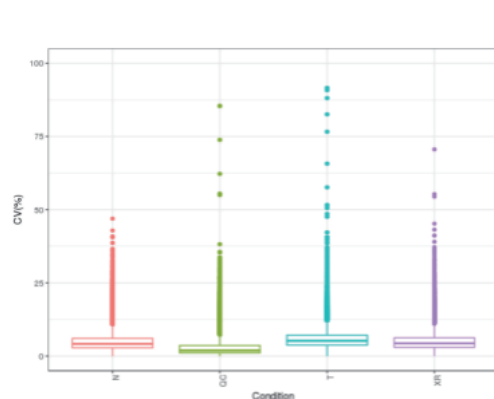
Standard:

01	Project overview	02	Data quality control	03	Protein identification and quantification list
04	Differential proteins data statistics and volcano plot	05	Principal component analysis (PCA)	06	Expression pattern cluster analysis
07	Time series analysis	08	Protein GO/COG/KOG/ Pathway annotation	09	Protein-protein interaction analysis
10	GO/COG/KOG enrichment analysis of differential proteins	11	Repeatability analysis	12	Protein subcellular localization analysis

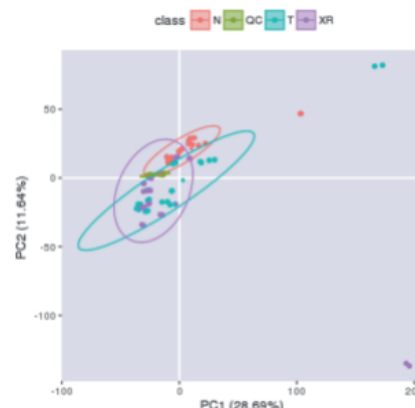
Customized:

Proteome and transcriptome/RNA-seq correlation analysis
 Quantitative proteomics and phosphoproteomics correlation analysis
 Proteome + metabolome correlation analysis

Examples of Data QC Analysis - Stability and Repeatability

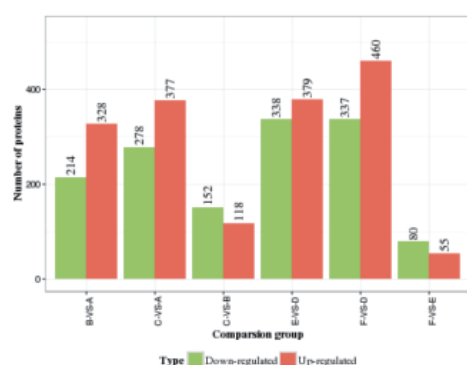


CV Distribution

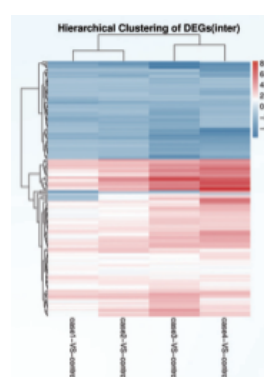


PCA Analysis

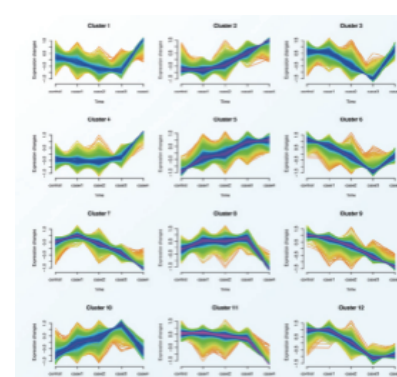
Examples of Protein Quantification Analysis



Quantification Statistics



Cluster Analysis



Time Series Analysis

Application Example

Serum DIA proteomics indicate PI3 could be a potential biomarker for psoriasis

Xu M etc. In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. *Theranostics*. 2019

Plasma DIA proteomics show PIGR and ALDOB are significantly associated with NAFLD

Niu L L etc. Plasma proteome profiling discovers novel proteins associated with non-alcoholic fatty liver disease. *Molecular Systems Biology*. 2019

DIA quantification in BGI Genomics shows high coverage and reproducibility

Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. *Nature communications*. 2017 (BGI Genomics contribution No.10)

Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. *Nature communications*. 2020 (BGI Genomics contribution No.7)

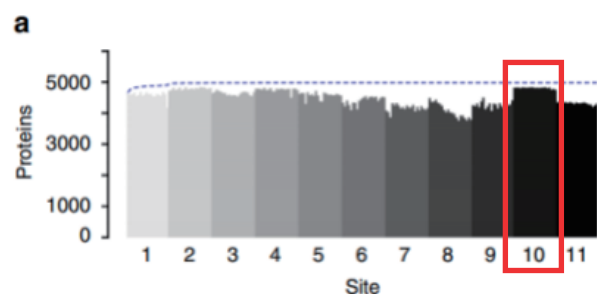


Figure 1. The number of proteins detected in SWATH-MS analyses is shown ordered by site of data collection

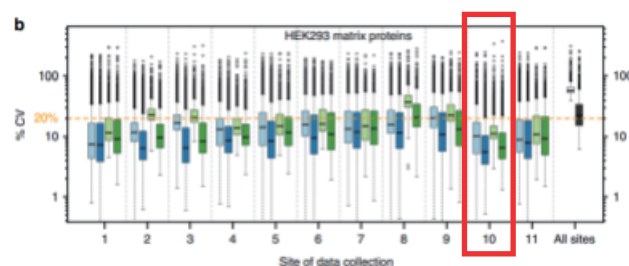


Figure 2. The CV of protein abundances for the 4077 proteins that were detected in >80% all samples in different sites

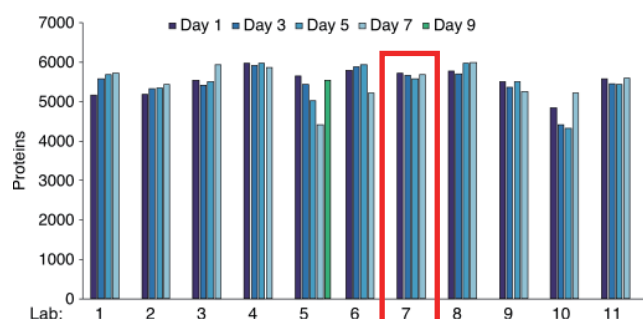


Figure 3. The number of proteins identified (with a 1% FDR) from the HRMS1-DIA analyses of QC sample

Sample Requirements

Amount of human plasma, serum: $\geq 100 \mu\text{L}$

Turn Around Time

Typical 3-4 weeks from sample QC acceptance to data report delivery for Blood DIA Quantitative Proteomics

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.

info@bgi.com
www.bgi.com

For Research Use Only. Not for use in diagnostic procedures (except as specifically noted).

Copyright© BGI Genomics 2025. All trademarks are the property of BGI Genomics or their respective owners. This material contains information on products targeted to a wide range of audiences and could contain product details or information otherwise not accessible or valid in your country. Please be aware that we do not take any responsibility for accessing such information, which may not comply with any legal process, regulation, registration, or usage in the country of your origin. Unless otherwise informed, certain sequencers and sequencing reagents are not available in selected countries or regions. Please get in touch with a representative for regional availability. The company reserves the right of final interpretation.



www.bgi.com



BGI Genomics

