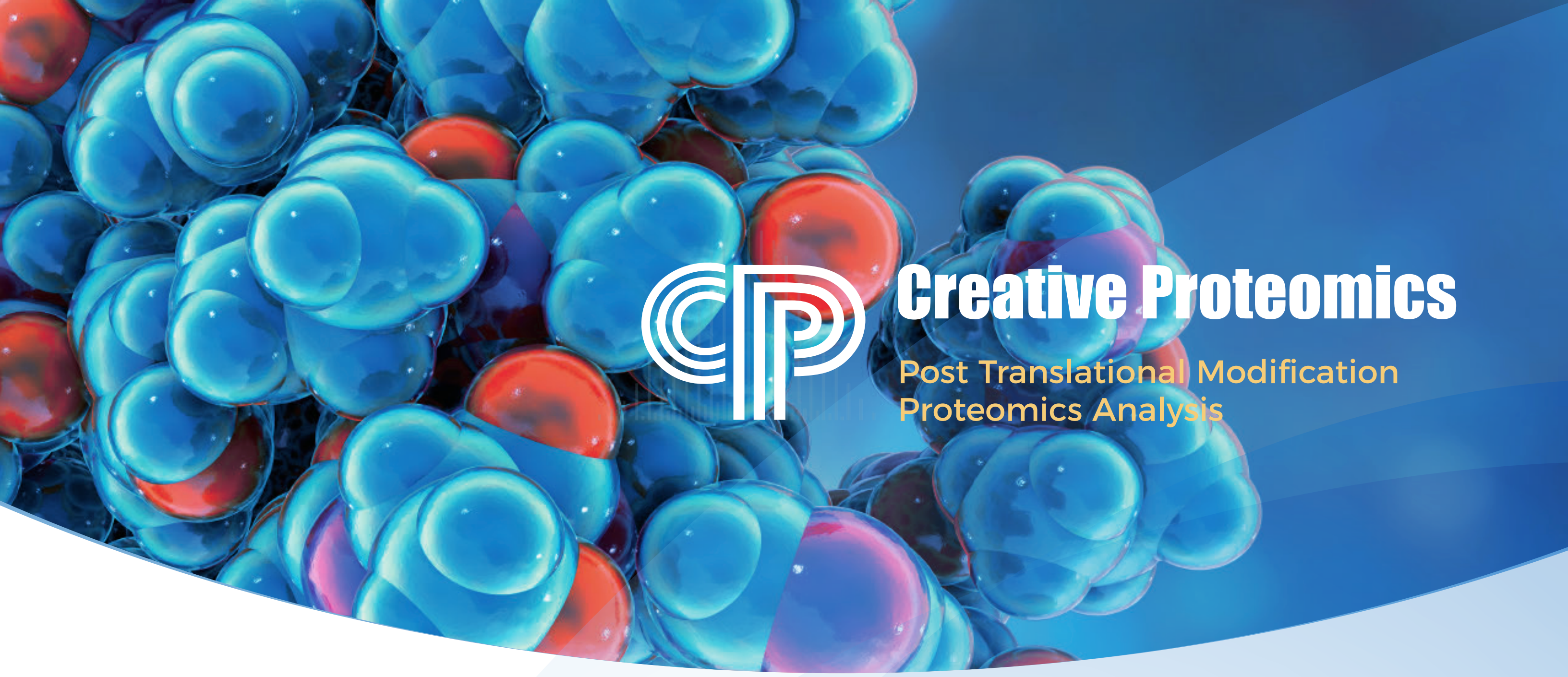


Creative Proteomics

Post Translational Modification Proteomics Analysis

Proteomics Analysis of Post Translational Modification

Post-translational modifications (PTMs) are involved in almost all cellular life processes, such as cell division, proteolysis, signaling, regulatory processes, regulation of gene expression and protein interactions, etc. PTMs enable more types of proteins, more complex structures, more precise regulation, more specific roles and better functions. More than 400 types of post-translational modifications have been identified, including common PTMs such as phosphorylation, acetylation, ubiquitination, glycosylation, methylation, etc.

The proteomic study of post-translational modifications is very challenging because of their low expression level at the whole proteome and wide dynamic range in samples, and different enrichment and mass spectrometry methods are required for different modification types. The combination of affinity enrichment, multidimensional separation, and biomass spectrometry provides an opportunity for the development of post-translational modification analysis at the whole proteome.

Equipped with the LC-MS/MS platform, Creative Proteomics enables the identification and relative quantification of protein PTM sites for either purified proteins or at the whole proteome level.

PTM analysis for targeted protein

- Isolate or purify target protein (>90% purity) from biological samples for downstream mass spectrometry analysis
- Identifiy PTMs sites due to mass shift before and after the modification.

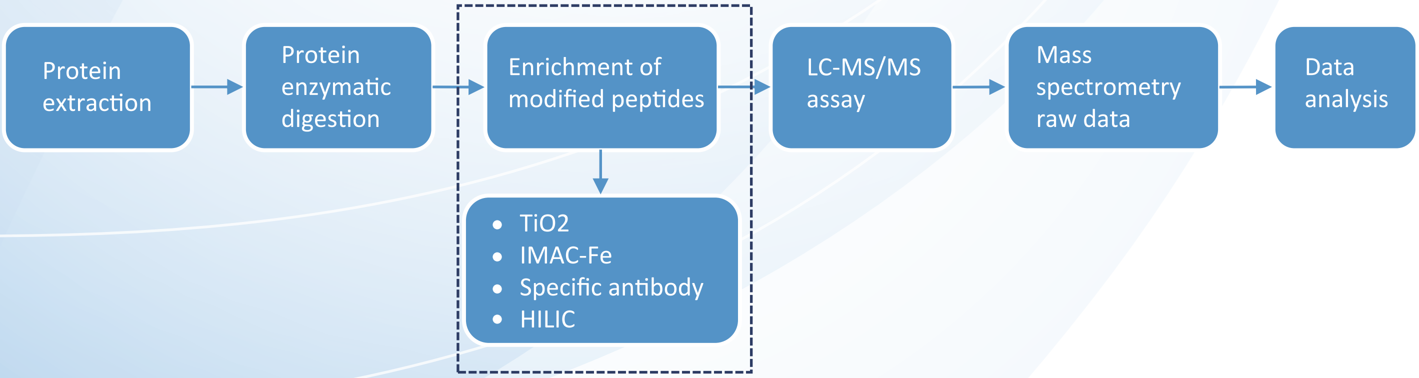
PTM analysis for the whole proteome

- Identify and relatively quantify modified proteins in the whole biological samples.
- Investigate the relationship between dynamic changes in the modified proteome by using iTRAQ, TMT or label-free quantification method.

Types of PTMs Analysis Service We Provide

Phosphorylation	Acetylation	Methylation
Phospho-proteomics	Acetyl-proteomics	Methyl-proteomics
Ubiquitination	SUMOylation	Di-Sulfide Bond Analysis
Ubiquitinated-proteomics	SUMOylated-proteomics	Glycosylation Analysis
Biotinylation Analysis	S-Nitrosylation Analysis	S-palmitoylation Analysis
Histone PTMs Analysis		

Workflow of Post-Translational Modification Analysis



Research Applications

- Investigating disease biomarkers
- Assessing the effectiveness of drugs
- Studying plant resistance to diseases and insects
- Examining how microbes respond to stress and adversity
- Researching cell signaling and recognition mechanisms
- Investigating the development of cancer cells

Feature Post-Translational Modification Proteomics in Creative Proteomics

Modification Type		Amino Acid Loci	Enrichment Methods	Applications
Phosphorylation		Ser/Thr/Tyr	IMAC (immobilized metal ion affinity chromatography), TiO2	Commonly used to study signal transduction, cell cycle, regulatory mechanisms, resistance, growth and development, and cancer mechanisms
Methylation		Lys/Arg	Motif specific antibody	Histone function, transcription and epigenetic regulation
Acetylation		Lys	Motif specific antibody	Gene expression regulation, cellular defense mechanisms, apoptosis and metabolism, cell cycle, transcriptional activation and silencing, protein stability, neurodegenerative pathologies, etc.
Ubiquitination		Lys	Motif specific antibody	Cell cycle, apoptosis, protein degradation, defense mechanisms, photomorphogenesis, signal transduction, plant growth and development, cancer and neurodegeneration
Glycosylation	N-Glycosylation	Asn	HILIC	Cell recognition, differentiation, stress response, signaling, immune response, neurodegenerative diseases, metabolic diseases and infectious diseases research
	O-Glycosylation	Ser/Thr		

Service Advantages

◉ **High Enrichment Efficiency**

We have a wealth of expertise in employing various techniques for enhancing peptide enrichment, in order to achieve the most effective enrichment outcomes for different peptides.

◉ **High Resolution**

With our specialized knowledge, we are capable of precisely pinpointing protein modification locations, enabling us to detect single amino acid site modifications with great accuracy.

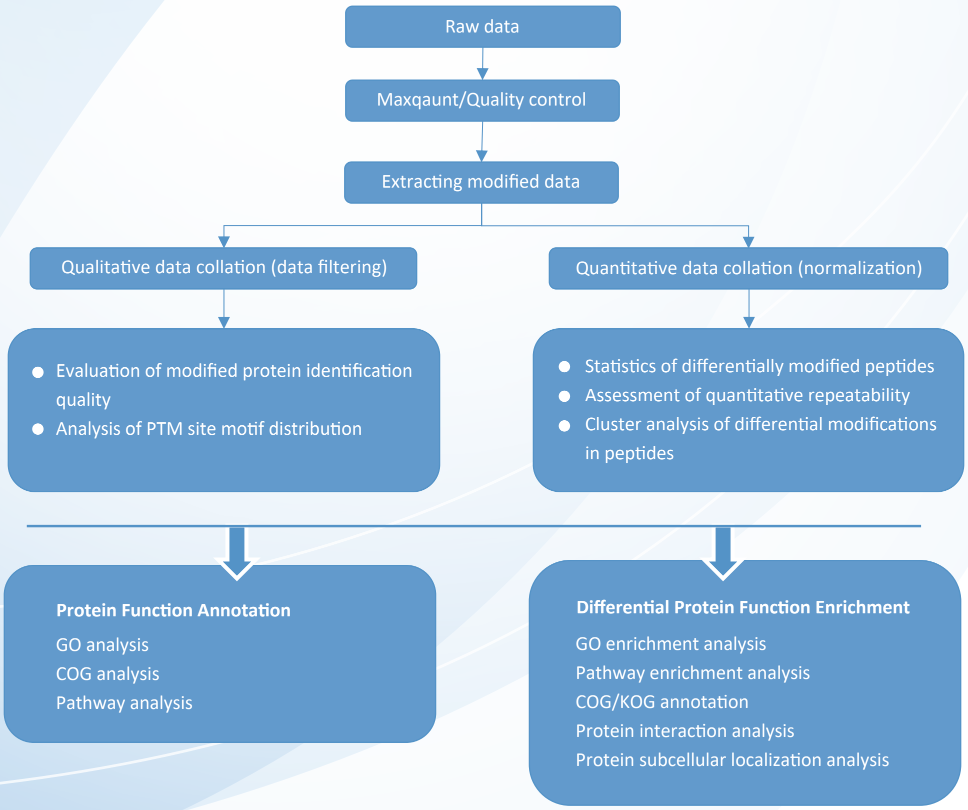
High Quantification Accuracy

Through our provision of isobaric labeling method, we are able to achieve precise quantification of modified peptides.

Comprehensive Information Analysis

We offer a range of customized bioinformatics solutions as per client requirements

Bioinformatics Analysis Workflow



Raw data

Maxqaunt/Quality control

Extracting modified data

Qualitative data collation (data filtering)

Quantitative data collation (normalization)

- Evaluation of modified protein identification quality
- Analysis of PTM site motif distribution

- Statistics of differentially modified peptides
- Assessment of quantitative repeatability
- Cluster analysis of differential modifications in peptides

Protein Function Annotation

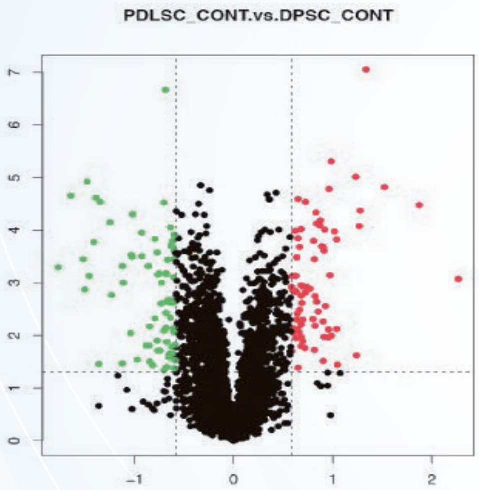
GO analysis
COG analysis
Pathway analysis

Differential Protein Function Enrichment

GO enrichment analysis
Pathway enrichment analysis
COG/KOG annotation
Protein interaction analysis
Protein subcellular localization analysis

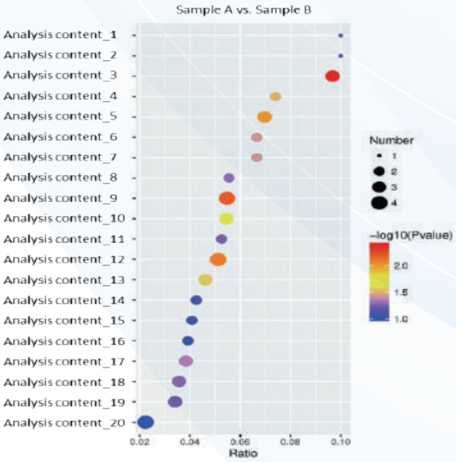
Results Presentation

Identification of phosphorylation sites



Differential protein volcano map

GO enrichment analysis



Differential protein volcano map