

PTM BIO Discovery-Driven Proteomics Solutions

—
Not just greater proteome
coverage, but deeper
biological insight.

Reproducible Proteome Coverage

In-Depth Biological Data Mining

High-Precision Quantification

Integrated Multi-omics Interpretation

Enhanced
Discovery
Proteomics

Deep
Insight
Proteomics

Proteomics: Proteins are active biological macromolecules that carry out biological functions. Proteomics is a systems biology technology that comprehensively analyzes the entire state of proteins. Compared to genomics and transcriptomics, proteomics directly and comprehensively resolves the protein abundance or post-translational modification levels in samples, uncovering protein specific regulatory mechanisms that cannot be determined at the gene and transcriptional levels. It is the core content of the 'post-genome' era and holds great significance for deepening our understanding of the essence of life phenomena, disease mechanisms disease diagnosis, and even drug development.

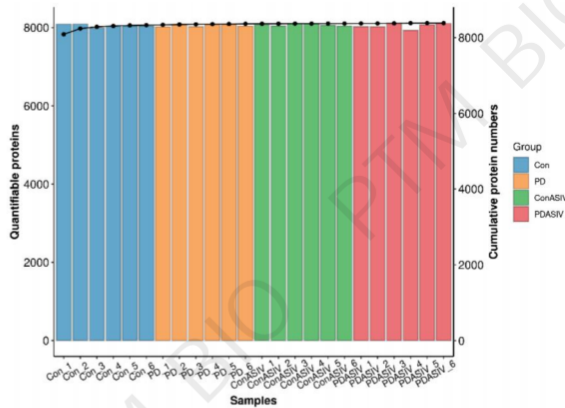
Quantitative Proteomics Strategies and PTM BIO Recommended Solutions

	Approach	Quantification Strategy	Key Advantages	Best Fit For	Notes
Label-free	DIA / Label-free Proteomics	MS-based label-free quantitative proteomics	Broad applicability, flexible design, suitable for large sample sets	Discovery proteomics for cells, tissues, and biofluids	A mainstream approach for protein profiling and differential analysis
Label-based	TMT / iTRAQ Proteomics	Isobaric labeling-based multiplex quantification	High reproducibility, multiplexing capability, suitable for parallel comparison	Comparative studies with moderate sample numbers	Ideal for simultaneous multi-sample analysis
Targeted	PRM Targeted Proteomics	Targeted quantification of predefined proteins or peptides	High sensitivity, specificity, and quantitative accuracy	Validation of candidate biomarkers or proteins of interest	Best suited for follow-up verification rather than discovery

PTM BIO Recommended Discovery Proteomics Solutions

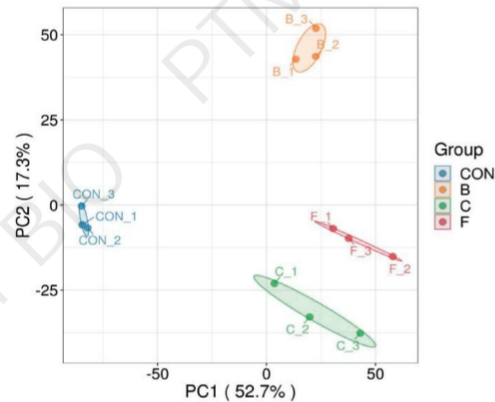
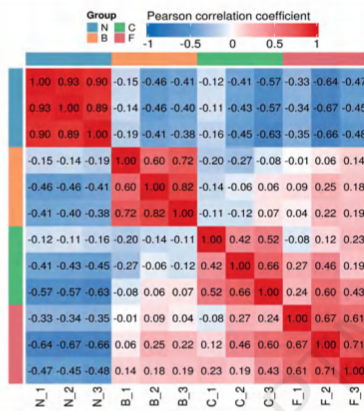
Products	Typical Needs	What We Deliver
Enhanced Discovery Proteomics	For routine discovery studies requiring reliable protein quantification and standard biological interpretation.	A complete quantitative proteomics workflow with standard bioinformatics reporting, including QC assessment, protein identification and quantification, reproducibility analysis, differential protein analysis, GO/KEGG functional annotation, enrichment analysis, clustering analysis, and PPI network analysis. It helps researchers rapidly identify candidate proteins and key biological pathways from proteome-scale data.
Deep Insight Proteomics	For high-value projects requiring deeper proteome coverage, stronger data mining, and more comprehensive scientific support.	Built on the same report framework, but with deeper proteome coverage and greater potential for downstream data mining. The expanded protein coverage helps reveal more regulatory proteins, candidate biomarkers, and mechanistic pathways. After report delivery, PTM BIO provides more comprehensive one-on-one scientific support to help customers interpret differential proteins, key pathways, PPI networks, WGCNA modules, candidate targets, and follow-up validation strategies.

Protein Quantification Depth of Each Sample / Cumulative Protein Quantification Curve



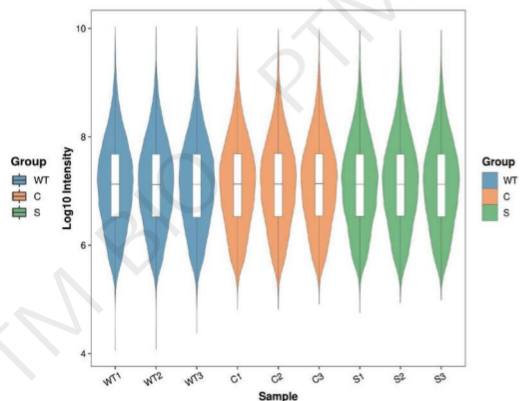
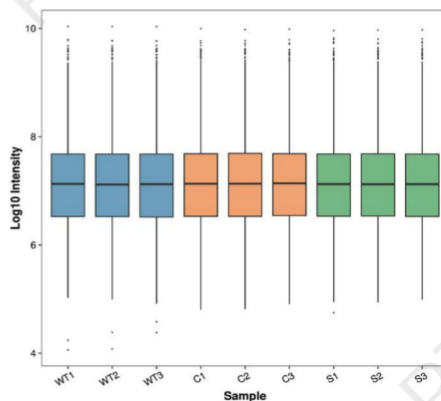
Consistent protein quantification depth is the foundation of high-quality proteomics research. Through standardized mass spectrometry workflows and rigorous quality control procedures, PTM BIO helps researchers **obtain robust, reliable, and quantitatively reproducible proteomics** data for downstream mechanistic analysis.

PCC Correlation Heatmap / PCA Plot



Using multidimensional reproducibility assessments, including Pearson correlation coefficient analysis, principal component analysis, and relative standard deviation analysis, we enable researchers to directly evaluate whether biological replicates are **consistent**, whether the overall **data quality is stable**, and whether the proteomics dataset is suitable for downstream differential protein screening and mechanistic interpretation.

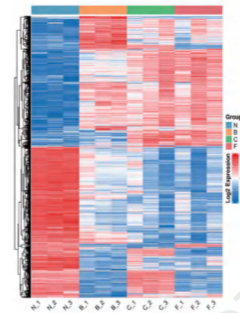
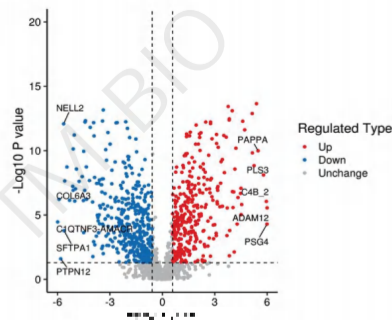
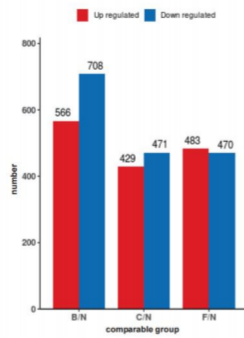
Protein Intensity Box Chart / Violin Chart



PTM BIO performs comprehensive quality control at the sample, peptide, and protein levels, helping ensure the **stability, comparability, and biological interpretability** of proteomics data from the earliest stages of analysis.

2

Differential Protein Discovery: Rapid Identification of Candidate Proteins



Differential Protein Statistics Bar Chart:

The differential protein statistics chart provides a quick overview of the scale of protein expression changes across experimental comparisons, helping researchers prioritize key comparison groups and guide downstream candidate protein selection and mechanistic analysis.

Differential Protein Volcano Plot:

The volcano plot simultaneously visualizes fold change and statistical significance. Significantly upregulated and downregulated proteins can be prioritized as candidate targets for downstream mechanistic studies, PRM validation, or biomarker screening.

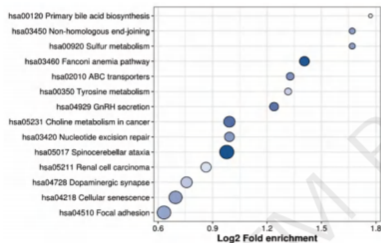
Differential Protein Expression Heatmap:

The clustering heatmap visualizes the expression patterns of differentially expressed proteins across samples and groups, helping researchers move beyond individual protein changes to understand coordinated expression patterns among protein groups.

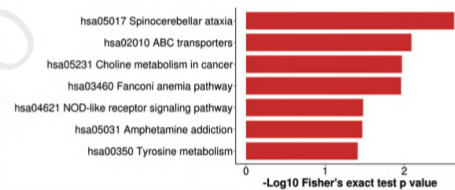
3

Functional Annotation and Enrichment Analysis: From Protein Lists to Biological Interpretation

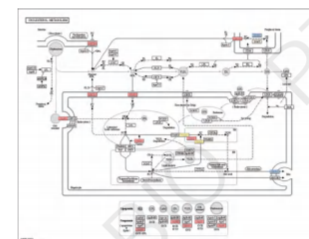
High-throughput proteomics studies often generate large sets of differentially expressed proteins. Simple statistical summaries alone are insufficient to connect these protein changes with the biological phenotype under investigation or its underlying molecular mechanisms. Functional annotation and enrichment analysis help researchers extract biological patterns from complex proteomics datasets, identify significantly involved pathways, and uncover key molecular mechanisms underlying the biological process of interest.



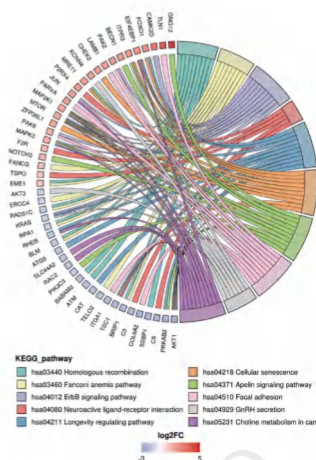
Enrichment Bubble Chart



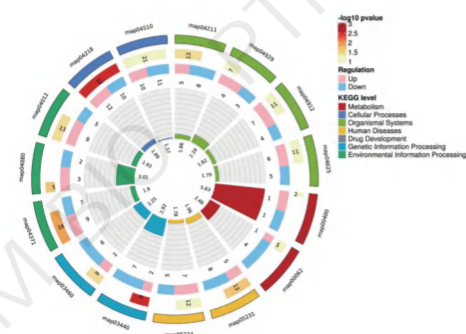
Enrichment Bar Chart



KEGG Pathway Map Enriched Analysis of Differentially Expressed Proteins

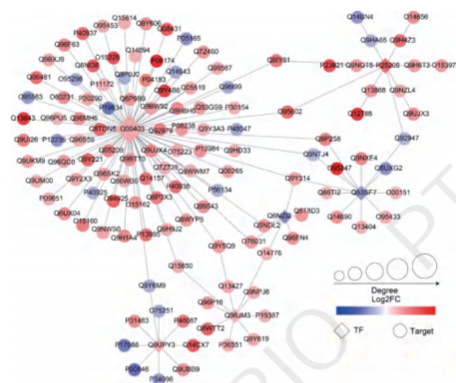


Enrichment Chord Diagram



Enrichment Circos Diagram

Network and Advanced Analysis: Identification of Key Regulatory Proteins and Mechanistic Modules



PPI Network Analysis:

Protein–protein interaction (PPI) network analysis reveals potential interactions among differentially expressed proteins.

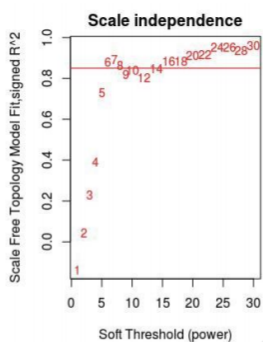
The topology of the interaction network helps identify proteins that may occupy central regulatory positions, making them suitable candidates for downstream functional validation and mechanistic investigation.

Protein–protein Interaction Network

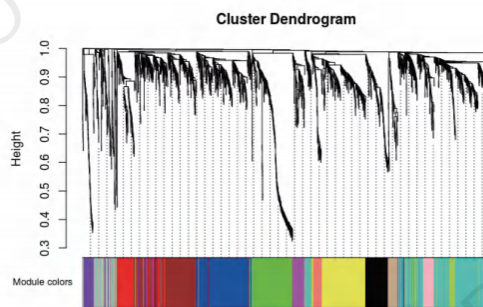
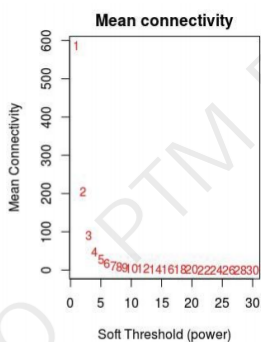
WGCNA Analysis:

Weighted gene co-expression network analysis (WGCNA) constructs a protein co-expression network to identify modules of co-regulated proteins and further evaluates their associations with disease groups, treatment conditions, or clinical phenotypes.

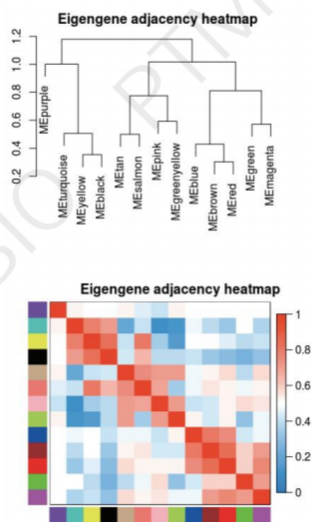
For **Deep Insight Proteomics**, WGCNA-based advanced analysis can further extend the interpretation from individual differentially expressed proteins to phenotype-associated protein modules, helping researchers identify regulatory networks and potential hub proteins with mechanistic relevance.



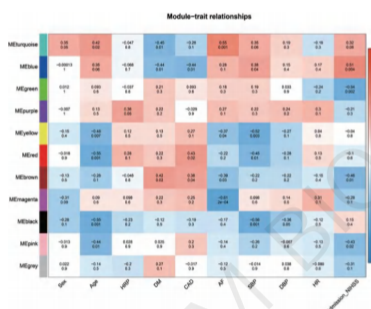
Soft-threshold Power Selection



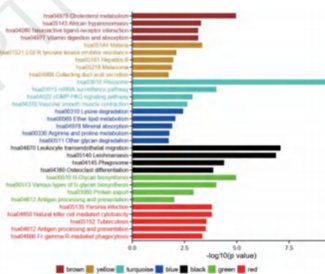
Protein Modules Detection



Inter-Module Correlation Heatmap Based on Protein Abundance Clustering



Module–Trait Relationship Heatmap



Functional Enrichment of Key Modules

PTM BIO Brand Advantages

01 Technological Innovation



Integrated with PTM BIO's proprietary **ProTeoMaster™ automated sample preparation platform**, sample preparation efficiency has been increased by nearly **10-fold**, enabling higher experimental consistency, stability, and analytical reproducibility.

02 Industry-Leading Platform Capacity



PTM BIO operates an extensive and highly diversified high-resolution mass spectrometry platform, significant improvements, acquisition speed, mass accuracy, and quantitative precision.

- **5 × Orbitrap Astral high-resolution mass spectrometers**
- **3 × timsTOF HT high-resolution mass spectrometers**

03 Proven Scientific Excellence



· **2,900+ high-impact original research publications** supported by PTM BIO, including **36 full-length research articles in Nature, Cell, and Science.**

- Quantitative proteomics analysis completed for **over 10,000 samples**
- Multiple benchmarks established in proteome identification depth across diverse proteomics applications

04 Comprehensive Post-project Support



- Providing one-on-one project support and customized analysis
- Free access to premium online training courses and technical documentation
- Cloud-based project reports with flexible reanalysis and parameter adjustment
- Free access to **40+ proteomics bioinformatics tools**

