

Service Description

Proteome profiling analysis refers to the analysis of an entire proteome from complex samples like complete cells, tissues and body fluids. It is most often used to identify as many peptides and proteins as possible. Proteome profiling analysis based on mass spectrometry (MS) can provide reference information for high-throughput quantitative proteomics and protein modification analysis.

At present, proteome profiling analysis mainly includes two separation methods. The first is the sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) method based on protein molecular weight. The second is the reverse-phase high performance liquid chromatography (RP-HPLC) method based on peptide hydrophobicity.

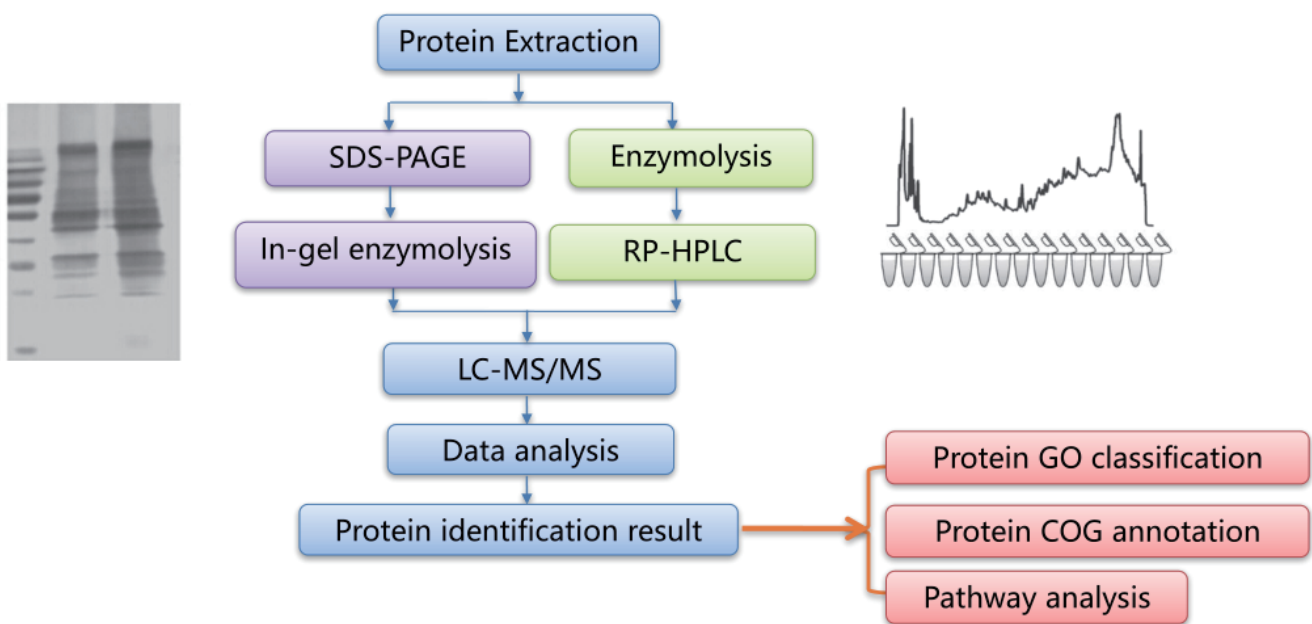
BGI has extensive experience in the field of Proteome Profiling with well developed and reliable workflows using market leading technologies, and a bioinformatics infrastructure that is second to none.

Research Applications



- Regulation mechanism of protein expression in the development of diseases
- Plant and animal growth and development research
- Stress resistance and disease resistance mechanism study

Proteome Profiling Analysis Workflow

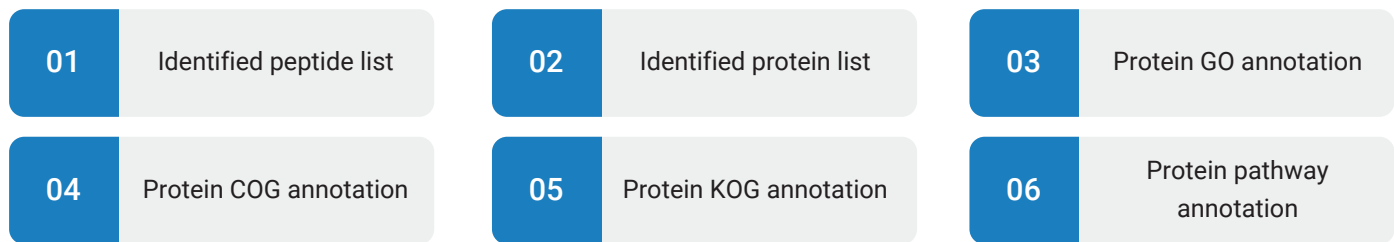


BGI Service Advantages

<h3>Efficient Sample Separation</h3>	<h3>High Identification Rate</h3>	<h3>Wide Range of Applications</h3>
<p>Choose from SDS-PAGE or RP-HPLC separation methods according to the sample nature</p>	<p>High resolution and high mass precision MS platforms can identify 12,000 different proteins</p>	<p>No species-specific restrictions</p>

Bioinformatics Analysis Workflow

Standard:



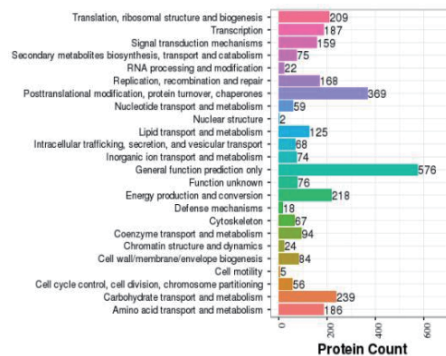
Customized Solutions:

Quantitative analysis of protein relative abundance in a single sample (iBAQ)

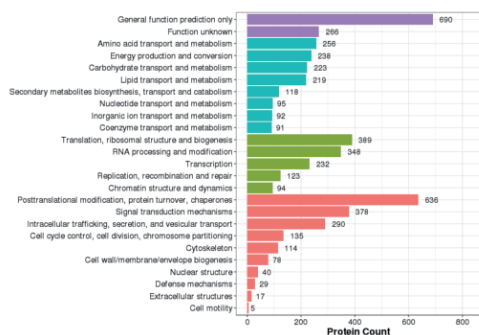
Examples of Protein Function Annotation



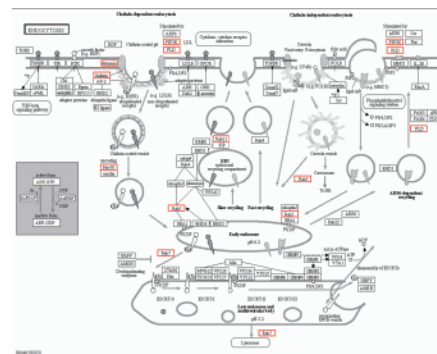
Protein GO Annotation



Protein COG Annotation



Protein KOG Annotation



Protein pathway annotation

General Sample Requirements

	SAMPLE TYPE	AMOUNT	
		RECOMMEND	MINIMUM
Animal	Animal internal organs (heart, liver, spleen, lung, kidney), skin, muscle, brain, etc	≥ 10 mg	≥ 5 mg
	Mollusks (Toxoplasma, Schistosomiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	≥ 10 mg	≥ 5 mg
Cell	Suspended cells, adherent cells	≥ 1×10 ⁷	≥ 1×10 ⁶
	Cell culture supernatant	≥ 20 mL	
Exosome	Exosome isolated by customer	≥ 100 µg, ≥ 0.5 µg/µL	
Fluid	Plasma, serum (remove highly-abundant protein)	≥ 200 µL	≥ 200 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	≥ 50 mL	≥ 20 mL
	Tear	≥ 25 µL	≥ 20 µL
Plant	Twigs of plants (leaf buds, tender leaves), algae	≥ 500 mg	≥ 250 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	≥ 200 µg, ≥ 0.5 µg/µL	≥ 100 µg, ≥ 0.5 µg/µL
Others	Feces	≥ 500 mg	≥ 100 mg

Turn Around Time

4-5 weeks



To Learn More

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

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BGI Genomics



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