## Service Description

Protein identification analysis mainly includes gel spot identification and gel band identification, which can be used when it is necessary to identify a specific range of proteins, or when there are only a few kinds of proteins in a sample.

Gel spot identification is mainly used for MS identification of the designated gel spot in two-dimensional (2D) electrophoresis gel. Firstly, the gel spot sample is decolorized and enzymolysised, and then detected by LC-MS/MS. Using the obtained mass spectra, the target protein can then be identified via cross referencing established databases.

Gel band identification is mainly used for MS identification of a protein solution in which protein type is relatively small (dozens to 100) or the designated band in sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Firstly, the gel band or protein solution samples are enzymolysised, and then detected by LC-MS/MS. Using the obtained mass spectra, the proteins are then identified via cross referencing established databases.
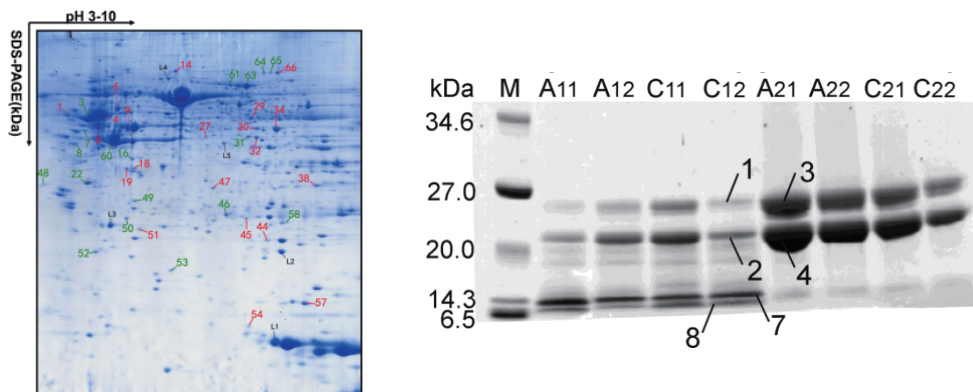
Gel spot (left) and gel band (right)

Zhan X Q, et al., How many proteins can be identified in a 2DE gel spot within an analysis of a complex human cancer tissue proteome, (2018)
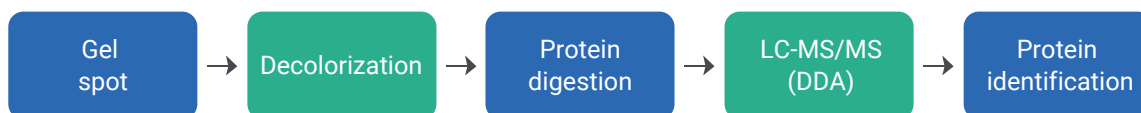
BGI has extensive experience in the field of Protein Identification with reliable workflows using nano LC-MS/MS and a bioinformatics infrastructure that is second to none.
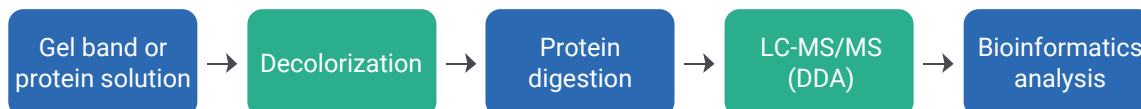
Research Applications

- Identification of target proteins
- Identification of protein mixture
- Protein-protein interaction studies

Protein Identification Analysis Workflow
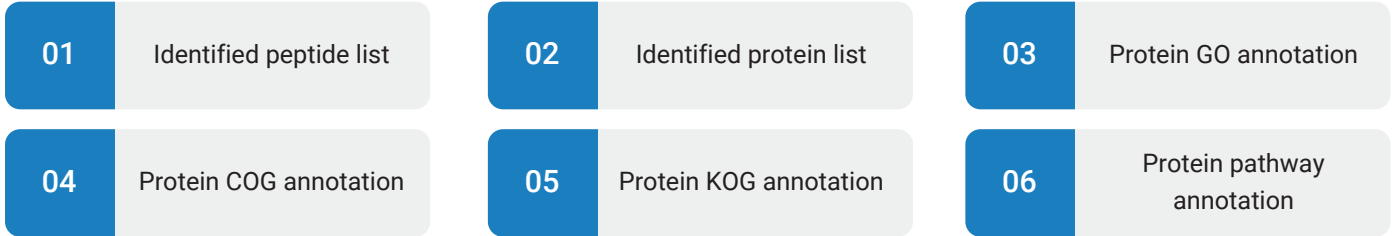
Gel spot identification:

Gel spot → Decolorization → Protein digestion → LC-MS/MS (DDA) → Protein identification

Gel band identification:

Gel band or protein solution → Decolorization → Protein digestion → LC-MS/MS (DDA) → Bioinformatics analysis

Bioinformatics Analysis Workflow

Standard:

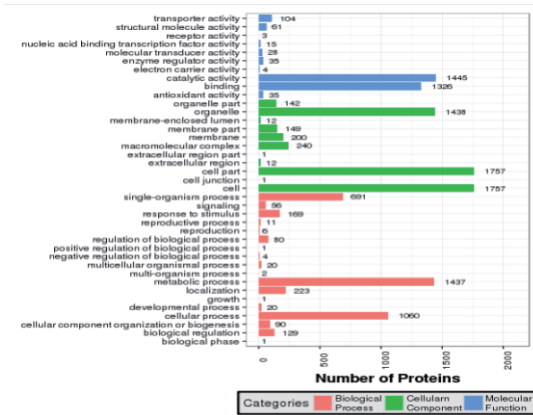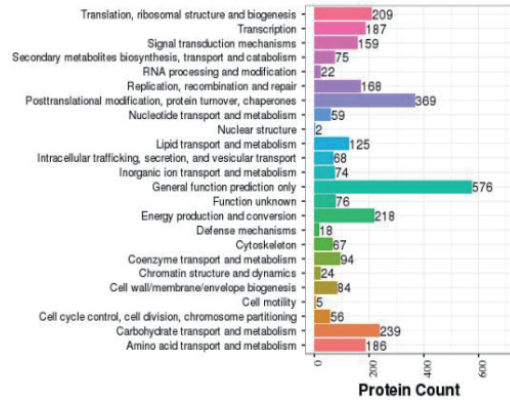|		
01 Identified peptide list	**02** Identified protein list	**03** Protein GO annotation
04 Protein COG annotation	**05** Protein KOG annotation	**06** Protein pathway annotation

Customized Solutions:

Quantitative analysis of protein relative abundance in a single sample (iBAQ)
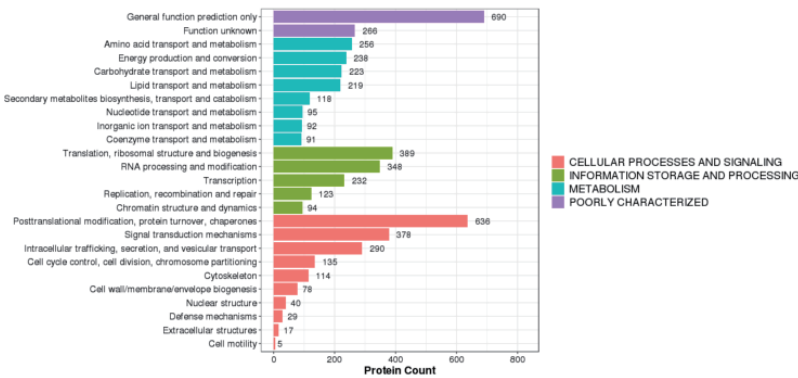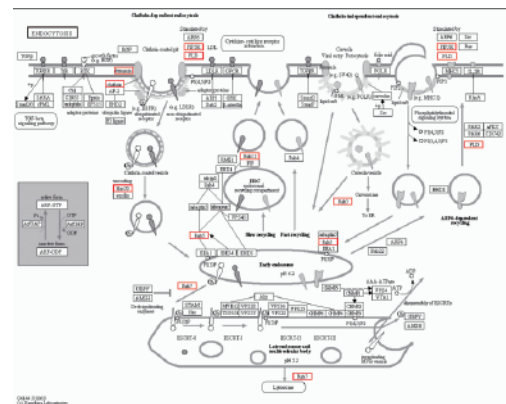
Examples of Protein Function Annotation

Protein GO Annotation

Protein COG Annotation

Protein KOG Annotation

Protein pathway annotation

General Sample Requirements

SAMPLE \ PRODUCT	GEL SPOT IDENTIFICATION	GEL BAND IDENTIFICATION	MODIFICATION SITE IDENTIFICATION
Coomassive or silver stained gel spot/band	Visible spot	Protein ≥ 1 µg	Protein ≥ 1 µg. Projects that need enrichment is not accepted.
Single protein (protein solution purified after IP or CO-IP)	/	≥ 5 µg, ≥ 0.5 µg/µL	≥ 10 µg, ≥ 0.5 µg/µL. If enrichment is required, the amount of sample sent needs to be increased by 3 times.

To Learn More

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

International Head Offices

BGI Americas

One Broadway, 3rd Floor
Cambridge, MA 02142,
USA
Tel: +1 617 500-2741

BGI Europe

Ole Maaløes Vej 3,
DK-2200 Copenhagen N,
Denmark
Tel: +45 7026 0806

BGI Asia

16 Dai Fu Street,
Tai Po Industrial Estate,
New Territories, Hong Kong
Tel: +852 36103510

BGI Australia

L6, CBCRC, 300 Herston
Road, Herston, Brisbane,
Queensland 4006, Australia
Tel: +61 (07) 3362 0475

BGI Genomics   BGI_Genomics

We Sequence, You Discover