PTM BIO
Pioneer in Proteomics

Proteomics Solutions for Life Science Research

Jingjie PTM BioLab (PTMBIO) is China's most innovative leader in the development and application of proteomics technologies. We provide integrated solutions for high-throughput proteomics and modification proteomics, and develop highly specific, high-sensitivity antibodies for protein modifications to empower your research.

Proteomics

Protein Modification Proteomics

Bioinformatics and Data Services

Antibody Products

Technical Service Product List

Proteomics

- 10X High-Depth Proteomics
- High-Depth Blood Proteomics
- Spatial Proteomics
- Plant Spatiotemporal Proteomics
- Single-Cell Proteomics
- Plant Single-Cell Proteomics
- 4D-Fast DIA
- Blood+DIA
- LFQ/4D-LFQ
- TMT/iTRAQ
- SILAC
- Protein Identification
- SpatialX Holographic Spatial Proteomics
- Holographic Spatial Proteomics
- Urine Proteomics
- Peptidomics
- .....

Modification Proteomics

- Phosphorylation
- Ubiquitination
- Intact N-Glycopeptide
- O-GalNAc
- Methylation
- Acetylation
- Propionylation
- Palmitoylation
- L-/D-Lactylation
- Crotonylation
- Succinylation
- 2-Hydroxyisobutyrylation
- 3-Hydroxybutyrylation
- Redox Modification
- SUMOylation
- Spatial Phosphorylation
- Tyrosine Phosphorylation
- Full-Spectrum Phosphorylation

Targeted Proteomics

- PRM
- 4D-PRM
- Modification-PRM
- 4D-Modification-PRM
- Blood600

Platform Advantages

Full Coverage: Covering 26 modification types and hundreds of modification-specific antibodies.

Multi-level: In-depth analysis of proteomics, modification proteomics, and bioinformatics.

High Performance: Industry-leading high-resolution, high-sensitivity mass spectrometry platform.

Pioneer: Pioneering series of omics technologies, holding multiple records for proteomics and modification site quantification.

Professional: Experienced proteomics research team, with 3,500+ high-impact collaborative publications.

NEW~

Orbitrap Astral

NEW~

timsTOF HT

timsTOF Pro/Pro 2

Exploris 480

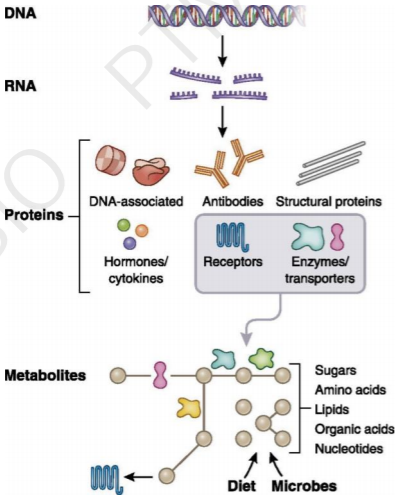
Q Exactive HF-X

Orbitrap Fusion Lumos

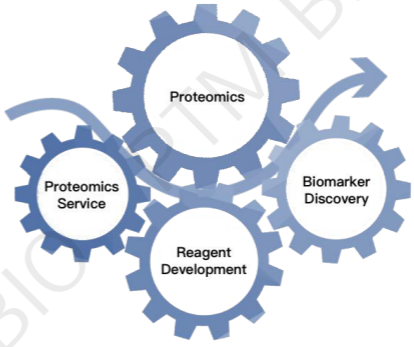
Proteomics Technology

Technology Overview

Proteomics: Proteins are active biological macromolecules that carry out biological functions. Proteomics is a systems biology technology that comprehensively analyzes the overall 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.



The basic flow of information in biological systems, from DNA (genome) to RNA (transcriptome) to proteins (proteome) to metabolites (metabolome).



Proteomics-Driven Precision Medicine

Proteomic studies can reveal the physiological mechanisms of animals and plants, such as growth and development, and neural signal transduction. They also provide theoretical foundations and solutions for elucidating the mechanisms of various diseases, such as tumor metastasis and cardiovascular diseases. Furthermore, screening protein biomarkers can provide molecular markers for the early diagnosis and treatment of diseases.

Research Methods

Quantitative Proteomics Analysis: 10X Proteomics, 4D-FastDIA/4D-LFQ, TMT/iTRAQ, Label Free, etc.

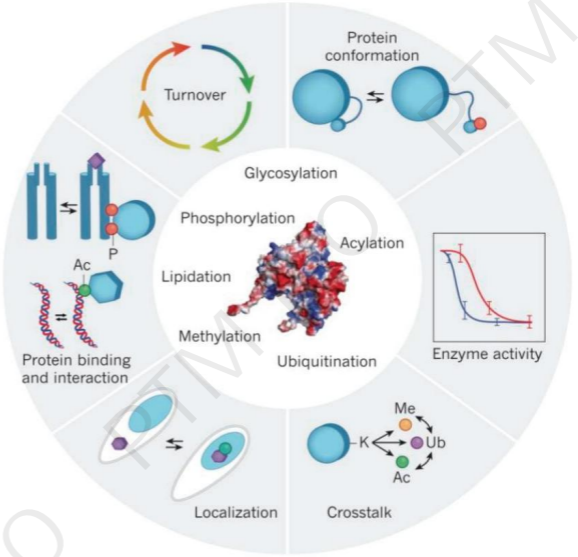
	Method Type	Technical Principle	Advantages	Limitations	Applications
Label-free Methods	10X Proteomics	>300 Hz acquisition speed, achieving near 100% ion utilization	Higher throughput, deeper coverage, higher sensitivity	Requires special instrument equipment	Large-scale proteomics and modification proteomics detection for all types of samples
	4D-FastDIA	Combining ion mobility window acquisition to achieve near 100% ion utilization	Good reproducibility, higher detection depth, and no need for pre-library construction	Requires special instrument equipment	Proteomics analysis for large-scale samples
	Label-free	First-level ion intensity quantification	Flexible and convenient, wide applicability	Many missing values, slightly poorer reproducibility	Proteomics and modification proteomics detection for all types of samples
	4D-LFQ	Quantitative analysis of primary ion intensity under 4D alignment conditions	Good throughput, depth, and qualitative accuracy	Requires special instrument equipment	Protein and modification proteomics detection for all types of samples
Labeling Methods	TMT/iTRAQ	Label-free ion quantification	Good reproducibility, mature method	Contains ratio compression effects	Generally suitable for comparing 2-18 samples simultaneously; requires "bridging" for more than that; relatively accurate quantification
Labeling Methods	4D-PRM/PRM	Targeted detection of peptide targets, secondary ion quantification	High sensitivity, good accuracy, can achieve precise absolute quantification	Can only detect a limited number of preset proteins and cannot perform comprehensive proteomics analysis	Subsequent validation work for the experiment

Protein Modification Proteomics Technology

Technology Overview

Protein post-translational modification (PTM) refers to the addition of chemical modifications to specific amino acids after translation.

Post-translational modifications can alter the structure of proteins, contributing to the diversity of protein structure and function. Increasingly, research findings show that many important life processes and disease occurrences are not only related to the abundance of proteins but are more importantly regulated by various types of post-translational modifications. In-depth study of protein post-translational modifications is of great significance for revealing the mechanisms of life processes, screening clinical biomarkers for diseases, and identifying drug targets.



Jingjie PTM BioLab provides comprehensive research solutions for protein modification proteomics, enabling quantitative comparison of biological samples at the post-translational modification level under different physiological and pathological conditions, and deeply revealing the close relationship between PTM changes and life activities.

Modification Types	Biological Functions	Common Application Directions
Phosphorylation	The most widespread type of post-translational modification, participates in enzymatic reactions, mediates protein activity and receptors to regulate and control protein activity and function.	Widely applied, especially in signal transduction, development and differentiation, cancer mechanisms, stress responses,etc.
Acetylation	The most studied acetylation modification, participates in epigenetics, signal transduction, metabolic regulation, apoptosis, and other biological processes.	Immune responses, tumor formation, metabolic diseases, apoptosis, etc.
L- lactylation	First discovered in 2019, it is an important way for lactate, a carbon-containing metabolite in the cellular glycolysis pathway, to function, regulating diseases such as cancer and inflammation.	Tumor formation and progression, inflammation, metabolic regulation, etc
D- lactylation	Three isomers of lactoylation modification successfully identified in 2024.	Intestinal diseases, brain diseases, tumors, etc.
Succinylation	Affecting metabolic processes in mitochondria, it holds significant value for studying mitochondrial dysfunction-related diseases, participating in cellular differentiation, metabolic regulation, epigenetic regulation, signal transduction, and other physiological activities.	Inflammation, metabolic diseases, tumors, etc.
Crotonylation	One of ***Cell***'s 'Top Five Research Highlights' in 2011, regulating gene expression by combining with transcriptionally active chromatin regions.	Reproductive regulation, epigenetics, tumor metabolism, DNA damage repair, etc.
β-hydroxybutyrylation	First reported 16 years ago, closely related to cellular core metabolism.	Energy metabolism, tumor research, DNA damage repair, liver metabolism, liver cancer, etc.
2-hydroxyisobutyrylation	Chromatin function regulation.	Epigenetics, glycolytic metabolic pathway.
Malonylation	Energy metabolism, biosynthesis of antibiotics, metabolic regulation, and photosynthesis.	Metabolic disorder diseases, immune regulation.
Benzoylation	First discovered in 2018, it regulates glycerophospholipid metabolism, ovarian steroid biosynthesis, the signaling pathway of phospholipase D, and serotonin, compared to acetylation Synapses and the secretion process of insulin.	Epigenetics, metabolic regulation
N-glycosylation	A widely existing type of post-translational protein modification, primarily affecting protein proper folding, active state, intracellular transport, etc.	Cell-to-cell recognition, cell adhesion, signal transduction, immune response, cell transformation, etc.
O-glycosylation	Involved in regulating multiple signaling pathways, participating in processes such as growth, proliferation, and hormone response.	Individual development, cellular stress, transcriptional regulation, signal transduction, Metabolic diseases, tumor occurrence and development.
Intact N-glycopeptide	Listed as one of the focus technologies by Nature Methods, primarily affecting proteins spatial conformation, activity, transport, and localization, etc.	Physiological mechanisms, disease pathology, discovery of disease biomarkers. Pathogens interact with hosts, plant growth and development
Ubiquitylation	A key type of modification that downregulates protein expression, mediates protein degradation, and alters cellular localization, activity, and other factors affecting substrate function and activity.	Cell cycle, apoptosis, aging, neurodegenerative diseases, signal transduction.
SUMOylation	A common ubiquitin-like modification that participates invarious important physiological and biochemical reactions in cells, such as protein-protein and protein-DNA interactions regulating their functions, playing an indispensable role.	Cardiovascular diseases, cancer, neurodegenerative diseases, and immune diseases, etc. The occurrence and development of various diseases.
Methylation	Involved in the regulation of gene expression, the modulation of protein function, and the processing of ribonucleic acid(RNA).	Epigenetics, cancer mechanisms, aging, neurodegenerative diseases.
Cysteine-Redoxome Proteomics	Capable of reversibly regulating protein activity, interaction, and localization, thereby achieving precise control over many life processes.	The occurrence of major diseases, fat metabolism regulation, plant stress responses, etc.

Classic Cases

Cell

Metabolic Regulation of Homologous Recombination Repair by MRE11 Lactylation

Collaborating Institution: Shanghai East Hospital, Tongji University

Product Technology: L-lactylation Modification Proteomics, Pan-L-lactylation and Pan-Acetylation Antibodies, Custom Antibodies.

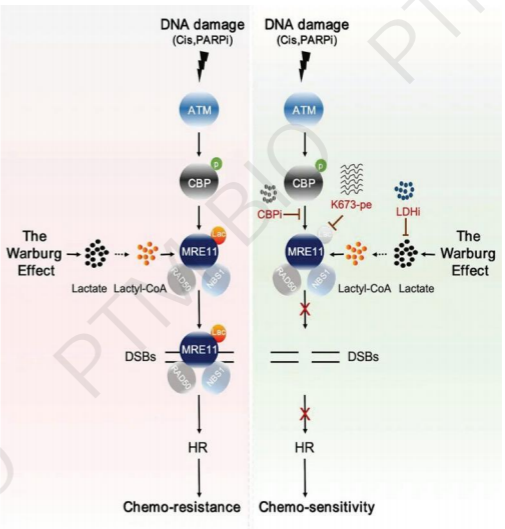
Research Overview

1.TCGA analysis showed that low LDHA expression was associated with higher homologous recombination deficiency (HRD) scores. Cellular studies further demonstrated that increased protein lactylation enhanced homologous recombination repair.

2.L-lactylation modification proteomics profiling identified the homologous recombination repair protein MRE11 and its lactylation site. Further validation demonstrated that CBP mediates MRE11 K673 lactylation.

3.Mechanistically, MRE11 lactylation enhances its DNA binding, promoting DNA end resection and facilitates homologous recombination repair.

4.Inhibiting MRE11 lactylation increased tumor cell sensitivity to chemotherapy, highlighting a potential mechanism of chemoresistance.



Nat Genet

Multiomic analysis of cervical squamous cell carcinoma identifies cellular ecosystems with biological and clinical relevance

Collaborating Institution: Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology

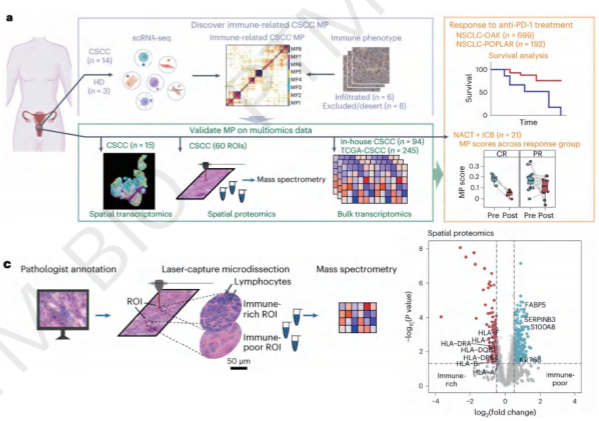
Product Technology: Product Technology: Spatial Proteomics

Research Overview

1.Spatial proteomics analysis was performed on 60 regions of interest (ROIs) (20 immune-rich regions, 40 immune-poor regions) with varying degrees of tumor-infiltrating lymphocytes.

2.It was discovered that tumors in the MP6 state interact with the tumor immune microenvironment through FABP5 and transforming growth factor β (TGFβ) signaling pathways, thereby remodeling the immune microenvironment. Moreover, more TGFβ-induced immunosuppressive cancer-associated fibroblasts exist around tumors in the MP6 state.

3.The study demonstrated that a significant decrease in MP6/7 scores after neoadjuvant chemotherapy is closely associated with complete pathological response after immunotherapy. Furthermore, FABP5 is a key molecule for CSCC tumor cells to remodel the tumor immune microenvironment.



PTM BIO Publications

Title	Journal
Metabolic regulation of gene expression by histone lactylation	***Nature*** (IF=48.5)
Disordered methionine metabolism in MTAP/CDKN2A-deleted cancers leads to dependence on PRMT5	***Science*** (IF=45.8)
Single-cell chromatin modification profiling reveals increased epigenetic variations with aging	***Cell*** (IF=42.5)
Global profiling of O-GlcNAcylated and/or phosphorylated proteins in hepatoblasto-ma	***Signal Transduct Tar*** (IF=52.7)
TRIM31 facilitates K27-linked polyubiquitination of SYK to regulate antifungal immunity	***Signal Transduct Tar*** (IF=52.7)
VAV2 is required for DNA repair and implicated in cancer radiotherapy resistance	***Signal Transduct Tar*** (IF=52.7)
Phosphoproteomics reveals therapeutic targets of esophageal squamous cell carcinoma	***Signal Transduct Tar*** (IF=52.7)
Direct phosphorylation and stabilization of MYC by Aurora B kinase promote T-cell leukemogenesis	***Cancer Cell*** (IF=44.5)
Increased glucose metabolism in TAMs fuels O-GlcNAcylation of lysosomal Cathep-sin B to promote cancer metastasis and chemoresistance *NEW*	***Cancer Cell*** (IF=44.5)
Acquired semi-squamatization during chemotherapy suggests differentiation as a therapeutic strategy for bladder cancer *NEW*	***Cancer Cell*** (IF=44.5)
Short-chain enoyl-CoA hydratase mediates histone crotonylation and contributes to cardiac homeostasis	***Cell Research*** (IF=25.9)
Landscape of the regulatory elements for lysine 2-hydroxyisobutyrylation pathway	***Cell Research*** (IF=25.9)
Global profiling of crotonylation on non-histone proteins	***Cell Research*** (IF=25.9)
Lysine 2-hydroxyisobutyrylation of NAT10 promotes cancer metastasis in an ac4C-dependent manner *NEW*	***Circulation*** (IF=38.6)





Jingjie PTM BioLab (Hangzhou) Co. Ltd
Tel:400-100-1145
Address: Building 8, Phase II, Biopharmaceutical Port Town, No. 291 Fucheng Road, Qiantang New District, Hangzhou, Zhejiang, China

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