

Empower the Future by Epigenetics and Proteomics

PTO BIO is dedicated to developing and providing innovative research products and services to fundamentally transform the way we understand, diagnose, and treat human diseases.

Products & Services An Integrated Platform



• **25+**

PTM Types

• **56000+**

PTM Sites Identified

• **400+**

PTM Antibodies
Expediting the Epigenetics Research

• **1500+**

Publications in Proteomics
Service

Proteomics Services

Proteomics Services

4D-LFQ/LFQ
In-Depth Blood Proteomics
4D-FastDIA
TMT/iTRAQ
PRM/4D-PRM

Profiling of PTMs

Classic PTMs

Phosphorylation
Methylation
Acetylation
Ubiquitination
SUMOylation
Cysteine-Redoxome

Novel Acylations

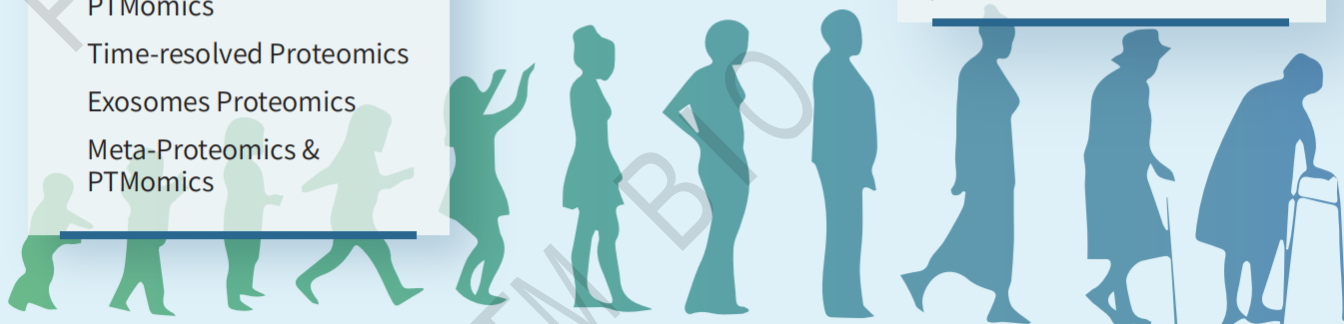
Lactylation (Kla)
 β -hydroxybutyrylation (Kbhb)
Crotonylation (Kcr)
Succinylation (Ksucc)
2-hydroxyisobutyrylation (Khib)
Malonylation (Kmal)
Glutarylation (Kglu)
Propionylation (Kpr)
Butyrylation (Kbu)

Glycosylation modification

O-GlcNAc
O-GalNAc
N-glycosites
Intact N-Glycopeptides

Proteomics Services

Single-cell Proteomics
Spatial Proteomics & PTMomics
Time-resolved Proteomics
Exosomes Proteomics
Meta-Proteomics & PTMomics

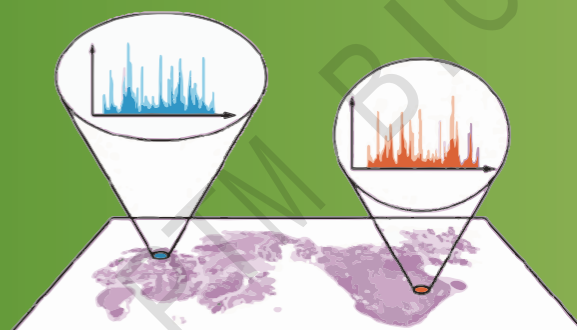


Featured Products

PTM Type	Subscript	PTM Functions	Selected Products
 Lactylation	First reported in Nature in 2019	Closely related to glycolysis and mitochondrial oxidative metabolism, regulating processes such as tumorigenesis, inflammation, metabolism, and hypoxia stress.	PTM-1401RM
 Succinylation	First reported in 2012	Extensively involved in metabolic regulation. Succinylation modification impacts numerous central metabolic enzymes, and is intricately linked with diseases such as cancer, cardiovascular diseases, and inflammation.	PTM-401, PTM-419
 Crotonylation	First reported in Cell in 2011	Regulates gene expression, stem cell differentiation, reproductive development, tumor metabolism, DNA damage repair, and more.	PTM-501, PTM-502
 β -hydroxybutyrylation	First reported in 2016	Closely linked to core cellular metabolism such as fatty acid oxidation, influencing the regulation of cell energy metabolism, DNA damage repair, and tumorigenesis.	PTM-1201RM
 2-Hydroxyisobutyrylation	First reported in 2014	Associated with processes like amino acid synthesis and glycolysis, participating in gene expression regulation, germ cell differentiation, and plant pathogen pathogenicity.	PTM-801, PTM-802
 Phosphorylation	Classic PTM	Regulates enzyme-catalyzed reactions, receptor binding activity, and plays a key role in signal transduction, development, differentiation, cancer development, and stress responses.	PTM-702RM(Tyr)、PTM-705RM(Thr)
 Methylation	Classic PTM	Modulates cancer, aging, neurodegenerative diseases, and other processes through the modulation of gene expression, protein function, RNA processing, and other epigenetic mechanisms.	PTM-602 (Kme1/2)、PTM-606 (Kme2)、PTM-601(Kme3)
 Acetylation	Classic PTM	Affects chromatin structure and gene expression, participating in the regulation of epigenetics, signal transduction, metabolic regulation, immune responses, tumorigenesis, apoptosis, and other biological processes.	PTM-105RM
N-Acetylation		Regulates protein stability, protein interactions, and membrane binding, with a significant role in cellular autophagy.	PTM-1601
Malonylation	First reported in 2012	Involved in the regulation of cellular energy metabolism, metabolic disorders, immune regulation, plant stress resistance, and other biological processes.	PTM-901, PTM-902
Benzoylation	First reported in 2018	Participates in the regulation of signaling pathways, hormone secretion, epigenetics, metabolic regulation, and other biological processes.	PTM-762
Glutarylation	First reported in 2014	Involved in nucleosome assembly, gene expression, DNA damage repair, cell cycle, and other chromatin-related functions.	PTM-1151, PTM-1152
Propionylation	First reported in 2007	Affects chromatin structure and gene expression, participating in the regulation of epigenetics, signal transduction, and metabolic regulation.	PTM-201, PTM-203
Butyrylation	First reported in 2007	Plays a role in gene expression, participating in the regulation of epigenetics, signal transduction, and plant stress responses.	PTM-301RM, PTM-329
 Methacrylation	First reported in 2021	Isomeric with crotonylation modification, with potential regulatory functions in epigenetics and cellular detoxification, and may be associated with neurological and liver diseases.	PTM-1501
Carboxyethylation		Involved in the regulation of oxidative damage and associated with various diseases such as atherosclerosis, diabetes, uremia, heart failure, and neurodegenerative diseases.	PTM-1701RM
O-linked Glycosylation	Classic PTM	Significant impact on protein folding, conformation, distribution, stability, and activity, regulating multiple signaling pathways controlling growth, development, hormone responses, cellular stress, transcription regulation, signal transduction, metabolic diseases, and tumor development.	PTM-951RM, PTM-952
 Ubiquitination	Classic PTM	Mediates protein degradation, altering protein subcellular localization and activity, affecting substrate function and activity, participating in the regulation of cell cycle, apoptosis, aging, neurodegenerative diseases, and signal transduction.	PTM-1107
SUMOylation		Involved in various physiological and biochemical reactions, including protein-protein and protein-DNA interactions, and participates in the regulation of diseases including cardiovascular diseases, cancer, neurodegenerative diseases, and immune-related diseases.	PTM-1109

Spatial Proteomics Service

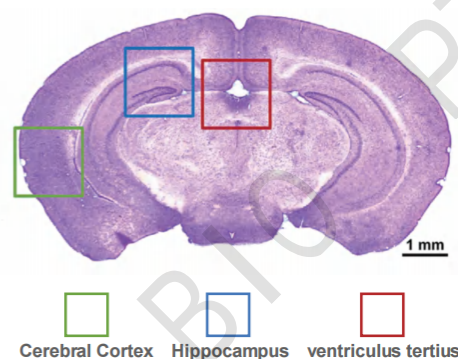
Spatial proteomics is a powerful approach that analyzes protein expression across various spatial locations by sampling at different points within samples. Unlike traditional large-scale tumor tissue analysis, spatial proteomics enables the profiling of protein expression in distinct cells and functional regions within tissues. In comparison to single-cell proteomics, spatial proteomics offers spatially-specific protein expression information.



Applications

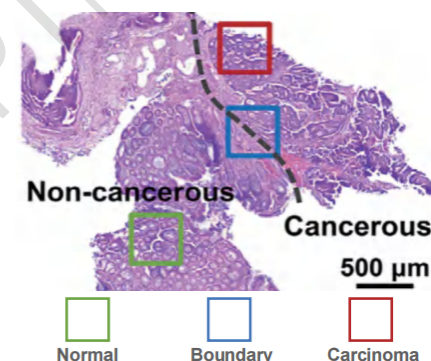
1. Proteomics analysis of functional regions of complex tissues

By dissecting and conducting proteomic analysis on the functional areas comprising complex brain tissue, such as the cerebral cortex, hippocampus, and the third ventricle, we can gain deep insights into the functions and activation states of neurons across different regions at the protein level.



2. Proteomics analysis of tissue heterogeneity

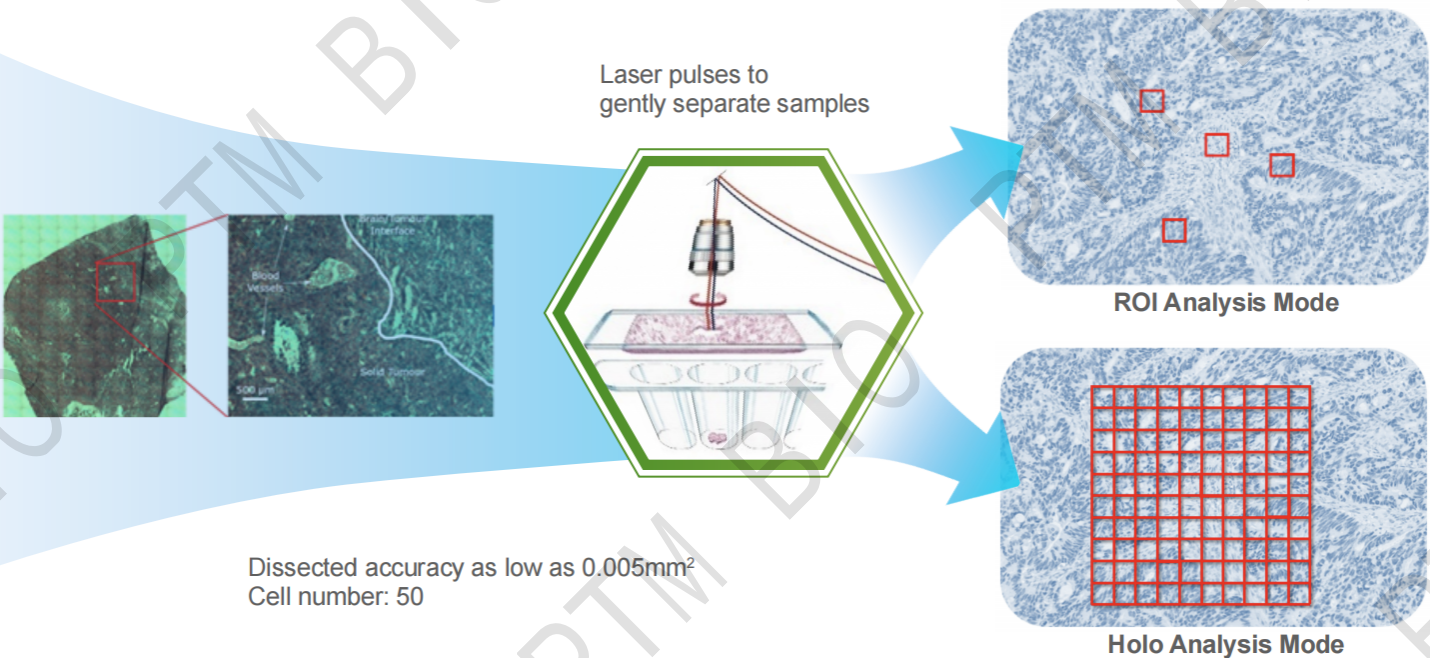
By regionally dissecting and conducting proteomic analysis on slices of cancer and normal tissues, we effectively address the heterogeneity present in cancer samples. This approach reveals abnormally activated pathways and potential therapeutic targets within cancer cells at the protein level.



PTM BIO provides high-precision, deep, and highly repetitive “one-stop” spatial proteomics & phosphorylation analysis service based on its self-sustaining high-precision instrument for the entire process.

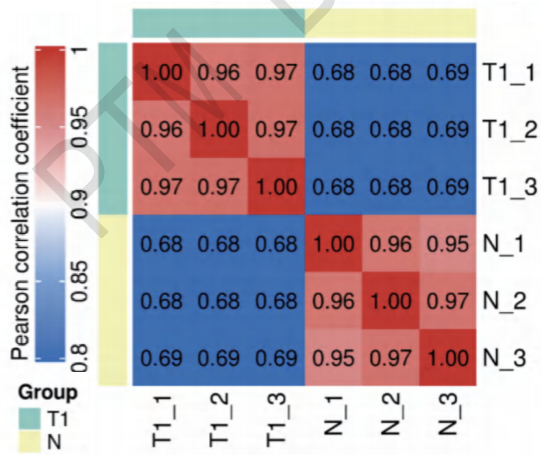
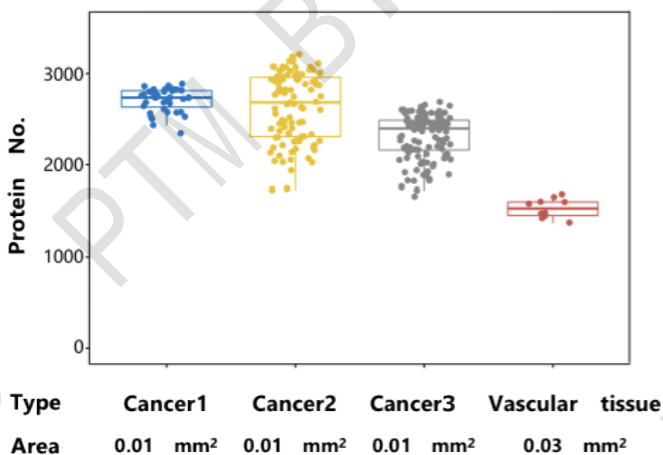
Individualized Dissection

Precise location and dissection of the ROI (region of interest), which greatly improves the flexibility and applicability of the research.



High-Depth Mass Spectrometry Quantification

4D & 10X Proteomics technology, to achieve high depth, high stability analysis.



High-Depth Quantification

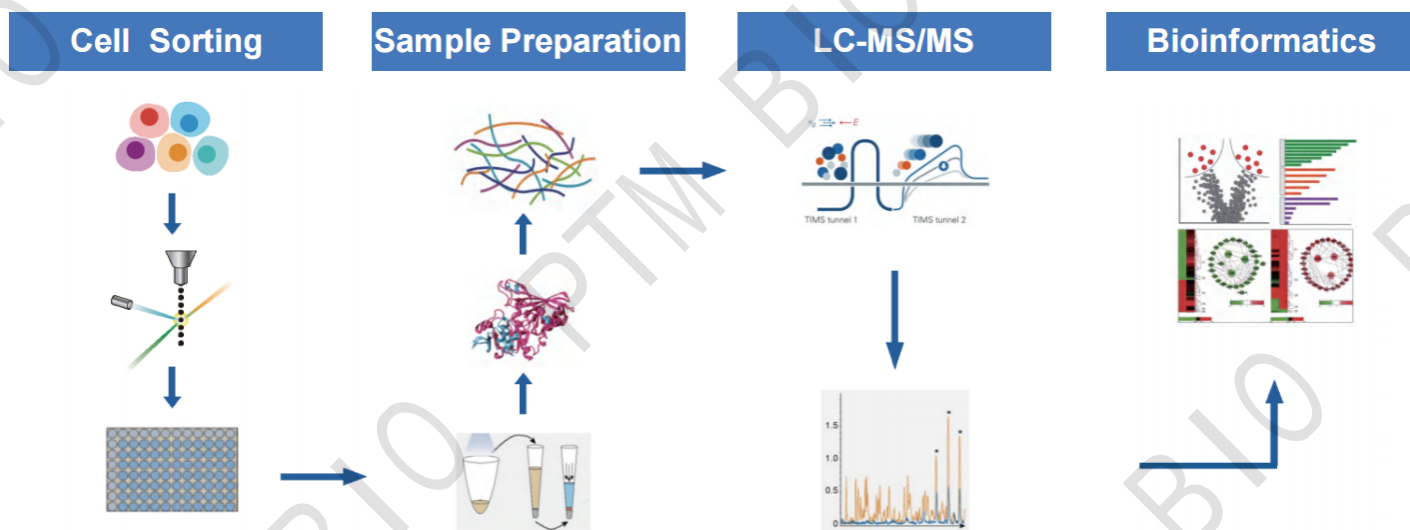
Over 2000 proteins per 0.01 mm²
2 times better than normal tech

High Technical Stability

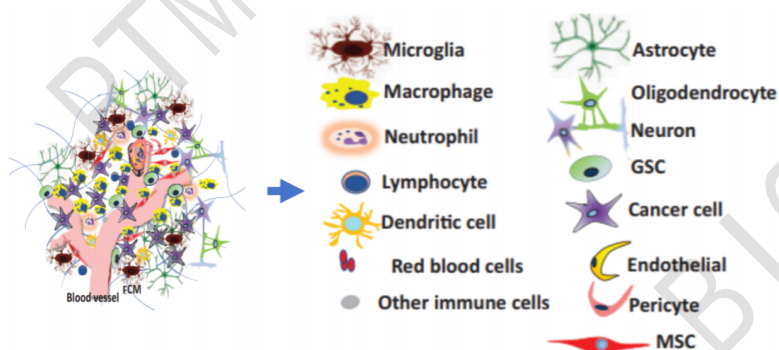
Pearson's correlation coefficients
among three replicates >0.95

Single-Cell Proteomics Service

MS-based single-cell proteomics analysis holds significant research and application value since proteins are the primary drivers of cell function. Single-cell proteomics can bridge the gap left by single-cell genomics and transcriptomics by detecting protein abundance, post-transcriptional regulation, and post-translational modifications. Furthermore, single-cell proteomic analysis furnishes precise information for investigating cell heterogeneity, constructing detailed protein molecular maps, and analyzing spatial protein networks in biological systems. It provides effective research methodologies for various fields, including tumor heterogeneity, stem cell differentiation, and germ cell development.



Applications



From *bulk* to *single cell*

- Proteomic Atlas
- Cell Therapy Analysis
- Tumor Heterogeneity and Drug
- Resistance Research
- Neurosciences Study
- Circulating Tumor Cell Analysis
- Reproductive Medicine Research
- High Throughput Drug Screening
- Immune System and Tumor
- Immunity Study

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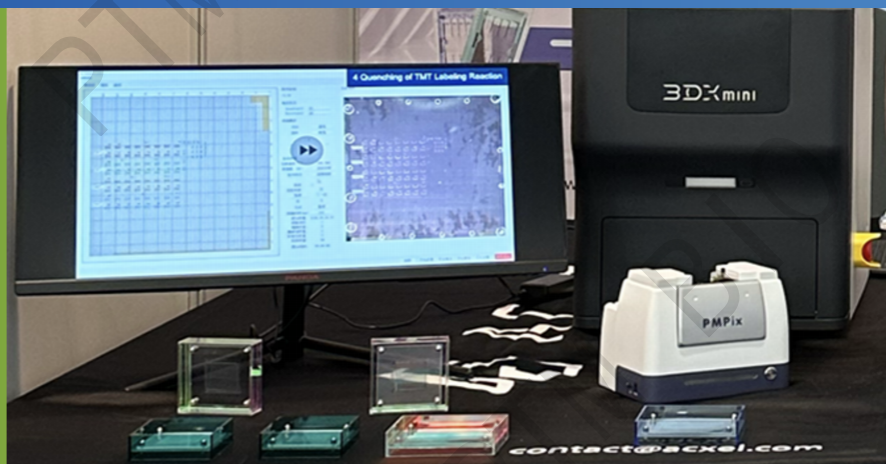
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Technical Advantages

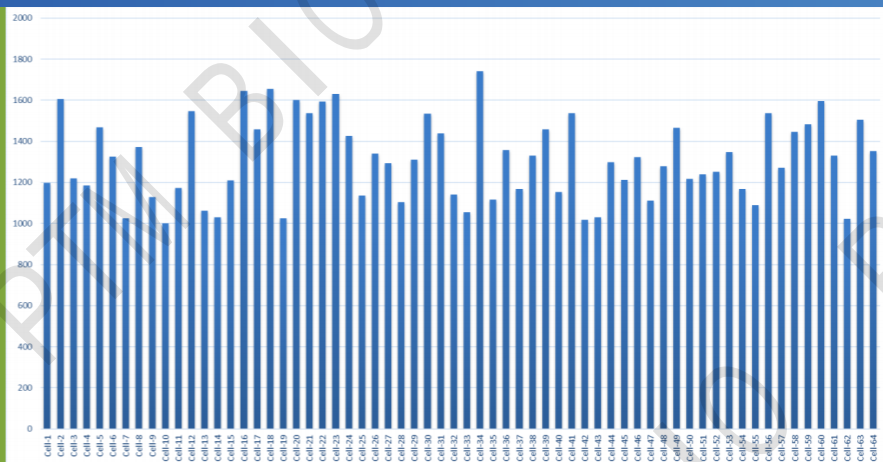
High Throughput Cell Sorting

- Ultra high throughput, >500 cells per day
- Fully automated with integrated chip
- Non destructive sample preparation



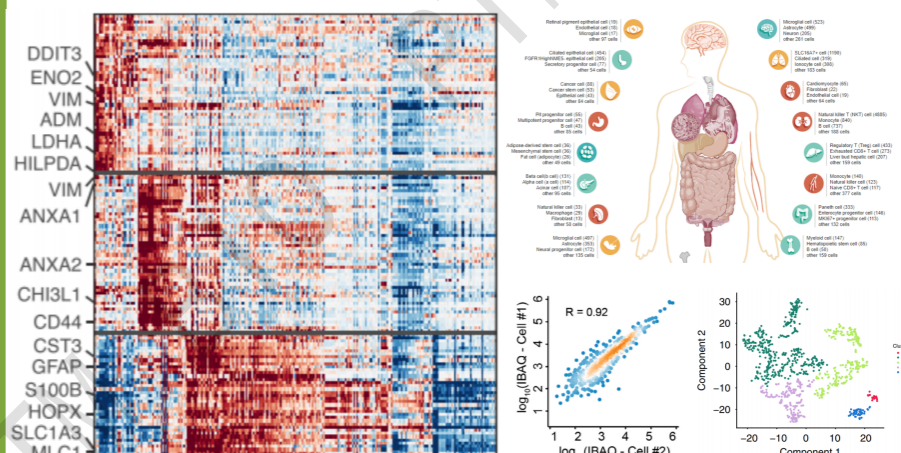
MS-based True Single Cell Analysis

- 4D & 10X proteomics analysis
- High specificity and accuracy
- High depth and sensitivity
- High stability platform



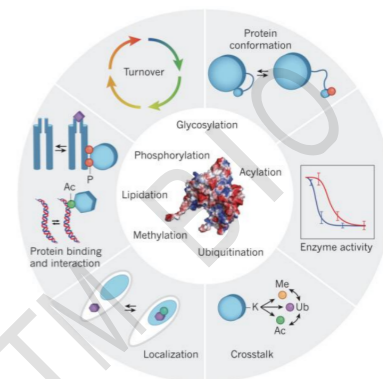
Advanced Bioinformatic Analysis

- Rich quality control for repeatability/missing rate, etc
- Scoring key characteristics such as cell cycle/stemness
- CellMarker library annotations - revealing potential cell types
- Conventional downstream analysis such as cell class differences and functional annotation



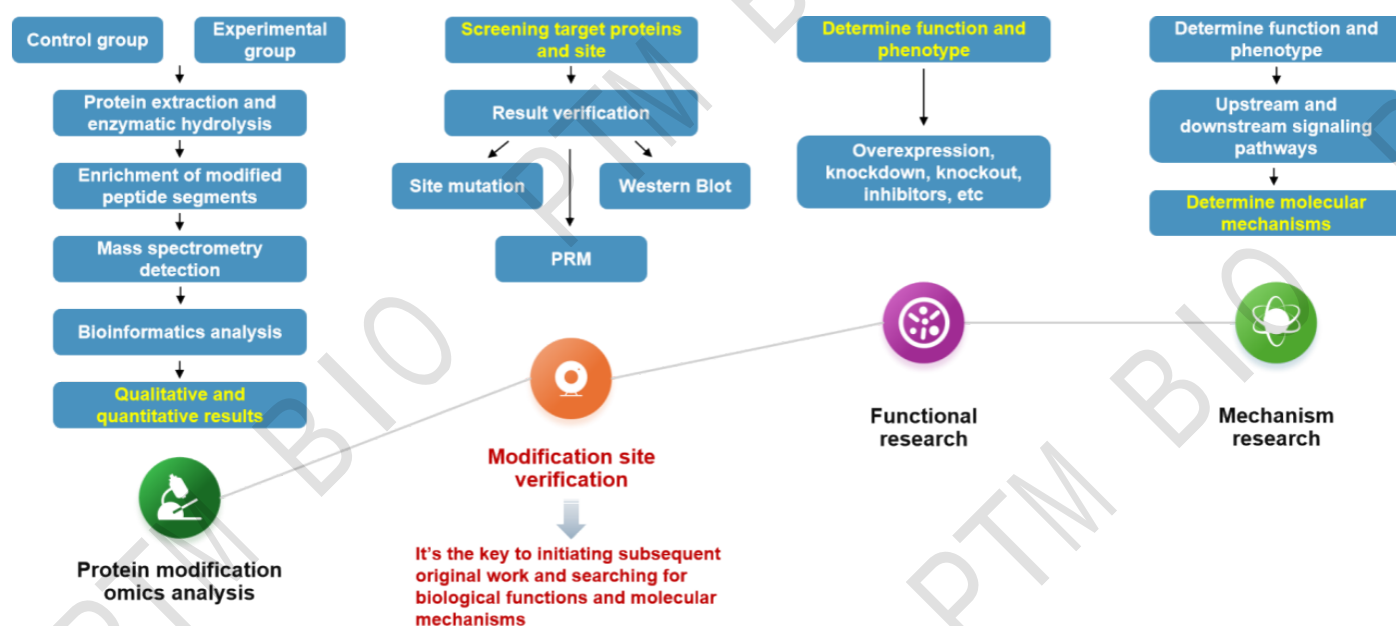
Post-Translational Modifications Proteomics Service

Post-translational modifications (PTMs) play a central role in the complexity and diverse functional roles of the proteome. They are involved in various physiological activities and pathological processes beyond mere protein expression disorders. Therefore, PTMomics is crucial for exploring biological mechanisms, discovering clinical biomarkers, and identifying therapeutic targets.



Solution for PTM research

As a leading and pioneering proteomic company, PTM BIO provides a comprehensive solution for PTM research with highly specific PTM antibodies and high-throughput PTM proteomics analysis service.



Research Methods

Methods

Identification of modification sites
Protein modification spectrum analysis
Quantitative analysis of PTM
Parallel Reaction Monitoring, PRM

Applications

Target protein function mining
Draw modification spectrum
In depth molecular mechanism research
Protein modification validation

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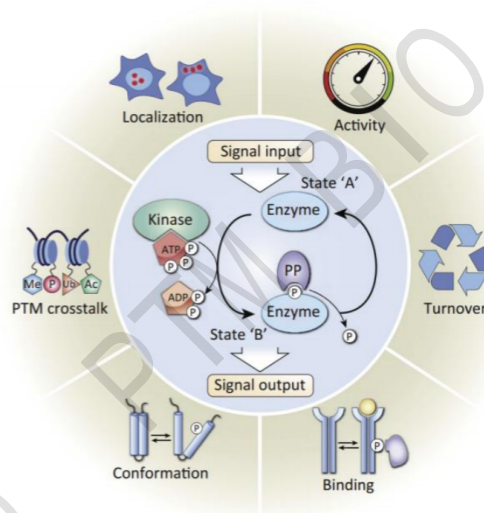
PTM Product Catalog

PTM	Biological Function	Applications
Phosphorylation	The most basic, common, and important mechanism for regulating and controlling protein viability and function	Widely applied in the research fields of signal transduction pathway, apoptosis, developmental differentiation, cancer Mechanism, etc
Acetylation	The most common type of acylation involved in epigenetic regulation, signal transduction, metabolic regulation, cell apoptosis, <i>etc</i>	Immune response, tumorigenesis, metabolic diseases, apoptosis, <i>etc</i>
Lactylation	First discovered on Nature in 2019. Lactate, a metabolic byproduct, can serve as a precursor for lactylation modification	Inflammation, cancer, metabolic diseases, <i>etc</i>
Succinylation	Common in many metabolic enzymes of central metabolism and intermediate metabolism , especially in mitochondrial metabolism	Inflammation, metabolic diseases, tumors, <i>etc</i>
Crotonylation	First discovered on Cell in 2011. involved in important biological processes such as gene expression regulation	Reproductive regulation, epigenetic regulation, tumor metabolism, DNA damage repair, <i>etc</i>
β -hydroxybutyrylation	First reported in 2016. closely related to cellular core metabolism	Energy metabolism, tumor research, DNA damage repair, liver metabolism, liver cancer, <i>etc</i>
2-Hydroxyisobutyrylation	Chromatin function regulation	Epigenetics and glycolytic metabolic pathways
Malonylation	Energy metabolism, antibiotic biosynthesis, metabolic regulation, and photosynthesis	Metabolic disorders, immune regulation
Benzoylation	First reported in 2018. Compared to acetylation, it regulates the metabolism of glycerophospholipids, synthesis of ovarian steroids, signaling pathways for phospholipase D hydrolysis, serotonin synapses, and insulin secretion processes	Epigenetics and metabolic regulation
N-glycosylation	A widely existing type of protein post-translational modification that mainly affects the correct folding, active state, intracellular transport of proteins, <i>etc</i> .	Intercellular recognition, cell adhesion, signal transduction, immune response, cell transformation, <i>etc</i>
O-glycosylation	Participate in the regulation of multiple signaling pathways, and participate in regulating processes such as growth, proliferation, and hormone response	Individual development, cellular stress, transcriptional regulation, signal transduction, metabolic diseases, tumor occurrence and development, <i>etc</i>
intact N-glycopeptide	Listed as one of the technologies of concern by Nature Methods , it mainly affects the protein's spatial conformation, activity, transportation, and localization	Physiological mechanisms, disease pathology, discovery of disease biomarkers, interaction between pathogens and hosts, plant growth and development, <i>etc</i>
Ubiquitination	An important type of modification that downregulates protein expression, mediates protein degradation, alters protein cellular localization, activity, and affects 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 the regulation of protein-protein, protein-DNA interactions, and plays an indispensable role	The occurrence and development of various diseases such as cardiovascular disease, cancer, neurodegenerative diseases, and immune diseases
Methylation	Participates in gene expression regulation, protein function regulation, and ribonucleic acid (RNA) processing	Epigenetics, cancer mechanisms, aging, neurodegenerative diseases
Redox modification	Can reversibly regulate protein activity, interactions, and localization, thereby achieving precise regulation of various life activities	Major disease occurrence, regulation of fat metabolism, plant stress, <i>etc</i>

Phosphorylation

Phosphorylation stands as the fundamental, ubiquitous, and essential mechanism for regulating and controlling protein function and viability.

PTM BIO has initiated an in-depth quantitative analysis of phosphorylation modifications, leveraging proprietary IMAC materials for the enrichment of phosphorylation-modified peptides, thereby effectively reducing sample complexity. This powerful combination, combined with rigorous double quality control and bioinformatics analysis, finds widespread application in studying phosphorylation mechanisms under both physiological and pathological conditions.



Protein extraction and trypsin digestion



Enrichment of phosphorylated peptides



LC-MS/MS



Qualitative and quantitative analysis



Phosphoproteome data

Applications

Signal transduction

Cancer mechanism

Immune inflammation

Metabolic regulation

Apoptosis

Adversity stress

Food science

Science: In vivo brain gpcr signaling elucidated by phosphoproteomics.

Nature: Proteomics identifies therapeutic targets of early-stage hepatocellular carcinoma.

Immunity: Integrative proteomics and phosphoproteomics profiling reveals dynamic signaling networks and bioenergetics pathways underlying T cell activation.

Cell Metab: Phosphoproteomics reveals the GSK3-PDX1 Axis as a key pathogenic signaling node in diabetic islets.

Autophagy: Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy.

Mol Cell: Reciprocal regulation of the TOR Kinase and ABA receptor balances plant growth and stress response.

J Agric Food Chem: Comparative quantitative phosphoproteomic analysis of the Chicken Egg during Incubation based on tandem mass tag labeling.

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Advantages

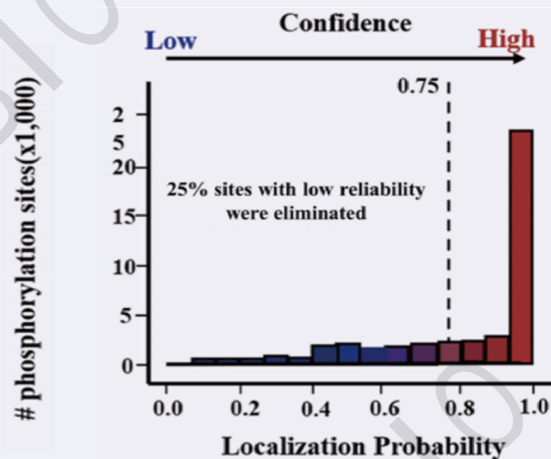
Technology upgrade-Deeper Coverage

Utilizing the IMAC enrichment strategy in combination with 4D proteomics technology has greatly enhanced detection sensitivity and significantly increased the number of identified phosphorylation sites.



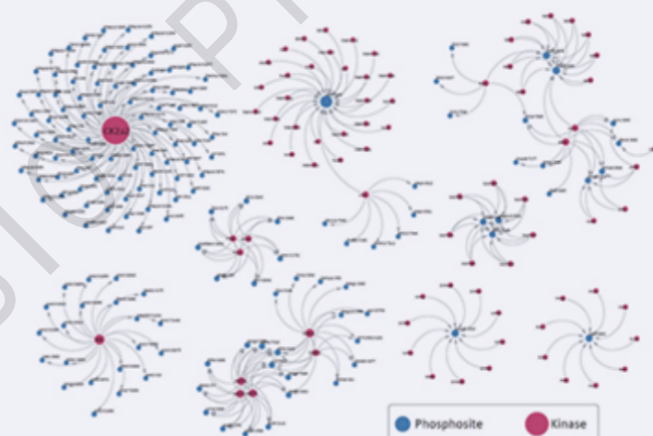
QC upgrade-Higher Credibility

Double quality control standards, including both FDR (False Discovery Rate, set at 0.75) and FLR (False Localization Rate, set at 0.75), are applied to exclude modification sites with lower reliability.



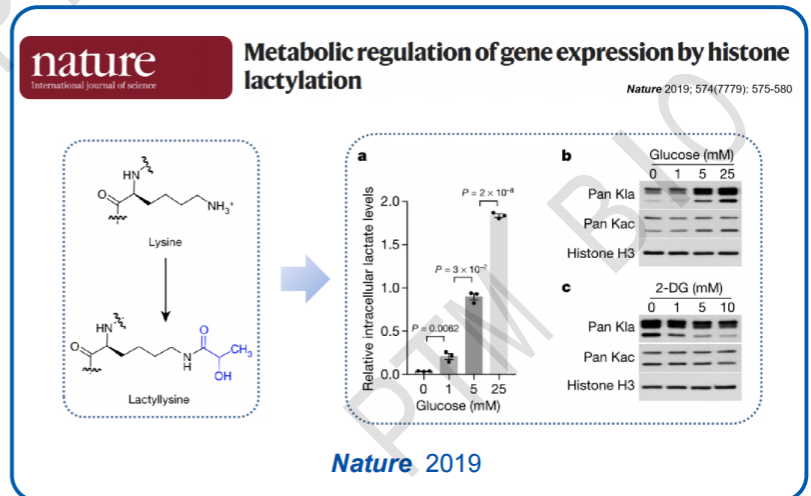
Bioinformatics upgrade-Deeper Mining

Kinase prediction, signal pathway analysis, and in-depth data mining are provided to explore the mechanisms under physiological and pathological conditions.



Lactylation

Lactylation is a newly discovered post-translational modification, initially described by Professor Ying-ming Zhao of the University of Chicago in 2019. Research has revealed that lactic acid, a metabolic byproduct, can act as a precursor for the lactylation modification of histone lysine. This modification plays a role in regulating the steady-state of M1 macrophages infected by bacteria and is implicated in the regulation of inflammation, cancer, and other diseases.



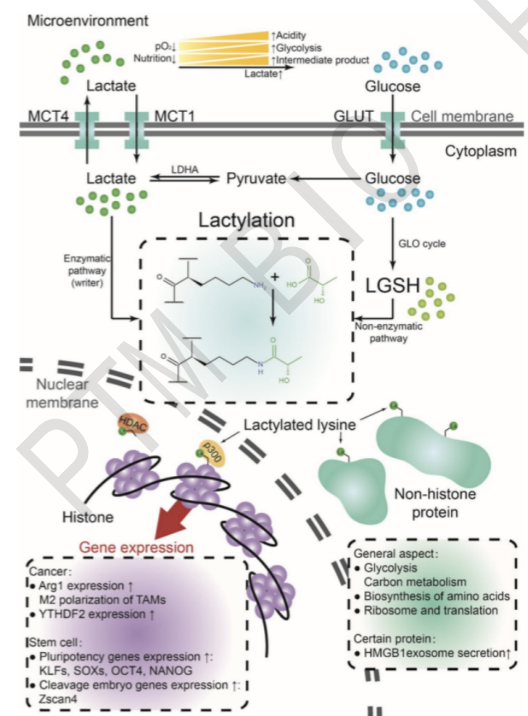
Applications

1. Regulatory mechanism studies

Further research is needed on enzymes that catalyze the production of lactyl-CoA intermediates, the site-specific functions of histone lactylation modifications, and the 'writers,' 'erasers,' and 'readers' of histone lactylation modifications.

2. Physiological and pathological function studies

Lactic acid is a widely existing metabolic substance, and the new histone modification mediated by lactate will play an important role in biological processes such as DNA damage repair and muscle movement, as well as in pathological processes such as inflammation and cancer.

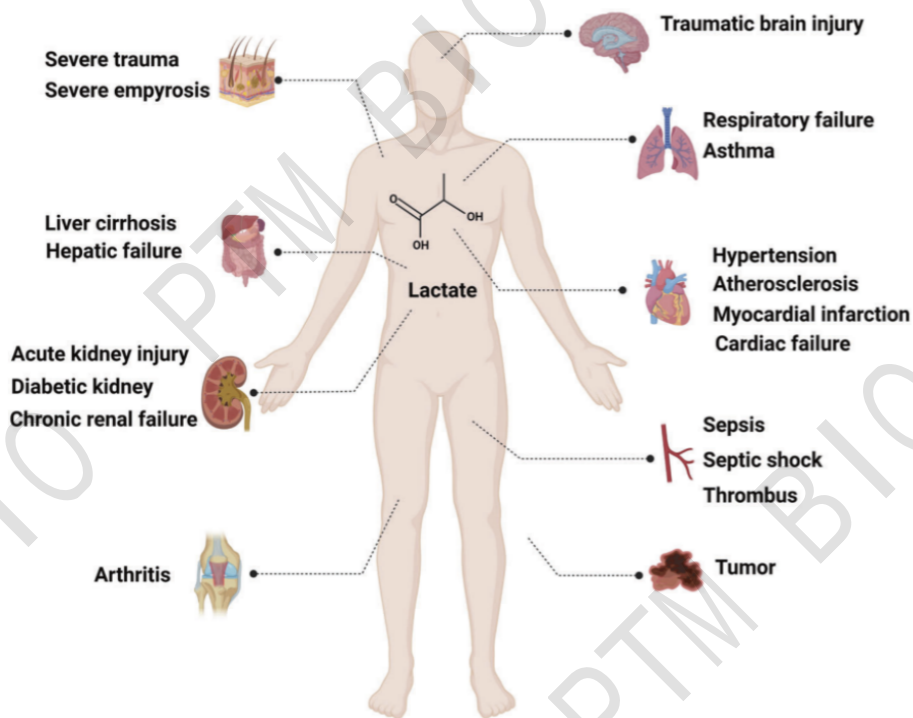


Nat Methods 2022

Hot Research Topics

Tumor Microenvironment

The significant amount of lactate produced by glycolysis in the tumor microenvironment was previously regarded solely as a metabolic waste. However, recent studies have revealed that lactic acid can actually promote tumor progression.



Lactate metabolism in human health and disease

Signal Transduct Target Ther. 2022

Mechanism Study

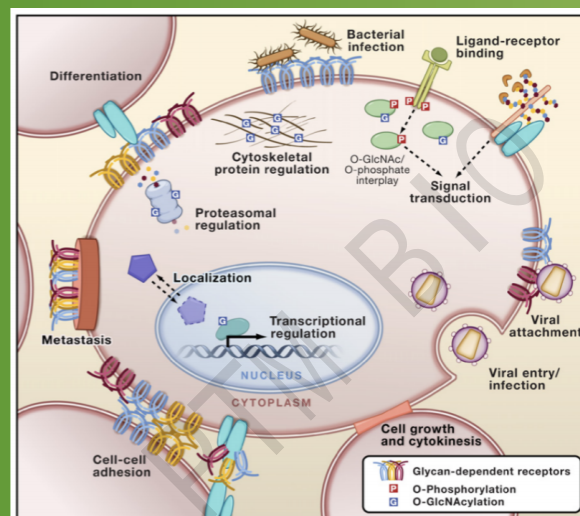
Lactate serves as a critical regulatory factor for tumor immunity and antiviral response. It suppresses the activation of inflammatory macrophages and fosters cellular homeostasis through diverse mechanisms across multiple subcellular levels. The discovery of lactylation modification underscores its pivotal role in inhibiting macrophage activation in an epigenetic context. Investigating the mechanisms governing the activation of various signaling pathways under hypoxic conditions and their synergistic interactions with canonical inflammatory pathways will be a crucial research direction.

Discovery of Drug Targets

Lactate in the blood is a byproduct of anaerobic respiration and indicates inadequate oxidative capacity. Clinical studies have revealed an association between lactate and hypertension, suggesting that insufficient oxidative capacity or mitochondrial dysfunction may contribute to hypertension. Furthermore, lactate levels can serve as diagnostic and prognostic tools for numerous diseases.

Glycosylation

Glycosylation is a significant and prevalent post-translational modification of proteins. It plays a crucial role in maintaining the normal physiological functions of the human body. Over half of the proteins in organisms undergo glycosylation modification, including transcription factors, enzymes related to glucose metabolism, and more.



Glycoproteomics Solution

PTM BIO offers comprehensive glycoproteomics research solution, provides powerful research tools for biomarker discovery and investigates disease pathogenesis.

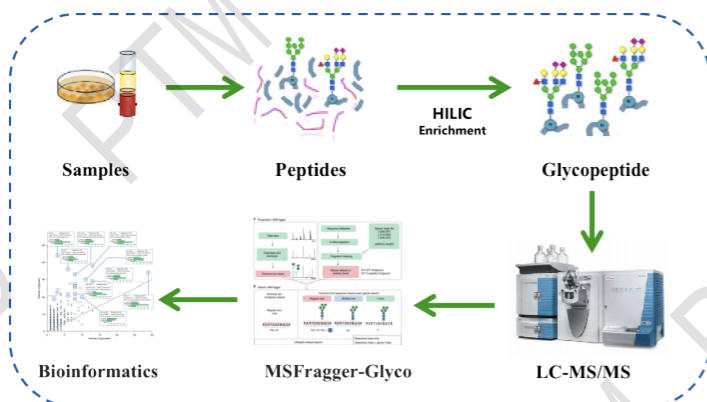
N-glycoproteomics

O-glycoproteomics

intact N-glycopeptide

intact O-GalNac glycopeptide

Analysis Protocol



Applications

- Tumor occurrence and mechanism
- Cellular development and metabolism
- Immunological research
- Neurobiology
- Discovery of biomarkers
- Glycosylation modification function

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Advantages

① Complete information discovery |

Provide glycoproteins, glycosylation modification sites, and complete sugar chain information

② High sensitivity |

Using ultra-high sensitivity mass spectrometer

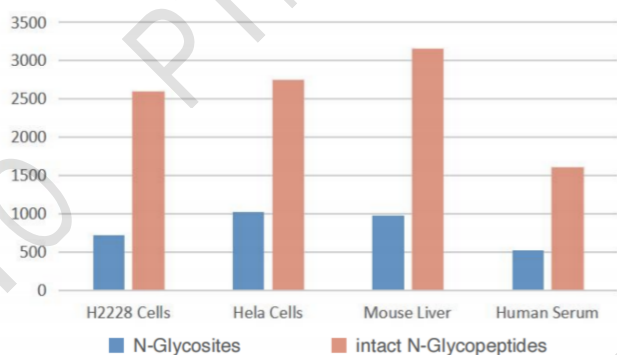
③ Stable and Reliable |

Experimental verification of clinical large queue organizational sample projects

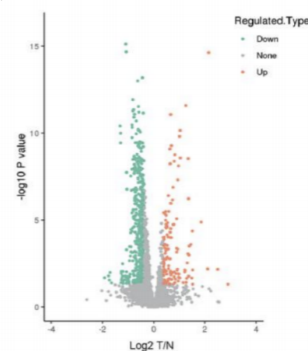
④ Deep bioinformatics analysis |

Innovative modification of multi omics, in-depth exploration of information

Demo Data



Glycans per glycosite



Conventional cells/tissues:

- 1 | Identified 800-1000 N-glycosylation sites
- 2 | Identified 2400-2600 intact N-glycopeptides

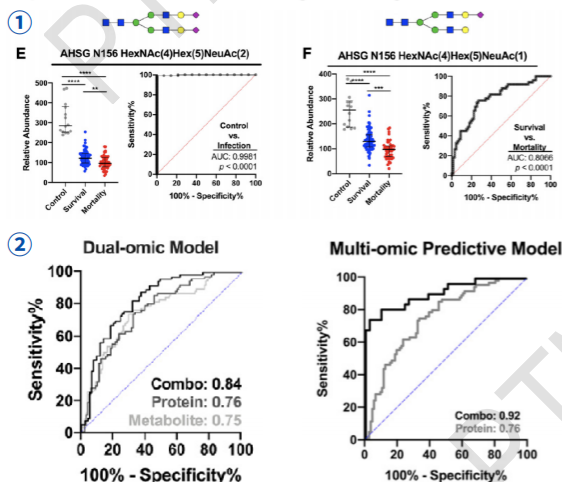
Clinical Large Queue Organizational Sample Project Testing:

- 1 | Identified over 3400 N-glycosylation sites
- 2 | Identified over 12000 intact N-glycopeptides
- 3 | Quantifiable proportion exceeding 80%

Application Cases

Cell

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



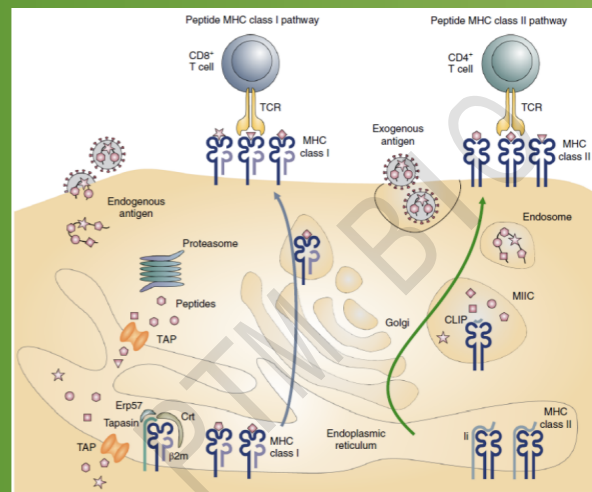
Resource

This study focuses on utilizing proteomics, metabolomics, and intact N-glycopeptides to discover highly accurate biomarkers that can be used to diagnose infections and predict infection-related mortality.

- ① Glycopeptides exhibit high accuracy in predicting both infection status and survival outcomes among infected individuals
- ② The multi-omic predictive model (combining protein, metabolite, and intact N-glycopeptide data) enhances the accuracy of predicting post-infection survival to an ROC-AUC of 0.92.

MHC Peptidomics

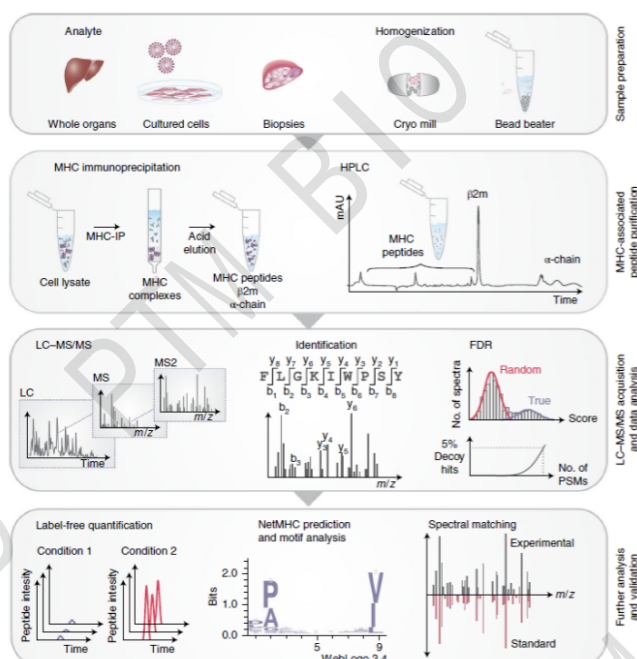
MHC (Major Histocompatibility Complex) is a group of genes that encode proteins involved in the immune system's recognition of foreign molecules. These proteins are crucial for presenting antigens to T cells, which are key players in the adaptive immune response. MHC plays a central role in immune surveillance and is essential for distinguishing self from non-self, thereby contributing to immune tolerance and defense against pathogens.



MHC class I and II antigen-presentation pathways.
Nat Protoc. 2019;14(6):1687-1707.

PTM BIO integrates independently developed high-performance antibodies with optimized enrichment and separation methods to offer high-quality MHC-associated peptide proteomics services, aiding in MHC research.

Analysis Protocol

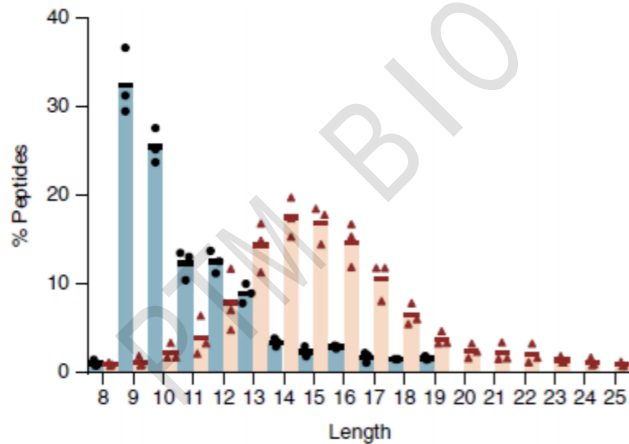


Applications

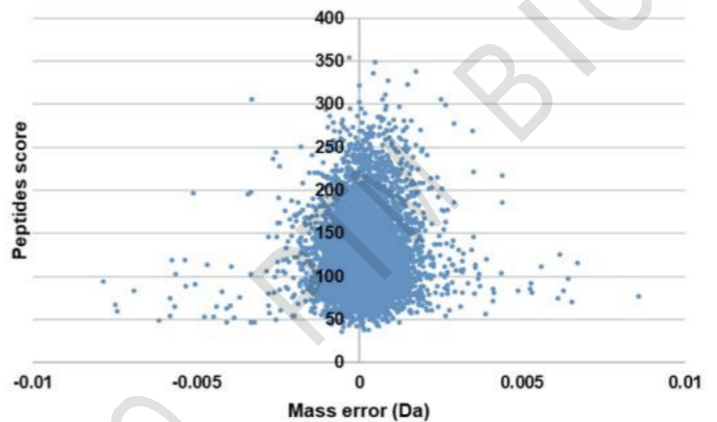
- Immune Response Study
- New Vaccines R&D
- Drug Discovery
- Early Diagnosis and Treatment
- Personalized Medicine

Advantages

- ① High affinity and high specificity MHC monoclonal antibodies;
- ② High specificity enrichment conditions for MHC molecules;
- ③ Efficient MHC complex separation method



Peptide length characteristic distribution as a quality control standard

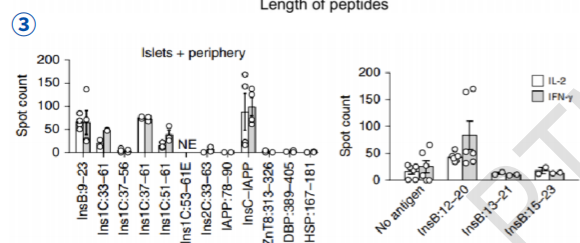
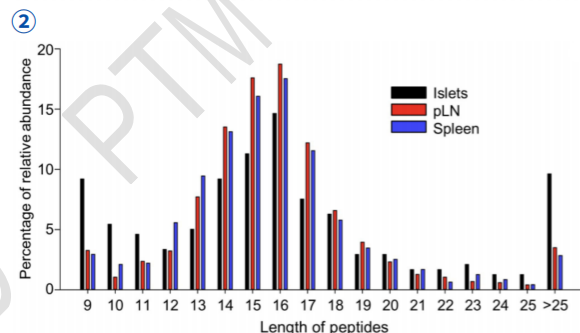
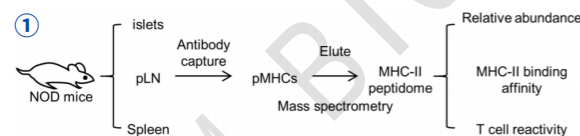


The mass error and high score of the identified MHC peptide segment indicating high reliability

Application Cases



The MHC-II peptidome of pancreatic islets identifies key features of autoimmune peptides



This study elucidates the main characteristics of autoimmune peptides induced by NOD mice, providing certain reference significance for the clinical diagnosis and treatment of type I diabetes.

- ① Analysis of MHC-II peptide composition in pancreatic islets, pancreatic lymph nodes, and spleen of NOD mice
- ② The distribution of MHC-II peptide segments in each organization conforms to the characteristics of 10-20 aa
- ③ Only 5 types of CD4+T cells that can activate autoimmunity, and the main antigenic epitopes recognized by pathological CD4+T cells are InsB: 12-20 epitopes

Title	Journal
Metabolic regulation of gene expression by histone lactylation	<i>Nature</i> (IF=64.8)
Single-cell chromatin modification profiling reveals increased epigenetic variations with aging	<i>Cell</i> (IF=64.5)
Disordered methionine metabolism in MTAP/CDKN2A-deleted cancers leads to dependence on PRMT5	<i>Science</i> (IF=56.9)
Direct phosphorylation and stabilization of MYC by Aurora B kinase promote T-cell leukemogenesis	<i>Cancer Cell</i> (IF=50.3)
Increased glucose metabolism in TAMs fuels O-GlcNAcylation of lysosomal Cathepsin B to promote cancer metastasis and chemoresistance NEW	<i>Cancer Cell</i> (IF=50.3)
Acquired semi-squamization during chemotherapy suggests differentiation as a therapeutic strategy for bladder cancer NEW	<i>Cancer Cell</i> (IF=50.3)
Landscape of the regulatory elements for lysine 2-hydroxyisobutyrylation pathway	<i>Cell Research</i> (IF=44.1)
Global profiling of crotonylation on non-histone proteins	<i>Cell Research</i> (IF=44.1)
Lysine 2-hydroxyisobutyrylation of NAT10 promotes cancer metastasis in an ac4C-dependent manner NEW	<i>Cell Research</i> (IF=44.1)
Global profiling of O-GlcNAcylated and/or phosphorylated proteins in hepatoblastoma	<i>Signal Transduct Tar</i> (IF=39.3)
TRIM31 facilitates K27-linked polyubiquitination of SYK to regulate antifungal immunity	<i>Signal Transduct Tar</i> (IF=39.3)
VAV2 is required for DNA repair and implicated in cancer radiotherapy resistance	<i>Signal Transduct Tar</i> (IF=39.3)
Phosphoproteomics reveals therapeutic targets of esophageal squamous cell carcinoma	<i>Signal Transduct Tar</i> (IF=39.3)
Short-chain enoyl-CoA hydratase mediates histone crotonylation and contributes to cardiac homeostasis	<i>Circulation</i> (IF=37.8)



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