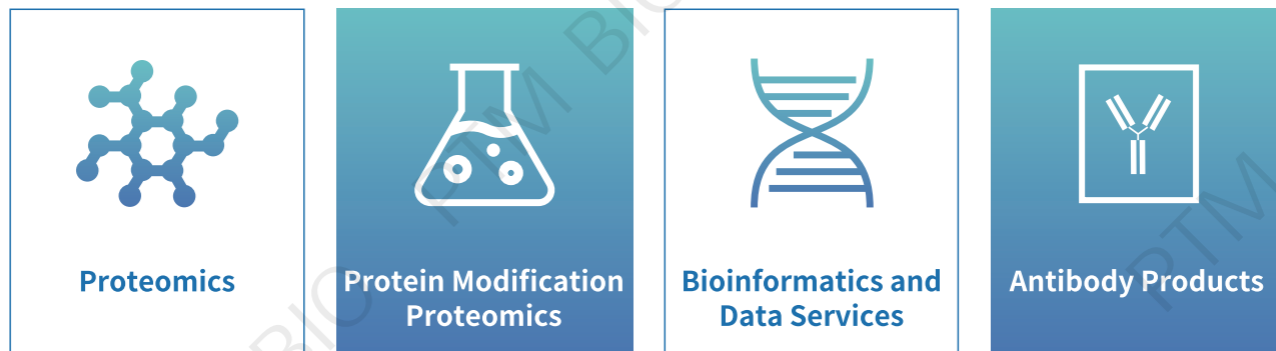




Proteomics Solutions for Life Science Research

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.



✚ Technical Service Product List

Proteomics		Modification Proteomics		Targeted Proteomics
Deep Insight Proteomics	LFQ/4D-LFQ	Phosphorylation	Crotonylation	PRM
Deep Insight Blood+DIA Proteomics	TMT/ITRAQ	Ubiquitination	Succinylation	4D-PRM
Spatial Proteomics	SILAC	Intact N-Glycopeptide	2-Hydroxyisobutyrylation	Modification-PRM
Plant Spatiotemporal Proteomics	Protein Identification	O-GalNAc	3-Hydroxybutyrylation	4D-Modification-PRM
Single-Cell Proteomics	SpatialX Holographic Spatial Proteomics	Methylation	Redox Modification	Blood600
Plant Single-Cell Proteomics	Holographic Spatial Proteomics	Acetylation	SUMOylation	
4D-Fast DIA	Urine Proteomics	Propionylation	Spatial Phosphorylation	
Blood+DIA	Peptidomics	Palmitoylation	Tyrosine Phosphorylation	
		L-/D-lactylation	Full-Spectrum Phosphorylation	

✚ 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.



Orbitrap Astral



timsTOF HT



timsTOF Pro/Pro 2



Exploris 480



Q Exactive HF-X

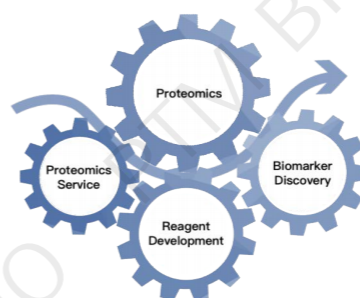
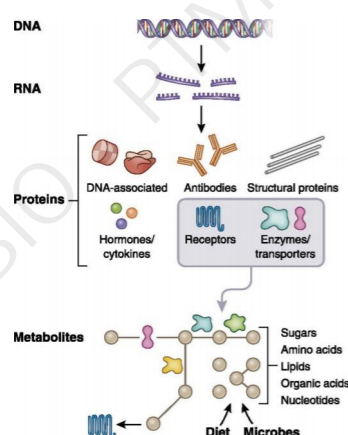


Orbitrap Fusion Lumos

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.



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: Enhanced Discovery Proteomics & Deep Insight Proteomics, 4D-FastDIA/4D-LFQ, TMT/iTRAQ, Label Free, etc.

	Method	Technical Principle	Advantages	Limitations	Recommended Applications
Label-Free	Enhanced Discovery Proteomics & Deep Insight Proteomics	Ultra-fast acquisition at >300 Hz, enabling near-complete ion utilization	Higher throughput, deeper proteome coverage, and improved sensitivity	Requires specialized MS instrumentation	Large-scale proteome and PTM profiling across diverse sample types
	4D-FastDIA	Ion mobility-assisted DIA acquisition for near-complete ion utilization	High reproducibility, deeper coverage, no need for library pre-building	Requires specialized MS instrumentation	Large-scale proteomics analysis
	Label-Free Quantification	MS1-based intensity quantification	Flexible workflow and broad sample compatibility	More missing values and relatively lower reproducibility	Proteome and PTMomics analysis across diverse sample types
	4D-LFQ	MS1-based intensity quantification with 4D feature alignment	Improved identification depth, quantification accuracy, and reproducibility	Requires specialized MS instrumentation	Proteome and PTMomics analysis across diverse sample types
Label-Based	TMT/iTRAQ	Isobaric labeling-based quantification	High reproducibility and well-established workflow	Subject to ratio compression	Comparative quantification of 2–18 samples per batch; commonly used for paired designs and accurate relative quantification
Targeted	4D-PRM/PRM	Targeted MS2-based quantification of selected peptides	High sensitivity and accuracy, enables precise absolute quantification	Limited to predefined proteins or peptides; not suitable for global proteome profiling	Follow-up validation of candidate proteins or peptides

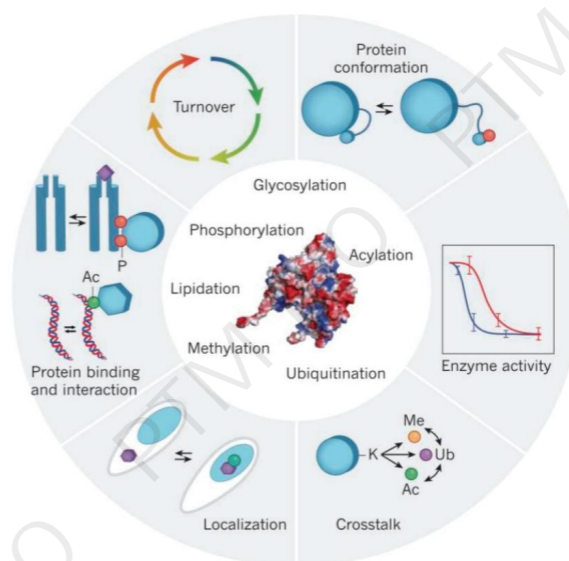
Protein Modification Proteomics Technology

🔧 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 in 2016, 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 in various 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

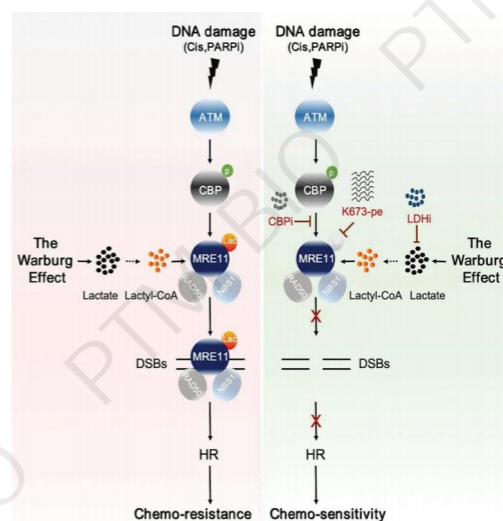
Metabolic Regulation of Homologous Recombination Repair by MRE11 Lactylation

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

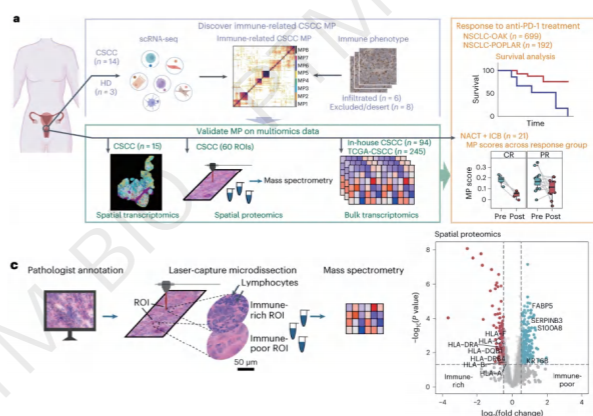
Multiomic analysis of cervical squamous cell carcinoma identifies cellular ecosystems with biological and clinical relevance

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

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



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