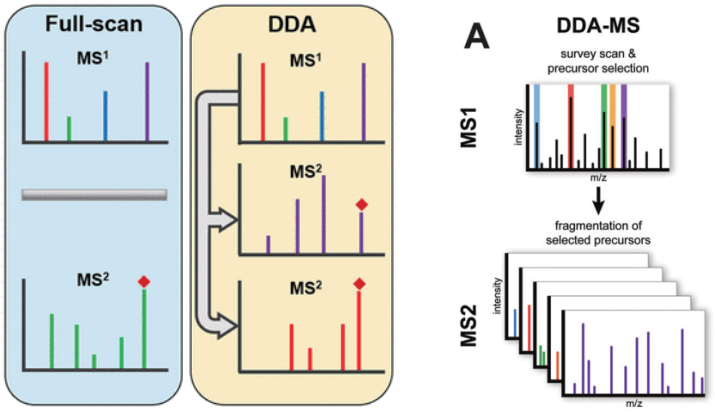
Label Free DDA Proteomics Service Overview

Service Description

Quantitative proteomics refers to the identification and quantification analysis of proteins in two or more samples to obtain the differential expression and function information of relevant proteins. It plays an important research role in the prevention, diagnosis, prognosis and efficacy monitoring of diseases, and can be used to help develop new therapeutic drugs.

Liquid chromatography - tandem mass spectrometry (LC-MS/MS) is currently the best method for unbiased, high-throughput proteomics analysis. In contrast to label-dependent quantitative proteomics such as the iTRAQ method, label-free data-dependent acquisition (DDA) proteomics doesn't need to use expensive a stable isotope for labeling of proteins. This allows accurate protein quantification of samples without additional error-prone in vitro labelling reactions and enables fast proteome identification and quantification.

In a typical DDA analysis, the mass spectrometer generates a full-scan mass spectra to determine the molecular weights of peptides and then acquires MS/MS spectra on the N most intense peptide ions. Hundreds of MS/MS spectra can be generated in a single run and downstream data analysis tools are applied for peptide identification and quantification. Since the peptides selected for fragmentation are usually the most abundant peaks in the survey scan, it is easy to cause the loss of low abundance peptides.



Schematic overview of the DDA-MS

Krasny L, et al., Data-independent acquisition mass spectrometry (DIA-MS) for proteomic applications in oncology, (2020)

DDA methods have been extensively utilized in the proteomics field since their inception. BGI has extensive experience in the field of label free DDA proteomics.

Research Applications

- Disease biomarker research
- Drug efficacy evaluation
- Special behavior mechanism and food/medicinal value research
- Plant growth and development research
- Plant disease resistance and insect resistance research
- Microbial stress and adversity physiology research

Label Free DDA Analysis Workflow

BGI Service Advantages

01 Fast Turnaround Time	02 Lower Cost	03 Low Complexity Analysis
No labeling enables fast proteome identification and quantification	Less pre-processing leads to less cost and retains the original sample information	Suitable for samples with low complexity and also can be used to analyze micro samples

Bioinformatics Analysis Standard Workflow

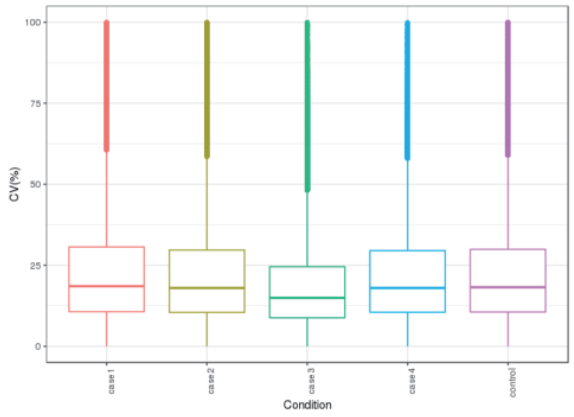
Standard:

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

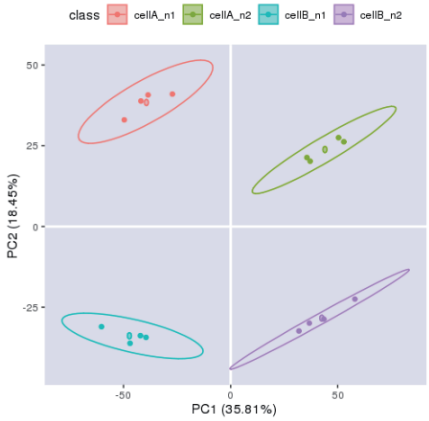
Customized Services:

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

Examples of Data QC Analysis - Stability and Repeatability

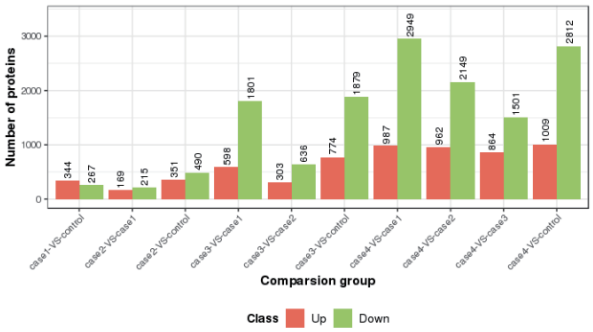


CV Distribution

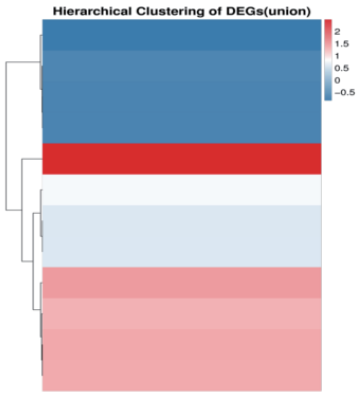


PCA Analysis

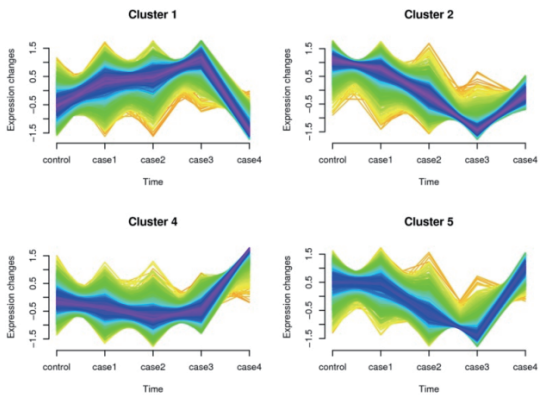
Examples of Protein Quantification Analysis



Quantification Statistics



Cluster Analysis



Time Series Analysis

General Sample Requirements

SAMPLE TYPE		AMOUNT	
		RECOMMEND	MINIMUM
Animal	Common animal tissues: animal internal organs (heart, liver, spleen, lung, kidney), skin, muscle, brain, etc	≥ 5 mg	≥ 1 mg
	Mollusks (Toxoplasma, Schistosomiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	≥ 5 mg	≥ 1 mg
Cell	Suspended cells, adherent cells	≥ 1×10^5	≥ 1×10^5
	Cell culture supernatant	≥ 5 mL	
Exosome	Exosome isolated by customer	≥ 10 μg, ≥ 0.5 μg/μL	
Fluid	Plasma, serum (remove highly-abundant protein)	≥ 200 μL	≥ 100 μL
	Plasma, serum (with highly-abundant protein)	/	
	Amniotic fluid, cerebrospinal fluid, semen, etc. (remove highly-abundant protein)	≥ 1 mL	≥ 500 μL
	Amniotic fluid, cerebrospinal fluid, semen, etc. (with highly-abundant protein)	≥ 100 μL	≥ 50 μL
	Saliva, milk	≥ 50 μL	≥ 20 μL
	Urine	≥ 20 mL	≥ 10 mL
	Tear	≥ 5 μL	≥ 3 μL
Plant	Twigs of plants (leaf buds, tender leaves), algae	≥ 200 mg	≥ 100 mg
	Old leaves, roots, stems, bark of plants	≥ 500 mg	≥ 500 mg
	Plant buds, pollen	≥ 20 mg	≥ 10 mg
	Plant seeds (rice/wheat seeds, etc.), fruits (apples, peaches, pears)	≥ 500 mg	≥ 200 mg
Microorganism	Prokaryotic bacteria (E. coli, Staphylococcus aureus, etc.), fungi (yeast, etc.)	Thallus ≥ 50 mg cells ≥ 5×10^6	
Protein solution	Complex protein solution, protein powder	≥ 200 μg, ≥ 0.5 μg/μL	≥ 5 μg, ≥ 0.5 μg/μL
Others	Feces	≥ 200 mg	≥ 100 mg

Turn Around Time

Sample size: 1-20, 3-4 weeks

To Learn More

To learn how your research can benefit from BGI's extensive experience in Label Free DDA Proteomics, visit www.bgi.com, write to us via info@bgi.com or contact your local BGI office.

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We Sequence, You Discover