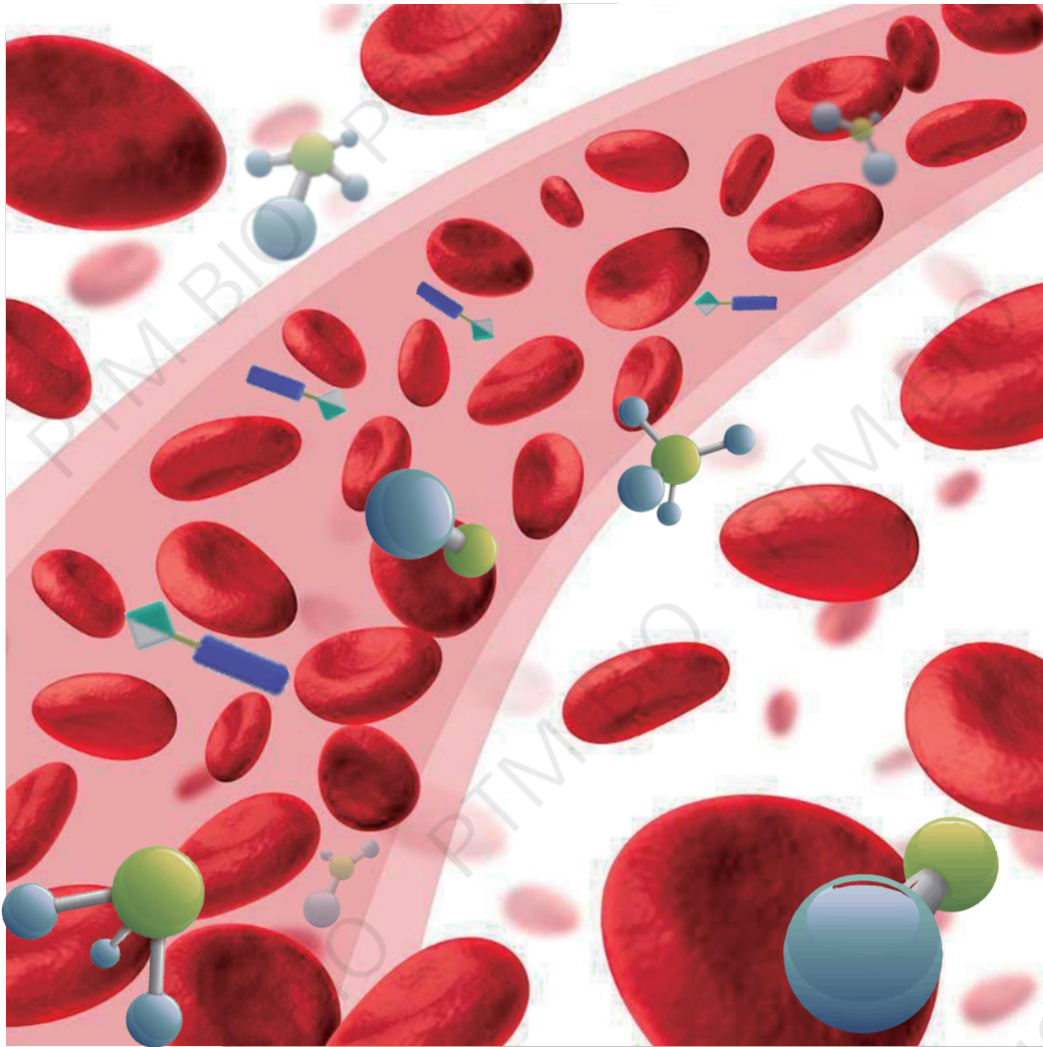




Advanced Blood Biomarker Discovery

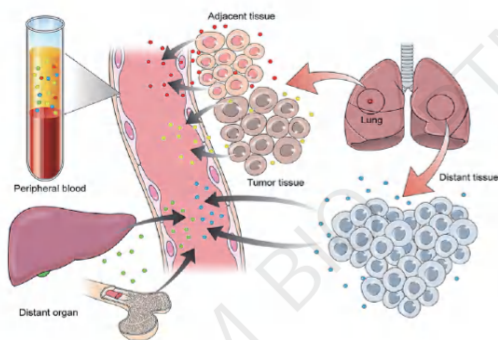
Deep-Coverage Proteomics

Peptidomics

Intact N-Glycopeptide Profiling

Blood: A Rich Source of Underexplored Biomarkers

Challenges in Blood-Based Research



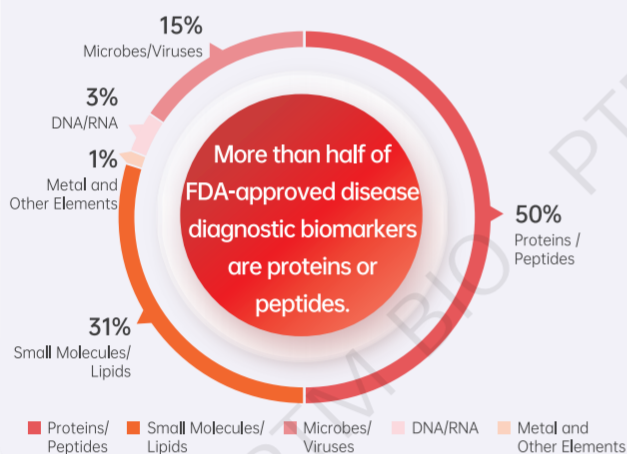
Blood is one of the most valuable clinical sample types. It carries molecular information from multiple organs and provides critical insights for disease mechanism studies and biomarker discovery. However, blood-based research still faces several key challenges:

- Limited protein coverage with conventional proteomics workflows.
- Insufficient exploration of blood-derived glycan biomarkers.
- Bioactive peptides and other non-canonical protein species play important biological roles, yet remain technically challenging to identify and characterize.

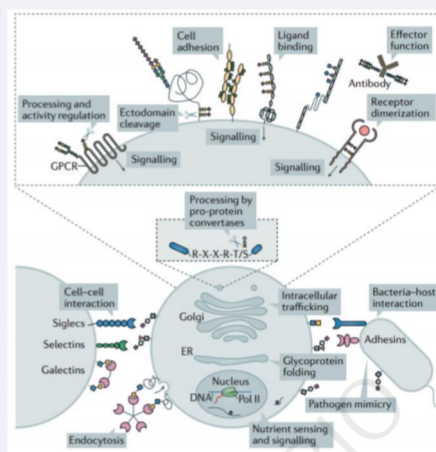
The Untapped Potential of Blood-Based Research

Proteins and Peptides Are Major Sources of Biomarkers

Distribution of Different Types of Biomarkers



Glycosylation Regulates Critical Biological Functions



Science. 2020 Jul 17;369(6501):330-333.

Peptides Are Key Molecular Targets in Body Fluid-Based Liquid Biopsy

Representative Peptides in Body Fluids and Their Physiological Functions

Peptide	Physiological Function
Thyrotropin-releasing hormone	Regulates thyroid hormone secretion
Oxytocin	Stimulates uterine contraction and lactation
Angiotensin	Regulates blood pressure
Calcitonin	Regulates bone turnover
Cholecystokinin	Regulates bile flow and pancreatic exocrine secretion
Insulin	Regulates blood glucose levels
Parathyroid hormone	Regulates bone turnover
Serum amyloid protein	Involved in inflammatory responses

Deep-Coverage Blood Proteomics

To address the key analytical challenges in blood proteomics, PTM BIO has developed the Blood+DIA deep-coverage blood proteomics platform, machine learning-enabled data processing, and an automated sample preparation system.

This platform delivers high throughput, high quantitative stability, low missing values, and reduced batch effects, making it particularly suitable for large-scale clinical cohort studies.

Key Advantages

- 1 Enhanced detection of low- and medium-abundance proteins, with signal intensities increased by 2- to 10-fold compared with the conventional workflow.
- 2 Greater protein identification depth Protein identification increased by up to 65%.
- 3 Improved quantitative reproducibility. More robust, accurate, and biologically meaningful quantification CV < 20%. Pearson correlation up to 0.99.
- 4 Automated sample preparation with ProTeoMaster™. The ProTeoMaster™ automated intelligent sample preparation system improves overall sample preparation efficiency by nearly 10-fold.

Blood+DIA Product Series	Blood+DIA Proteomics	Enhanced Blood+DIA Proteomics	Deep Insight Blood+DIA Proteomics
Mass Spectrometry Platform	tims TOF/ Exploris 480	Orbitrap Astral / timsTOF HT/ timsTOF/ Exploris 480	
Detection Depth	>2,500 proteins	>4,000 proteins	>6,000 proteins
*(Detection depth is based on internal laboratory test data. Actual results may vary depending on sample type, sample quality, and project conditions.)			

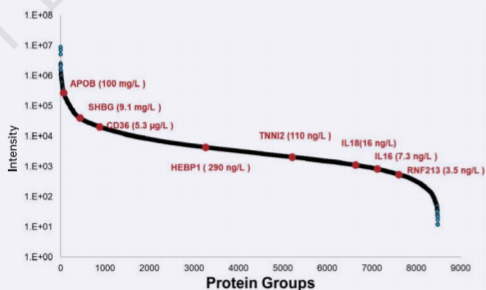
Advanced Blood Proteomics

High-Depth Identification of 8,000+ Blood Proteins



Deep Insight Blood+DIA Proteomics workflow enables deep blood proteome profiling, supporting the identification of 8,000+ blood proteins under optimized experimental conditions.

Broad Dynamic-Range Coverage Across the Plasma Proteomics



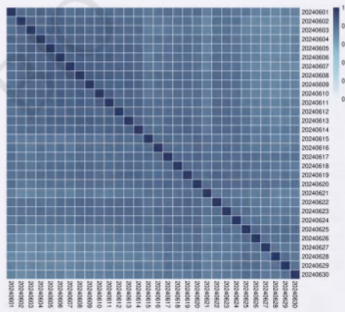
The 8,487 identified plasma proteins span a wide dynamic range and include a broad spectrum of functionally important proteins.

High-Quality Proteomics Data with Greater Biological Fidelity

No.	Workflow	Protein Identification Depth	Platelet Protein Proportion
1	Deep Insight Blood+DIA Proteomics	6,402	1.2%
2	Deep Insight Blood+DIA Proteomics	6,340	1.7%
3	Deep Insight Blood+DIA Proteomics	6,024	2.8%
4	Deep Insight Blood+DIA Proteomics	6,544	2.0%
5	Deep Insight Blood+DIA Proteomics	6,014	1.5%
6	Deep Insight Blood+DIA Proteomics	6,283	2.6%

Low platelet protein contribution, below 3%, helps ensure higher data fidelity and better representation of the circulating blood proteomics.

High Reproducibility for Large-Cohort Studies



Even after one month of continuous operation, the correlation remained >0.98, highlighting the outstanding stability of the mass spectrometry quantification workflow.

Blood Peptidomics: Uncovering Hidden Messengers

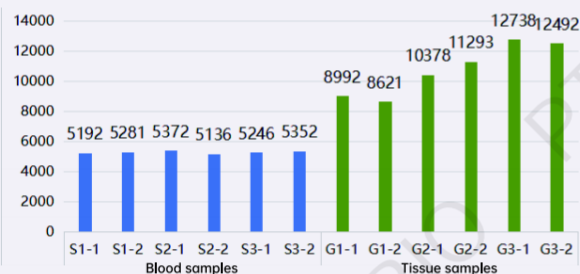
Peptides are short chains of amino acids generated primarily through proteolytic processing of precursor proteins and, in some cases, through translation of non-canonical open reading frames. Some function as endogenous signaling molecules, while others may serve as disease biomarkers or therapeutic leads.

PTM BIO's Blood Peptidomics platform enables high-confidence peptide discovery, identification, and functional characterization, overcoming challenges such as low abundance, difficult extraction, and complex validation.



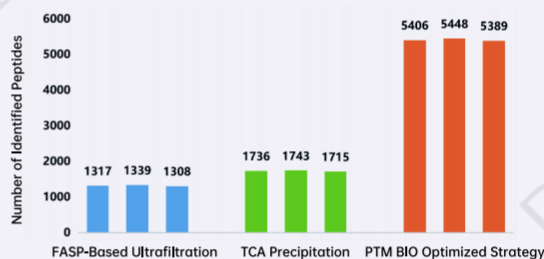
High-Quality Analytical Performance

Deep peptide profiling provides highly reproducible data



Depth peptide identification

High-depth peptide identification achieves up to a 4-fold improvement over conventional methods



Comparison of plasma peptidomics results across different enrichment strategies

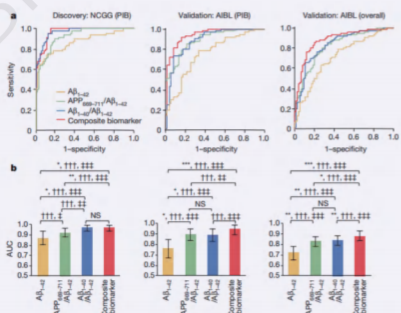
Representative Applications

Targets for Disease Diagnosis and Therapy

nature

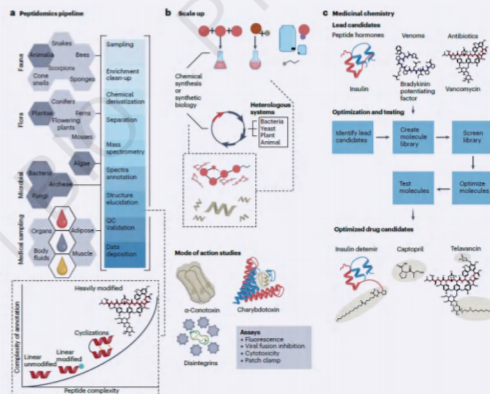
Letter | Published: 31 January 2018

High performance plasma amyloid- β biomarkers for Alzheimer's disease



Plasma A β peptides can be used for the diagnosis of Alzheimer's disease.

Peptide Drug Discovery and Development



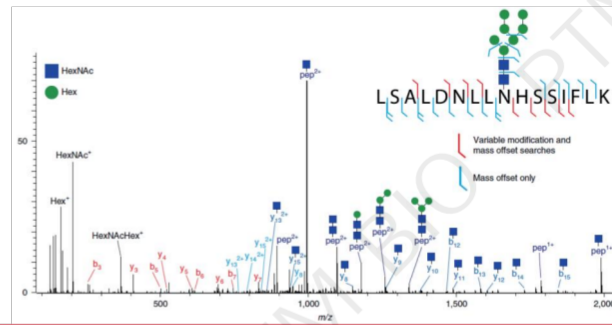
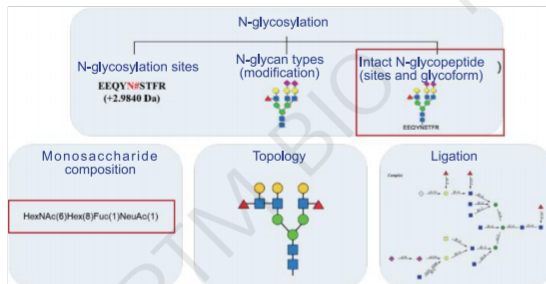
Peptide structural characterization and rational optimization support lead peptide development.

Intact N-Glycopeptidomics: Mapping Site-Specific Glycosylation Landscapes

N-glycosylation is one of the most extensively studied glycosylation modifications in blood. It regulates a wide range of biological processes and plays an important role in disease mechanisms, biomarker discovery, and drug development.

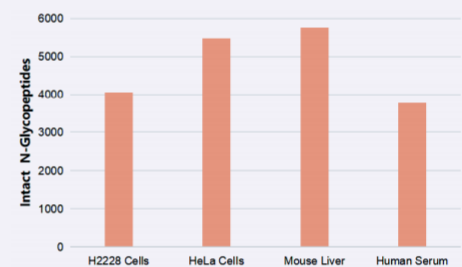
PTM BIO's intact N-glycopeptidomics platform enables simultaneous characterization of glycoproteins, glycosylation sites, and site-specific glycoforms, providing a powerful tool for biomarker discovery and disease mechanism studies.

Simultaneous Profiling of Glycosylation Sites and Glycan Structures



High-Quality Analytical Performance

- Complete profiling of glycoproteins, glycosylation sites, and site-specific glycoforms.
- Enhanced biomarker discovery and predictive modeling capability.
- Validated in clinical cohort and tissue sample studies.
- Maximum intact N-glycopeptide identification depth: 12,000+.



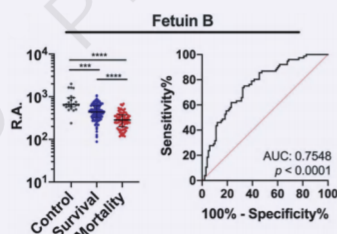
Representative Applications

Improving Prediction Accuracy with Protein + Glycopeptide Biomarkers

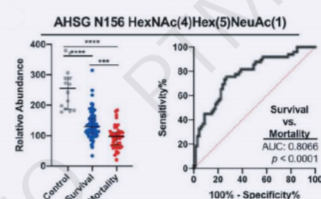
Cell

Resource

Mortality Risk Profiling of *Staphylococcus aureus* Bacteremia by Multi-omic Serum Analysis Reveals Early Predictive and Pathogenic Signatures

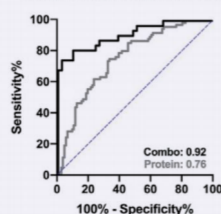


Protein biomarker AUC: 0.76



N-glycopeptide biomarker AUC: 0.81

Multi-omic Predictive Model

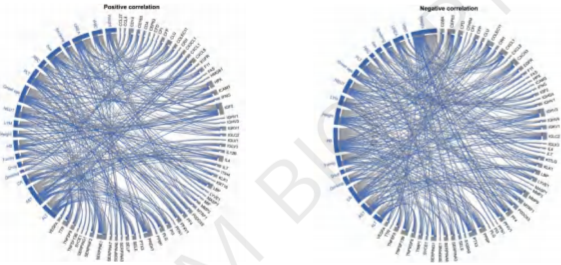


Large-Scale Cohorts, Multi-Omics Integration,
Machine Learning, and Clinical Validation

Data Mining: Dedicated Bioinformatics for Blood-Based Studies

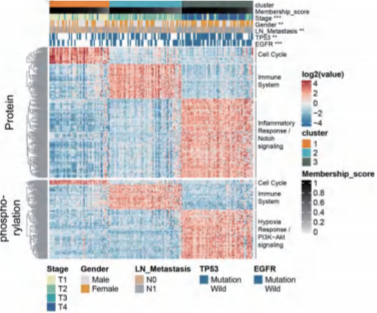
PTM BIO's AI-powered bioinformatics platform efficiently processes large-scale and complex omics datasets, enabling precise extraction of key biological insights. Customized analyses are tailored to each project's research objectives, providing comprehensive support for blood-based biomarker discovery and mechanism studies.

Clinical Phenotype-Protein Association Analysis



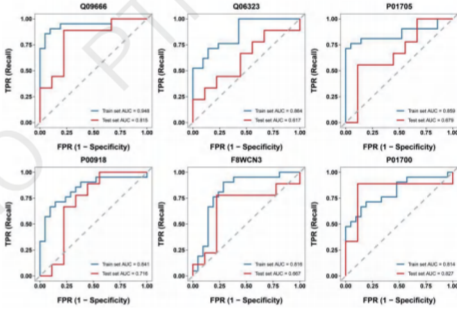
Integrates clinical phenotypes with differential protein expression profiles to identify disease-associated molecular features and potential clinical correlations.

Integrated Multi-Omics Clustering Analysis



Combines multi-omics datasets to reveal molecular subtypes, sample heterogeneity, and disease-related biological patterns.

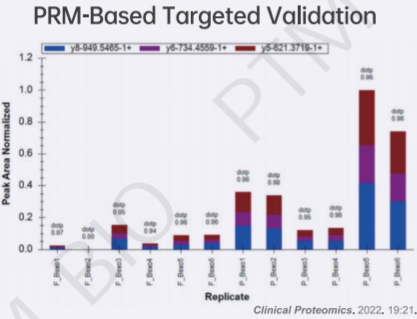
Predictive Biomarker Modeling



Applies statistical modeling and machine learning approaches to identify candidate biomarkers with diagnostic, prognostic, or stratification potential.

End-to-End Validation: From Discovery to Verification and Translation

PRM-Based Targeted Validation



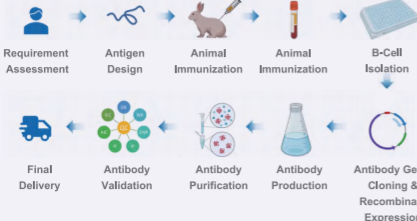
1 | **High-multiplex targeted verification**
Up to 40 candidate proteins can be quantified and verified in a single PRM assay.

2 | **Higher sensitivity and broader validation coverage**
Supports validation of a wider range of candidate proteins, including proteins within the top 60% intensity range.

3 | **Reference peptide spectral library construction**
Builds high-quality reference peptide libraries to improve the accuracy and reliability of validation results.

Antibody and Assay Kit Development

Development Process: Recombinant Monoclonal Antibody



1 | **In-house antibody development platform**
Supports the development of 4,000+ antibodies and IVD assay reagents.

2 | **Specialized Expertise in Custom PTM-Specific Antibody Development**
Successfully developed antibodies targeting 30+ types of post-translational modifications.

3 | **Rigorous validation for publication-ready data**
Custom antibodies developed by PTM BIO have been used in peer-reviewed studies published in leading journals.

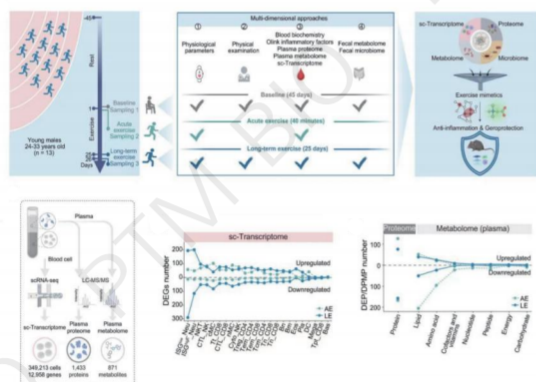
Selected Publications Supported by PTM BIO Products and Services

Blood Proteomics Reveals Exercise-Mimetic Mechanisms

Cell

Resource

Systematic profiling reveals betaine as an exercise mimetic for geroprotection



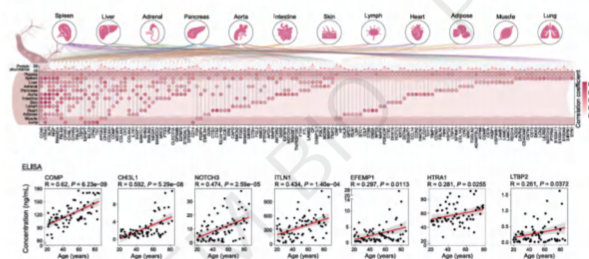
Plasma proteomics reveals distinct molecular responses across different exercise modalities.

Multi-Omics Reveals the Proteomic Code of Human Aging

Cell

Article

Comprehensive human proteome profiles across a 50-year lifespan reveal aging trajectories and signatures



Integrated plasma and tissue proteomics identified 211 shared age-associated proteins and highlighted GPNMB as a potential regulator of aging.

Collaborative Articles

Title	Journal
Metabolic regulation of gene expression by histone lactylation	Nature (IF=48.5)
Alanyl-tRNA synthetase, AARS1, is a lactate sensor and lactyltransferase that lactylates p53 and contributes to tumorigenesis NEW	Cell (IF=42.5)
Metabolic Regulation of Homologous Recombination Repair by MRE11 Lactylation NEW	Cell (IF=42.5)
Increased glucose metabolism in TAMs fuels O-GlcNAcylation of lysosomal Cathepsin B to promote cancer metastasis and chemoresistance	Cancel Cell (IF=44.5)
Branched-chain amino acid catabolism promotes thrombosis risk by enhancing tropomodulin-3 propionylation in platelets	Circulation (IF=38.6)
Sex-determining region Y gene promotes liver fibrosis and accounts for sexual dimorphism in its pathophysiology NEW	Journal of Hepatology (IF=33.0)
An integrated multi-omics analysis reveals osteokines involved in global regulation NEW	Cell Metabolism (IF=30.9)
Senescent immune cells release grancalcin to promote skeletal aging	Cell Metabolism (IF=30.9)
Proteogenomic insights into early-onset endometrioid endometrial carcinoma: predictors for fertility-sparing therapy response NEW	Nature Genetics (IF=29.0)

The PTM BIO Advantage

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 Capabilities



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**

