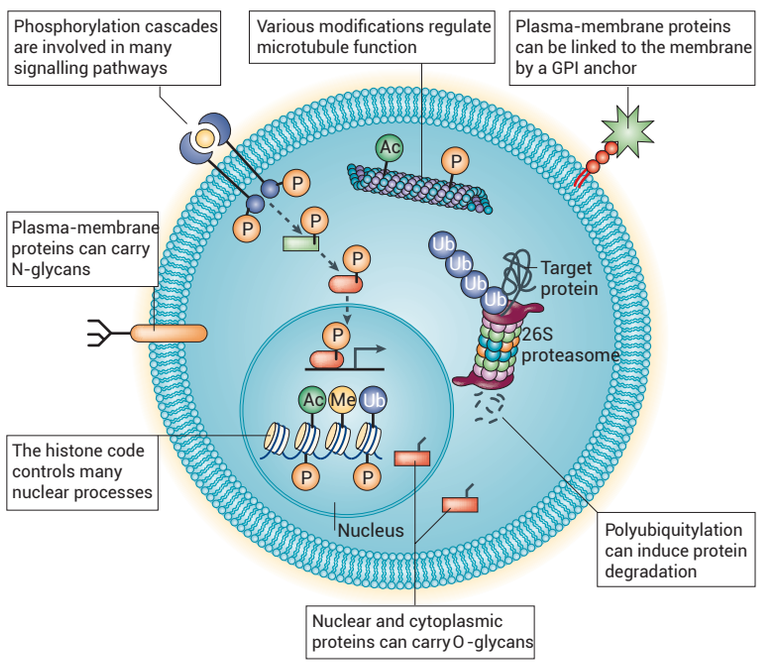
Post-Translational Modification Service Overview

Introduction

Post-translational modification (PTM) of proteins refers to the chemical changes proteins may undergo after translation. In other words, PTMs are chemical modifications of a polypeptide chain that occur after DNA has been transcribed into RNA and translated into protein.



Cellular post-translational modifications
Ole N. Jensen, et al., Interpreting the protein language using proteomics, (2006)

PTM modulates protein activity and macromolecular interactions and is involved in a range of fundamental molecular processes. Common PTMs include Phosphorylation, Glycosylation, Acetylation and Ubiquitination. As a result, identifying and understanding PTMs is key for the study of cell biology and the treatment and prevention of disease.

PTM TYPE	BIOLOGICAL FUNCTION	ENRICHMENT METHOD	PTM RESIDUES	MASS (ΔM, DA)
Phosphorylation	Phosphorylation is the most common mechanism of regulating protein function and transmitting signals throughout the cell.	IMAC (immobilized metal ion affinity chromatography),TiO_2, ZrO_2, Fe_2O_3,Antibody	Ser, Thr, Tyr	80
Glycosylation	Glycosylation is the reaction in which a carbohydrate is attached to a hydroxyl or other functional group of another molecule, and is key for molecular recognition, signal transduction and immune response.	HILIC, MAX, Lectin, Antibody Hydrazine chemical method	N-linked (Asn) O-linked (Ser, Thr) GPI anchor	> 800 203, > 800 > 1,000

Acetylation	Acetylation describes a chemical reaction that introduces an acetyl functional group into a chemical compound and is involved with gene expression regulation, chromatin structure, DNA damage repair and cancer development.	Antibody	N-terminal residue, Lys	42
Ubiquitylation	Ubiquitylation plays an important role in localization, metabolism, function, regulation, and degradation, and is closely related to the occurrence of diseases such as tumors and cardiovascular diseases.	Antibody	Lysine residue	114

BGI Genomics has extensive experience in the field of PTM Proteomics and has developed reliable workflows using market leading technologies and a bioinformatics infrastructure that is second to none.

Common Challenges with PTM Proteomics Studies

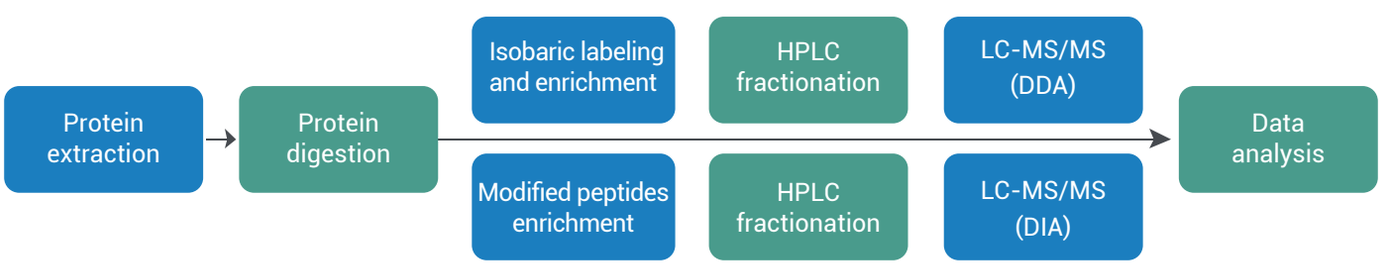
1. Various Kinds of PTM and High Complexity
2. Low Abundance
3. Dynamic Changes

Research Applications

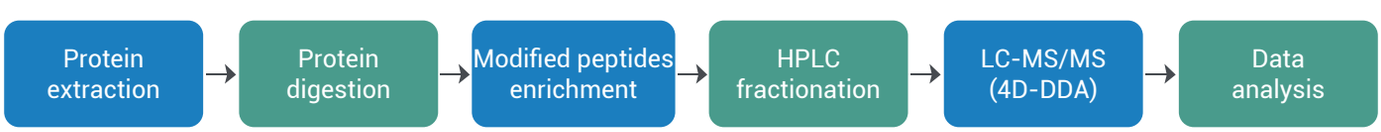
- Disease biomarker research
- Drug efficacy evaluation research
- Plant disease resistance and insect resistance research
- Microbial stress and adversity physiology research
- Cell recognition and signal transduction research
- Cancer cell development research

Post-Translational Modification Analysis Workflow

Phosphorylation:

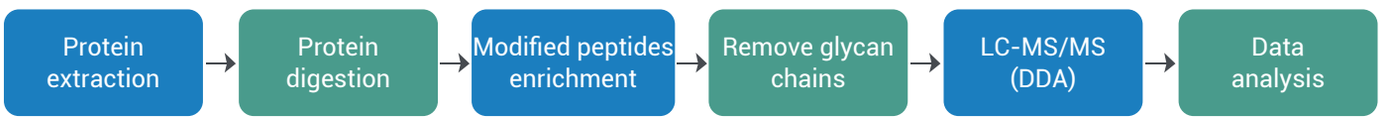


Acetylation/Ubiquitylation:

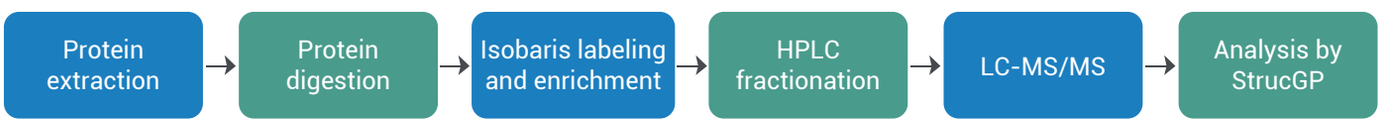


Glycosylaion

Quantification of N-glycosylated peptides:



Quantification of N-intact glycopeptides:

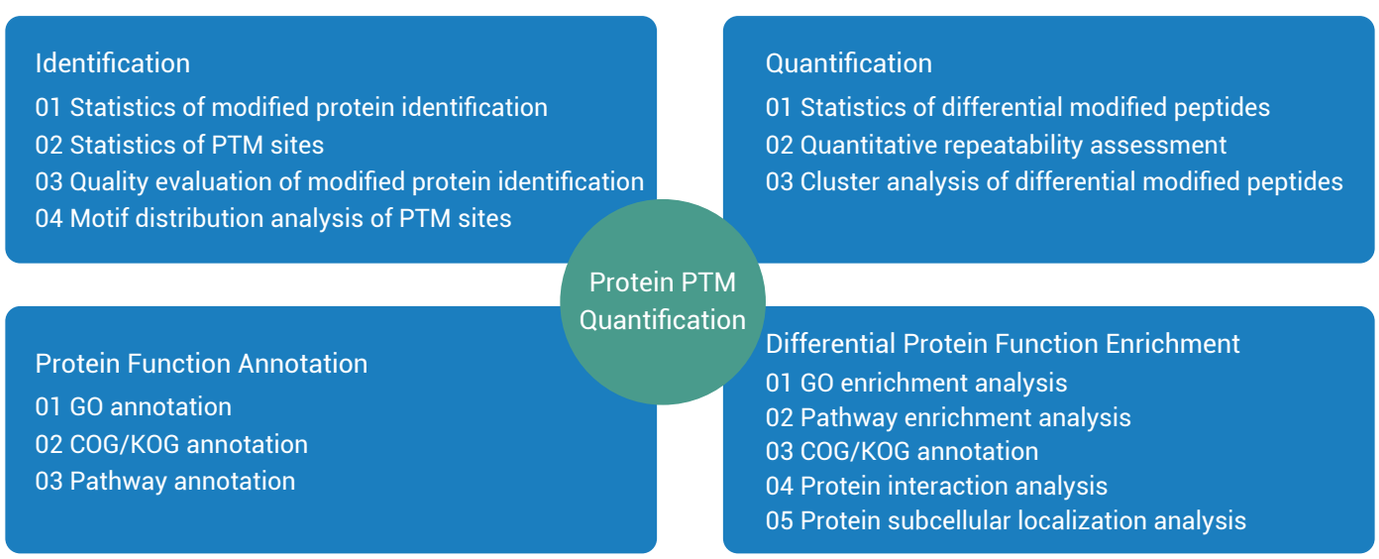


BGI Genomics Service Advantages

High Enrichment Efficiency	High Resolution	High Quantification Accuracy	Comprehensive Information Analysis
Our extensive experience in enrichment methods in order to ensure the optimum enrichment for different peptides.	Our expertise allows us to accurately identify protein modification sites in order to identify single amino acid site modifications.	Our isobaric labeling and DIA analysis services enables accurate quantification of modified peptides.	We provide motif analysis and kinase prediction analysis with other custom bioinformatics solutions available.

Bioinformatics Analysis Standard Workflow

Standard Protein PTM Quantification:



Standard Protein PTM Identification:

01 Data output statistics
02 PTM site localization
03 Modified peptide and protein identification

PTM identification of purified protein

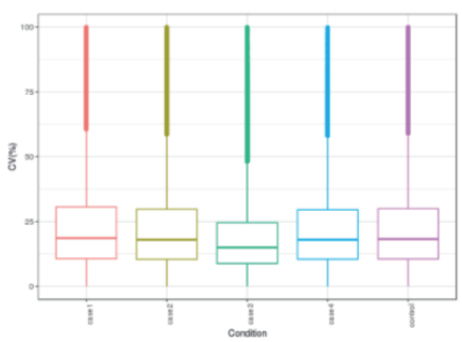
Modified protein profiling

01 Modified protein GO annotation
02 Modified protein COG annotation
03 Modified protein pathway analysis
04 Motif distribution of PTM sites

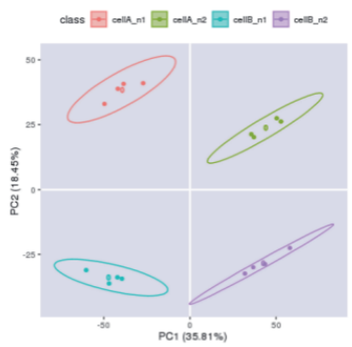
Customized Service:

Kinase prediction analysis
Quantitative proteomics and phosphoproteomics correlation analysis

Examples of Data QC Analysis - Stability and Repeatability

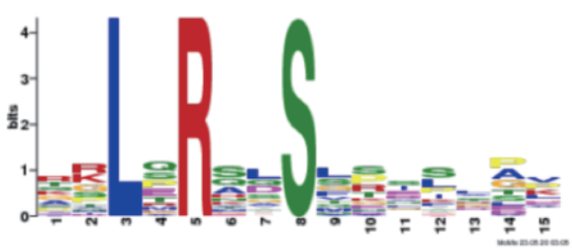


CV Distribution

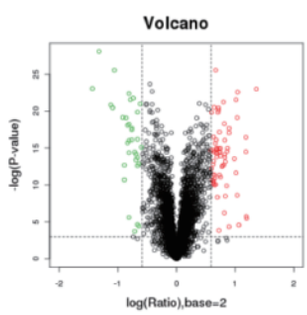


PCA Analysis

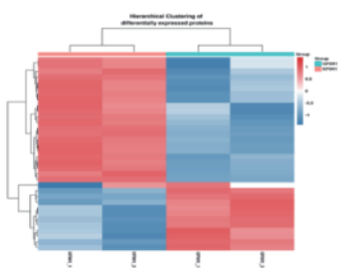
Examples of Identification and Quantification Analysis



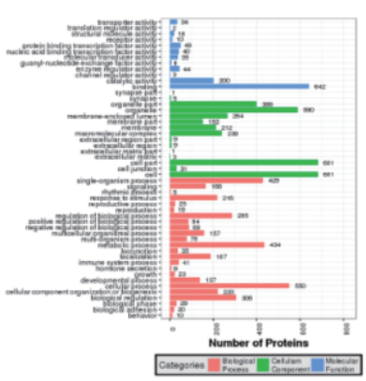
Motif Analysis of PTM Site



Volcano Plot

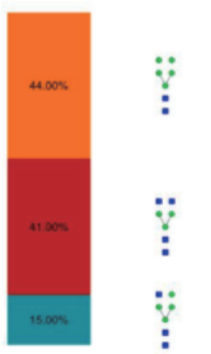


Cluster Analysis



GO Function Annotation

Summary of Glycan Structure



Glycoform Distribution

General Sample Requirements

Sample type		Sample amount category	Phosphorylation	Acetylation/ Ubiquitylation	Glycosylation
Animal	Common animal tissues: animal internal organs (heart, liver, spleen, lung, kidney), skin, muscle, brain, etc	Recommended	≥ 20 mg	≥ 2 g	≥ 100 mg
		Minimum	≥ 10 mg	≥ 75 mg	≥ 50 mg
	Mollusks (Toxoplasma, Schisto-somiasis, Drosophila, Acarid, Plutella xylostella, Laodelphax, Cestode, Cicada, Hematodinium, etc.)	Recommended	≥ 20 mg	≥ 2 g	≥ 100 mg
		Minimum	≥ 10 mg	≥ 75 mg	≥ 50 mg
Cell	Suspended cells, adherent cells	Recommended	≥ 2×10^7	≥ 5×10^8	≥ 1×10^8
		Minimum	≥ 2×10^7	≥ 3×10^7	≥ 5×10^7
Plant	Twigs of plants (leaf buds, tender leaves), algae	Recommended	≥ 2 g	≥ 3 g	/
		Minimum	≥ 1 g	≥ 3 g	
	Old leaves, roots, stems, bark of plants	Recommended	≥ 4 g	≥ 5 g	
		Minimum	≥ 2 g	≥ 50 mg	
	Plant buds, pollen	Recommended	≥ 200 mg	≥ 3 g	
		Minimum	≥ 100 mg	≥ 3 g	
	Plant seeds (rice/wheat seeds, etc.), fruits (apples, peaches, pears)	Recommended	≥ 500 mg	≥ 5 g	
		Minimum	≥ 200 mg	≥ 1 g	
Micro-rganism	Prokaryotic bacteria (E. coli, Staphylococcus aureus, etc.), fungi (yeast, etc.)	Recommended	Thallus ≥ 200 mg cells ≥ 2×10^7	150 mg-2 g	/
Protein solution	Complex protein solution, protein powder	Recommended	≥ 1 mg, ≥ 0.5 μg/μL	≥ 10 mg	≥ 5 mg
		Minimum	≥ 0.5 mg, ≥ 0.5 μg/μL	≥ 3 mg	≥ 3 mg

Turn Around Time

PTM TYPE	Phosphorylation	Glycosylation	Acetylation/Ubiquitylation
TURN AROUND TIME	3-5 weeks	4-5 weeks	3-5 weeks

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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www.bgi.com

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We Sequence, You Discover