

Isobaric Label Quantitative Proteomics Service Overview

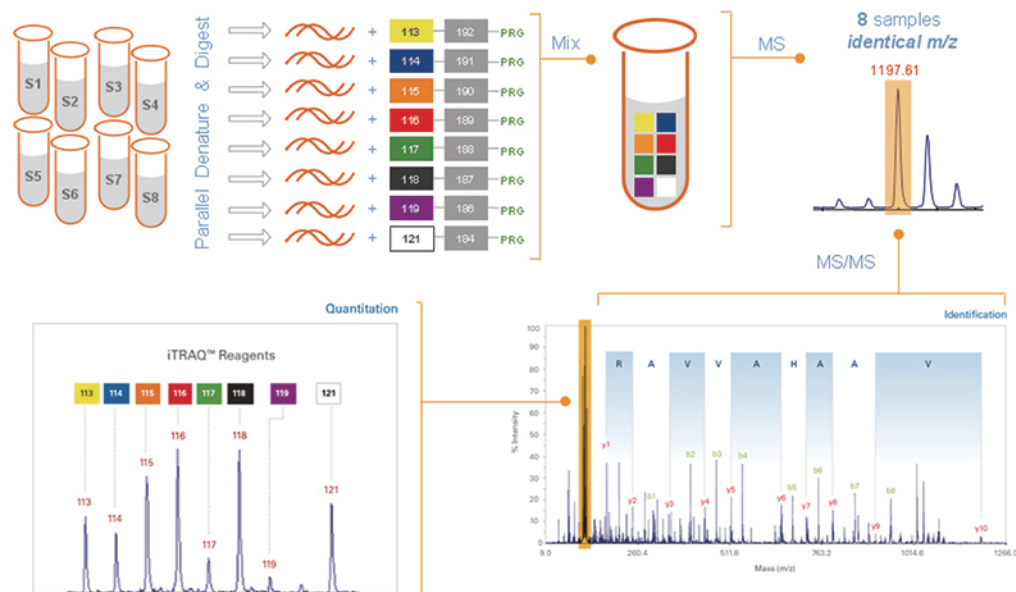


Service Description

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. Quantitative proteomics is most often applied in research concerning the prevention, diagnosis, prognosis and efficacy monitoring of diseases, and in helping to develop therapeutic drugs.

BGI Genomics provides Isobaric Label Quantitative Proteomics services using iTRAQ (Isobaric Tags for Relative and Absolute Quantitation), IBT (Isobaric Tags for Quantitation) and TMT (Tandem Mass Tags for Quantitation) technologies developed by AB SCIEX, BGI Genomics and Thermo Scientific, respectively.

The iTRAQ reagents are the first set of multiplexed, amine-specific, stable-isotope reagents that can label the lysine residues and N terminus of all peptides in between 2 to 8 (8-plex) different biological samples/treatments enabling simultaneous identification and quantitation.



Isobaric iTRAQ reagents 8-plex workflow

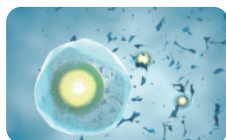
Williamson B, et al., Identification and quantitation of proteins using mass spectrometry-based peptide multiplex labelling methods, (2008)

IBT protein quantitative analysis is a BGI Genomics-developed upgraded version of conventional iTRAQ protein quantitative analysis, and IBT reagents can compare 16 different samples in parallel. TMT reagents have the same principle and compare up to 18 different samples in parallel.

Summary of Three Isobaric Label Reagent Options

TAG	ITRAQ		TMT		IBT	
Mode	4-plex	8-plex	16-plex	18-plex	10-plex	16-plex
Reporter 1	114	113	126	126	114	114
Reporter 2	115	114	127N	127N	115N	115N
Reporter 3	116	115	127C	127C	115C	115C
Reporter 4	117	116	128N	128N	116N	116N
Reporter 5		117	128C	128C	116C	116C
Reporter 6		118	129N	129N	117N	117N
Reporter 7		119	129C	129C	117C	117C
Reporter 8		121	130N	130N	118N	118N
Reporter 9			130C	130C	118C	118C
Reporter 10			131N	131N	119	119N
Reporter 11			131C	131C		119C
Reporter 12			132N	132N		120N
Reporter 13			132C	132C		120C
Reporter 14			133N	133N		121N
Reporter 15			133C	133C		121C
Reporter 16			134N	134N		122
Reporter 17				134C		
Reporter 18				135N		

Research Applications



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

Isobaric Label Analysis Workflow

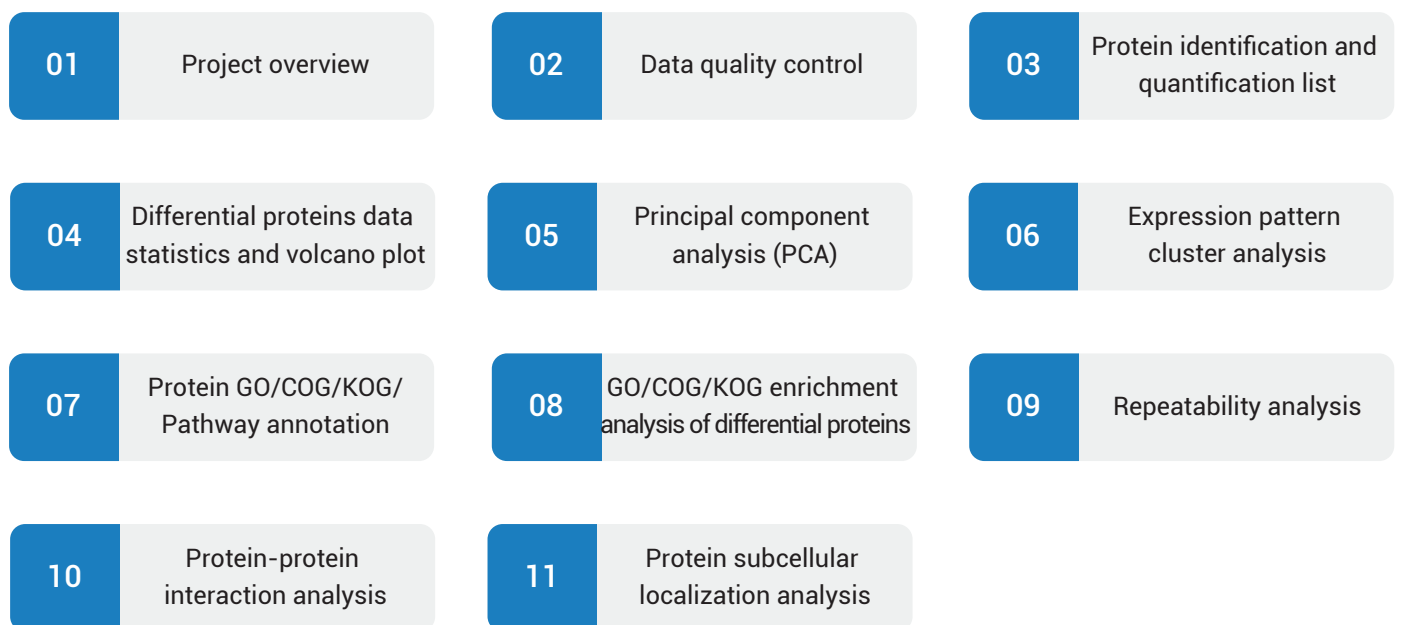


BGI Genomics Service Advantages

High Throughput and Short Project Cycle Simultaneous proteome quantification of less than 18 samples. More than 18 samples can be bridged by setting reference samples to realize the comparison of data, thus shortening project cycle	High Accuracy and Repeatability Analysis of multiple labeled samples at the same time avoids poor repeatability issues connected to testing separately and with traditional gel samples
Wide Range of Biological Samples Experience of wide range of species and various proteins including cytoplasmic protein, membrane protein, nuclear protein, extracellular protein. The protein abundance and molecular weight span are large	Cloud platform delivery The Dr. Tom cloud platform was used for data delivery, which was convenient for data mining and autonomous association analysis with the transcriptome

Bioinformatics Analysis Workflow

Standard:



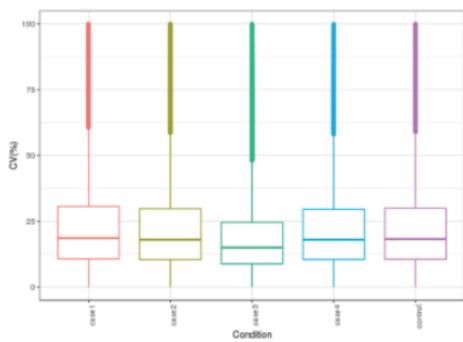
Customized Solutions:

01 Proteome and transcriptome/
RNA-seq correlation analysis

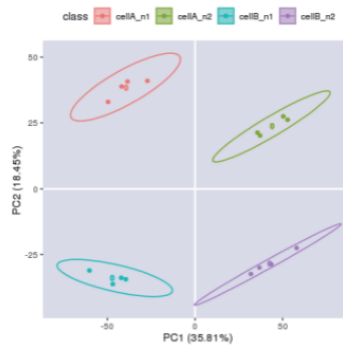
02 Proteome and metabolome
correlation analysis

03 Quantitative proteomics and
phosphoproteomics
correlation analysis

Examples of Data QC Analysis - Stability and Repeatability

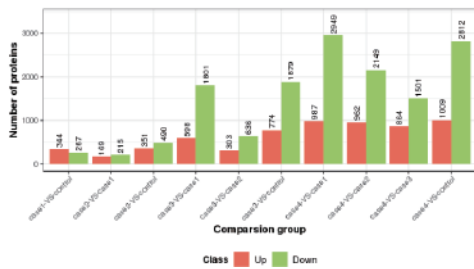


CV Distribution

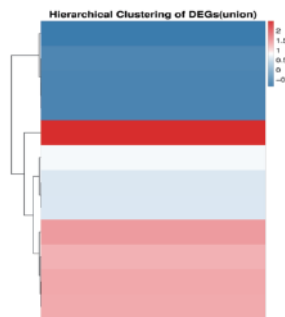


PCA Analysis

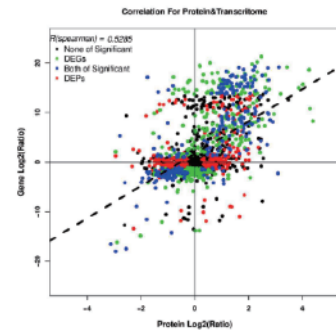
Examples of Protein Quantification Analysis



Quantification Statistics



Cluster Analysis



Proteome-Transcriptome
Correlation 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	≥ 10 mg	≥ 1 mg
	Mollusks (Toxoplasma, Schistosomiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	≥ 10 mg	≥ 2 mg
Cell	Suspended cells, adherent cells	≥ 1×10 ⁷	≥ 1×10 ⁶
	Cell culture supernatant	≥ 10 mL	
Exosome	Exosome isolated by customer	≥ 50 µg, ≥ 0.5 µg/µL	
Fluid	Plasma, serum (remove highly-abundant protein)	≥ 200 µL	≥ 200 µL
	Plasma, serum (with highly-abundant protein)	≥ 10 µL	≥ 3 µL
	Amniotic fluid, cerebrospinal fluid, semen, etc. (remove highly-abundant protein)	≥ 1 mL	≥ 500 µL
	Amniotic fluid, cerebrospinal fluid, semen, etc. (with highly-abundant protein)	≥ 200 µL	≥ 100 µL
	Saliva, milk	≥ 200 µL	≥ 100 µL
	Urine	≥ 30 mL	≥ 15 mL
	Tear	≥ 15 µL	≥ 10 µL
Plant	Twigs of plants (leaf buds, tender leaves), algae	≥ 300 mg	≥ 200 mg
	Old leaves, roots, stems, bark of plants	≥ 1 g	≥ 500 mg
	Plant buds, pollen	≥ 100 mg	≥ 50 mg
	Plant seeds (rice/wheat seeds, etc.), fruits (apples, peaches, pears)	≥ 1 g	≥ 500 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	≥ 100 µg, ≥ 0.5 µg/µL	≥ 50 µg, ≥ 0.5 µg/µL

Turn Around Time

Sample size: 1 batch, 4-5weeks



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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We Sequence, You Discover