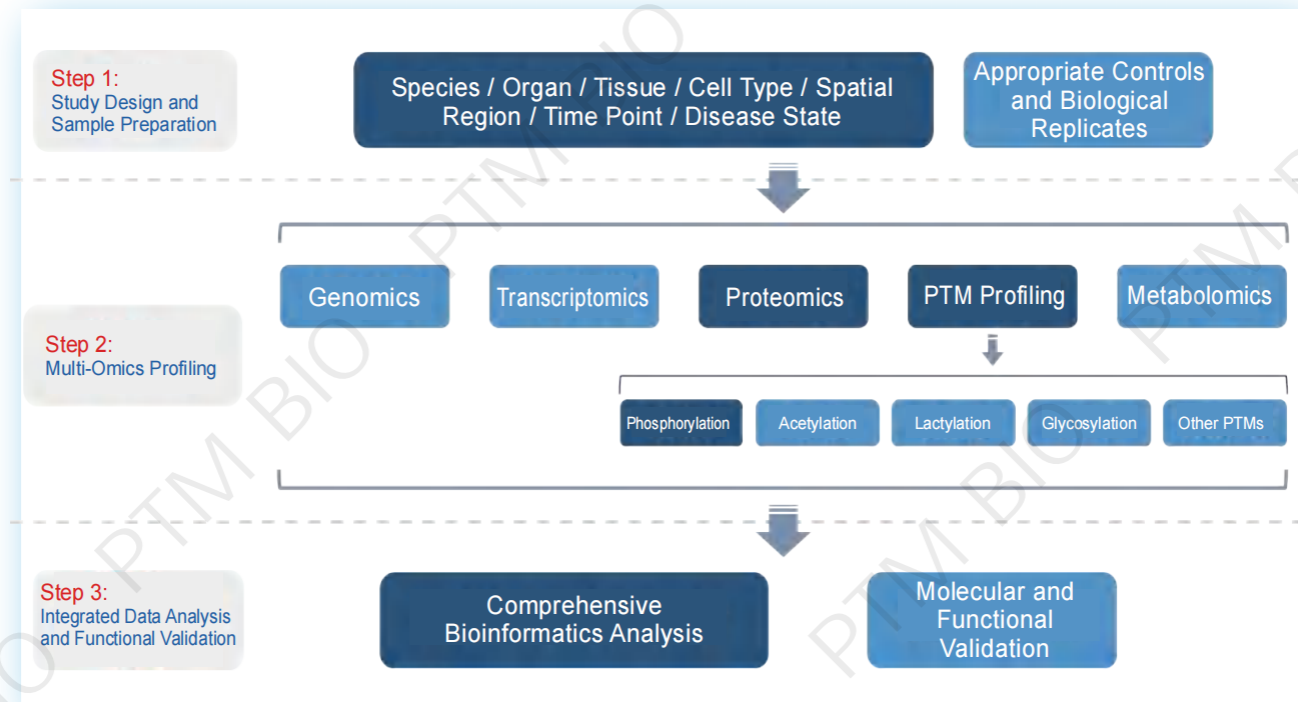


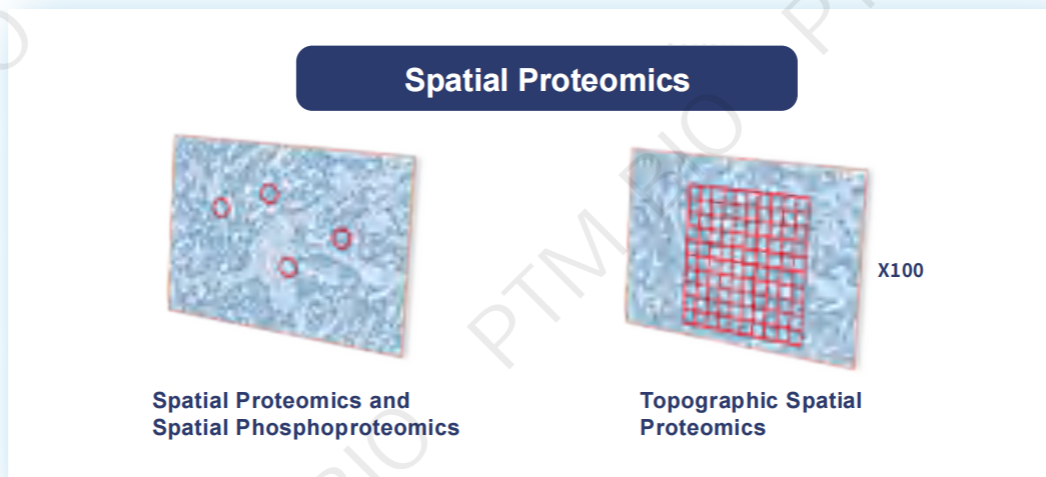
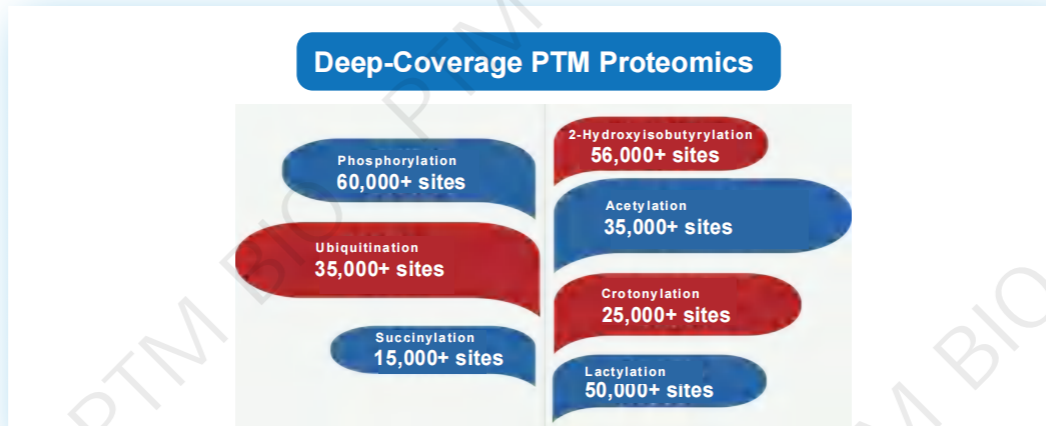
Multidimensional Proteomics Research Across Biological *From Global and PTM Proteomics to Spatial Proteomic Atlases*

From Global and PTM Proteomics to Spatial and Time-Resolved Proteomic Atlases

Proteome and PTM Atlases for Systems-Level Biology



Advanced Multi-Omics Technologies · High-Quality Data





High-Resolution Multidimensional Proteomic Atlases in Animal Models

Selected Research at the Frontier

Cell: An atlas of protein-protein interactions across mouse tissues

Generated a multi-organ protein-interaction atlas across mouse brain, liver, lung, skeletal muscle, kidney, heart, and thymus, **expanding the study of mammalian protein-interaction networks**.

Cell Stem Cell: Deciphering lineage specification during early embryogenesis in mouse gastruloids using multilayered proteomics

Generated single-cell proteomic and phosphoproteomic maps of mouse gastruloids and embryos across developmental stages, **revealing cell-type heterogeneity during early development**.

Featured Studies

Signal Transduct Target Ther (IF=52.7): Gefitinib and fostamatinib target EGFR and SYK to attenuate silicosis: a multi-omics study with drug exploration

Generated a time-resolved phosphoproteomic atlas of a mouse model of silicosis, **identifying disease-associated signaling pathways and candidate therapeutic targets**.

Nat Commun (IF=15.7): Multi-omics profiling reveals rhythmic liver function shaped by meal timing

Generated an integrated molecular atlas of mouse liver under time-restricted feeding, encompassing proteomics, phosphoproteomics, ubiquitinomics, succinylation profiling, N-glycosylation profiling, and lipid metabolism.

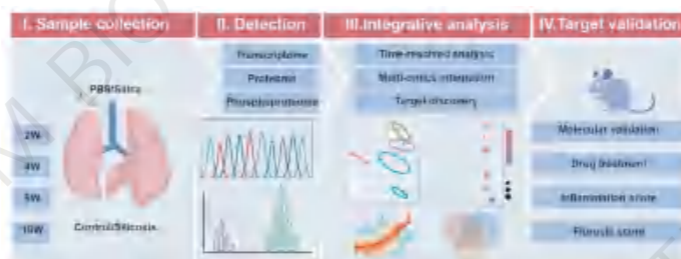
J Adv Res (IF=13): Comprehensive analysis of the lysine acetylome and succinylome in the hippocampus of gut microbiota dysbiosis mice

Profiled lysine acetylation and succinylation in a mouse model of gut microbiota dysbiosis, **revealing pathways that may link dysbiosis to depression and identifying candidate therapeutic targets**.

Signal Transduct Tar(IF=52.7): Time-Resolved Phosphoproteomic Profiling in a Mouse Model of Silicosis

Gefitinib and fostamatinib target EGFR and SYK to attenuate silicosis: a multi-omics study with drug exploration

Using PTM BIO proteomics services, researchers at the Chinese Academy of Medical Sciences and Peking Union Medical College applied time-resolved transcriptomics, proteomics, and phosphoproteomics to a mouse model of silicosis. Integrated analysis identified disease-associated signaling pathways and candidate drug targets. Preclinical evaluation further supported the activity of gefitinib and fostamatinib, providing a rationale for their further investigation in silicosis.



Nat Commun(IF=15.7): A Spatiotemporal Proteomic Atlas of the Cynomolgus Macaque Brain from Fetal to Neonatal Stages

Spatiotemporal proteomic atlas of multiple brain regions across early fetal to neonatal stages in cynomolgus macaques

Using PTM BIO proteomics services, researchers at Kunming University of Science and Technology generated a spatiotemporal proteomic atlas of multiple brain regions in cynomolgus macaques from fetal through neonatal stages. The study characterized region-specific proteomic dynamics during early primate brain development, providing a resource for investigating neurodevelopmental dysfunction and related disease mechanisms.



Landmark Studies in Plant Proteomic Atlases

Nature: Mass-spectrometry-based draft of the Arabidopsis proteome

The study generated a quantitative atlas of transcriptomes, proteomes, and phosphoproteomes across 30 *Arabidopsis* tissues, providing a resource for plant research.

Science: Integration of omic networks in a developmental atlas of maize

The study integrated matched transcriptomic, proteomic, and phosphoproteomic profiles across maize tissues to map developmental regulatory networks and improve functional annotation of the maize genome.

Featured Studies

Mol Plant (IF=24.1): A large-scale proteogenomic atlas of pear

Developed a proteogenomic atlas spanning 24 major pear tissues and organs, providing a reference framework for research in pear, other fruit crops, and non-model plant species.

Nat Commun (IF=15.7): Integration of multi-omics data accelerates molecular analysis of common wheat traits

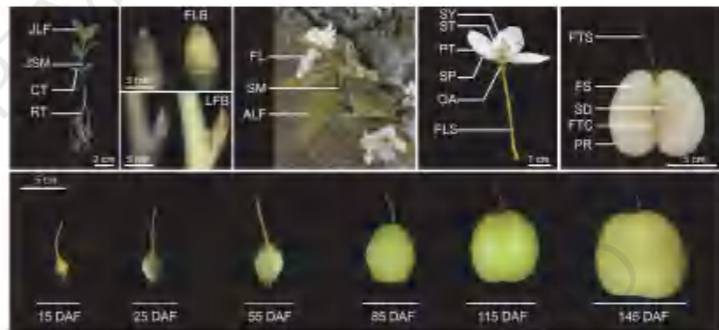
Built a deep multi-PTM atlas of wheat and examined molecular mechanisms underlying developmental and disease-resistance traits.

Adv Sci (IF=14.1): Lysine 2-hydroxyisobutyrylation- and succinylation-based pathways act inside chloroplasts to modulate plant photosynthesis and immunity

Generated lysine 2-hydroxyisobutyrylation and succinylation atlas in cotton, revealing how chloroplast protein PTMs help coordinate immunity and crop performance.

Mol Plant (IF=24.1): A Large-Scale Proteogenomic Atlas of Pear

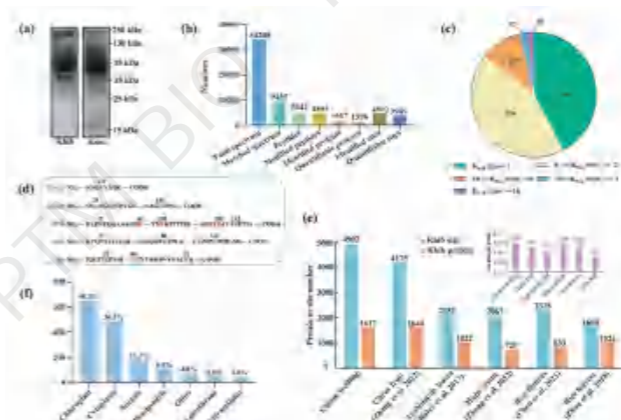
Researchers at Nanjing Agricultural University developed a proteogenomic atlas spanning 24 major pear tissues and organs across developmental stages, improving pear genome annotation. Gene-regulatory network analysis revealed relationships among key genes, identified five previously unannotated peptides involved in pollen-tube growth in the style, and proposed a receptor kinase-mediated PTM mechanism underlying stone-cell formation. The study also established PearEXP, an interactive resource for exploring pear transcript and protein expression atlas and newly annotated coding events.



Adv Sci (IF=14.1): Novel Acylation Profiling in Cotton Under Biotic Stress

Lysine 2-hydroxyisobutyrylation- and succinylation-based pathways act inside chloroplasts to modulate plant photosynthesis and immunity

Researchers generated lysine 2-hydroxyisobutyrylation (Khib) and succinylation (Ksuc) atlas in cotton seedlings and systematically examined immune responses to *Verticillium dahliae* infection. The study showed that the balance of Khib and Ksuc on chloroplast proteins contributes to the coordination of *Verticillium* wilt resistance and yield-related traits, suggesting potential directions for improving crop performance under pathogen stress.



Landmark Studies in Human and Clinical Proteomic Atlas Research

Selected Research at the Frontier

Cell: A quantitative proteome map of the human body

Generated a quantitative proteome map across **32 human tissues and organs**, providing new insights into **genetic disease mechanisms and nominating candidate therapeutic targets**.

Nature: A cross-species proteomic map reveals neoteny of human synapse development

Generated a **cross-species proteomic map of neocortical synapse development across six developmental time points** in humans, macaques, and mice, providing a framework for studying the molecular basis of human synaptic maturation.

Featured Studies

Cancer Cell (IF=44.5): Proteogenomic insights suggest druggable pathways in endometrial carcinoma

Generated **integrated proteomic, phosphoproteomic, acetylomic, and glycoproteomic atlas** of endometrial carcinoma, revealing candidate therapeutic targets.

Adv Sci (IF=14.1): Integrated lacylome characterization reveals the molecular dynamics of protein Regulation in gastrointestinal cancers

Generated a pan-cancer **lactylation proteomic atlas** across gastrointestinal malignancies, **identifying patterns of lysine lactylation associated with cancer biology**.

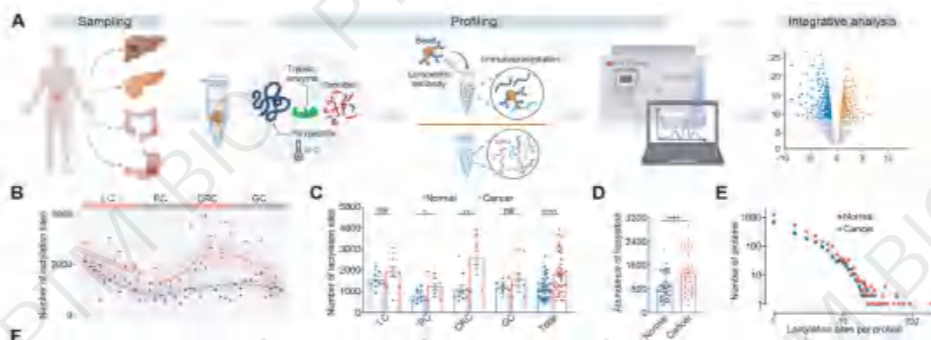
Cell Rep Med (IF=10.6): Organ-specific metabolic pathways distinguish prediabetes, type 2 diabetes, and normal tissues

Generated a **multi-organ proteomic atlas** from individuals with prediabetes and type 2 diabetes, revealing metabolic features associated with disease progression.

Adv Sci (IF=14.1): Pan-Cancer Lactylation Proteomic Atlas in Gastrointestinal Malignancies

Integrated lacylome characterization reveals the molecular dynamics of protein regulation in gastrointestinal cancers

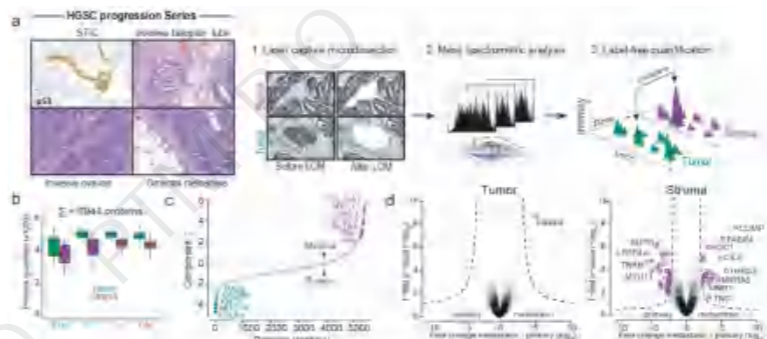
Using PTM BIO proteomics services, researchers at Shandong First Medical University performed integrated lacylome profiling of tumor and matched adjacent tissues from **40 patients** with gastrointestinal cancers, including **liver, pancreatic, colorectal, and gastric cancers**. The study characterized pan-cancer patterns of **lysine lactylation (Kla)**, providing a resource for biomarker discovery and the generation of therapeutic hypotheses.



Nature: Spatial Proteomics Identifies NNMT as a Key Regulator of Ovarian Cancer Metastasis

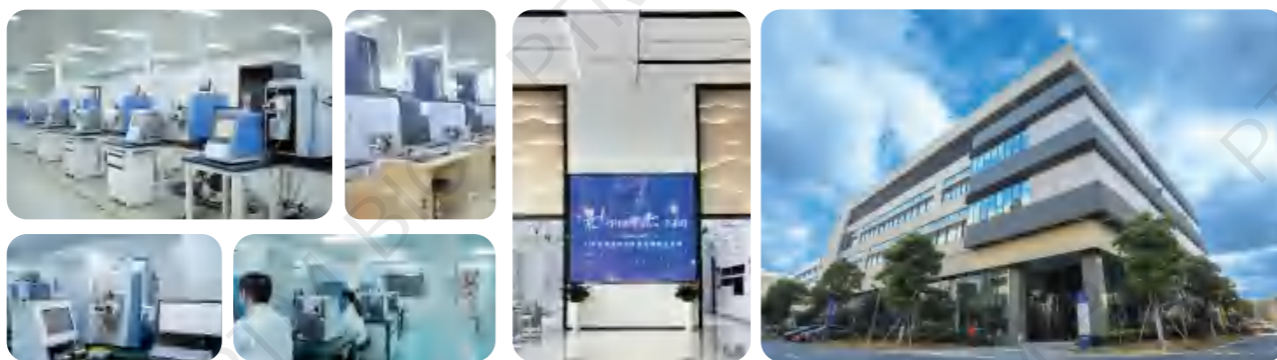
Proteomics reveals NNMT as a master metabolic regulator of cancer-associated fibroblasts

Using laser-capture microdissection, the study profiled **107 spatially distinct regions** from tissue specimens of **11 patients with high-grade serous carcinoma (HGSC)**. Spatial proteomics identified NNMT as a key metabolic regulator of cancer-associated fibroblasts and ovarian cancer metastasis. Inhibition of NNMT reversed cancer-associated fibroblast phenotypes and suppressed metastatic progression in preclinical models.



Selected Publications Featuring PTM BIO Products and Services

Title	Journal
Metabolic regulation of gene expression by histone lactylation	<i>Nature</i> (IF=48.5)
Alanyl-tRNA synthetase, AARS1, is a lactate sensor and lactyltransferase that lactylates p53 and contributes to tumorigenesis	<i>Cell</i> (IF=42.5)
Metabolic regulation of homologous recombination repair by MRE11 lactylation	<i>Cell</i> (IF=42.5)
Increased glucose metabolism in TAMs fuels O-GlcNAcylation of lysosomal Cathepsin B to promote cancer metastasis and chemoresistance	<i>Cancer Cell</i> (IF=44.5)
Branched-chain amino acid catabolism promotes thrombosis risk by enhancing tropomodulin-3 propionylation in platelets	<i>Circulation</i> (IF=38.6)
Sex-determining region Y gene promotes liver fibrosis and accounts for sexual dimorphism in its pathophysiology	<i>Journal of Hepatology</i> (IF=33.0)
An integrated multi-omics analysis reveals osteokines involved in global regulation	<i>Cell Metabolism</i> (IF=30.9)
Senescent immune cells release grancalcin to promote skeletal aging	<i>Cell Metabolism</i> (IF=30.9)
Proteogenomic insights into early-onset endometrioid endometrial carcinoma: predictors for fertility-sparing therapy response	<i>Nature Genetics</i> (IF=29.0)
Multimic analysis of cervical squamous cell carcinoma identifies cellular ecosystems with biological and clinical relevance	<i>Nature Genetics</i> (IF=29.0)
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	<i>Cell Research</i> (IF=25.9)
Targeting UBE2T potentiates gemcitabine efficacy in pancreatic cancer by regulating pyrimidine metabolism and replication stress	<i>Gastroenterology</i> (IF=25.1)



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