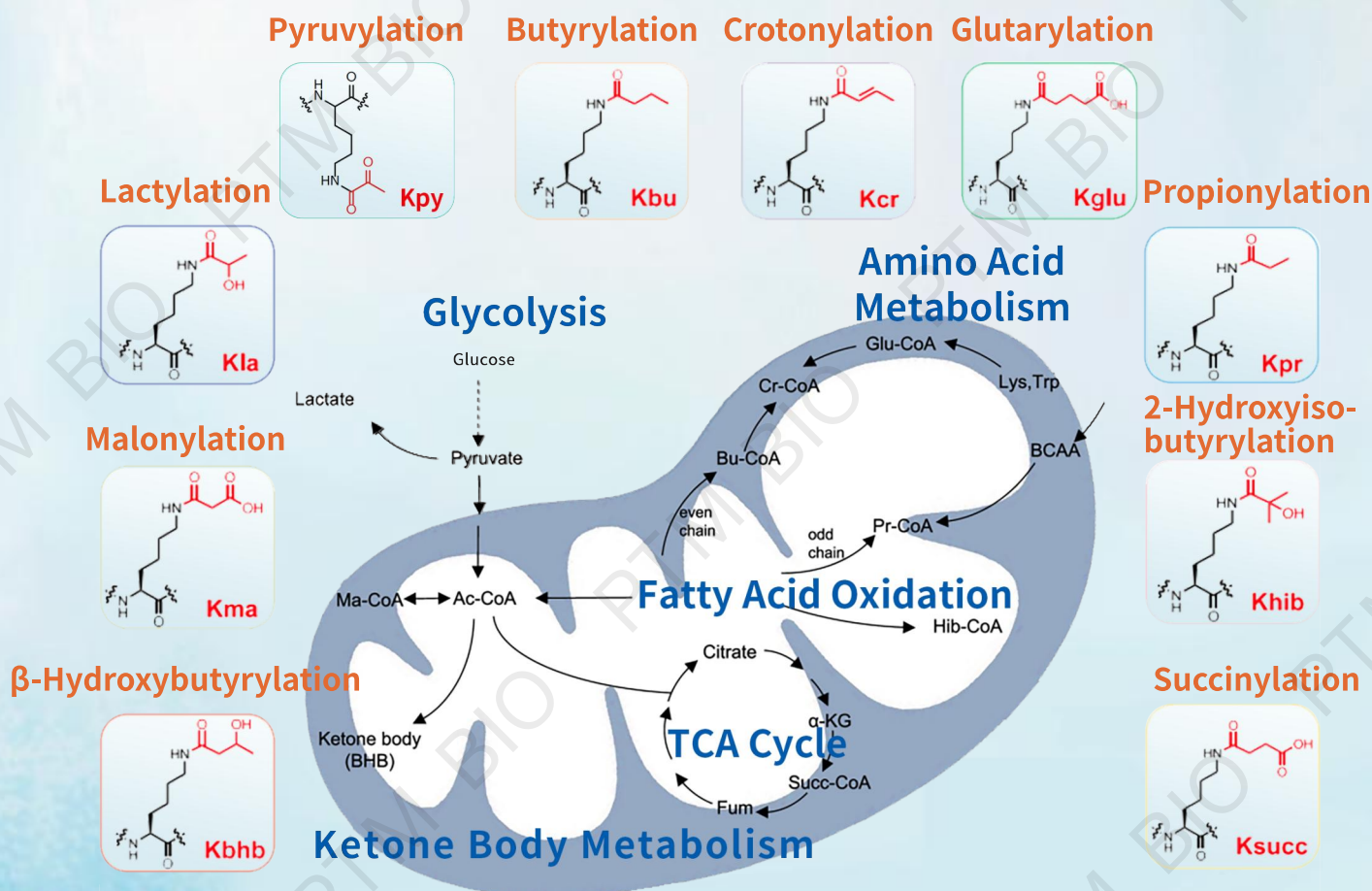


Comprehensive Profiling of Novel Protein Acylations



From Metabolic Reprogramming to Protein Function and Disease Biology

**Decode Metabolic Signals
Reveal Disease Biology
Advance Precision Medicine**

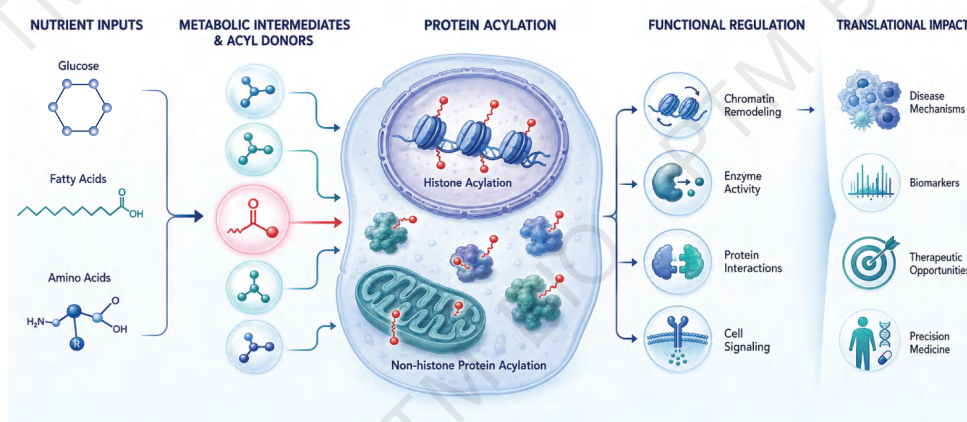
Post-Translational Modification Overview

Protein post-translational modifications (PTMs) are covalent chemical changes that occur after protein synthesis. By altering protein structure, activity, stability, localization, and molecular interactions, PTMs greatly expand proteome diversity and function. PTM BIO provides comprehensive PTM proteomics solutions for identifying and quantifying modification sites across biological conditions, helping researchers elucidate how PTM dynamics regulate biological processes and disease.

Novel Protein Acylations: Where Metabolism Meets Regulation

Metabolic reprogramming reshapes the intracellular pool of metabolites and acyl donors. These metabolic signals can be written onto histones and non-histone proteins as lysine acylations, altering chromatin states, enzyme activity, protein interactions, and cellular signaling.

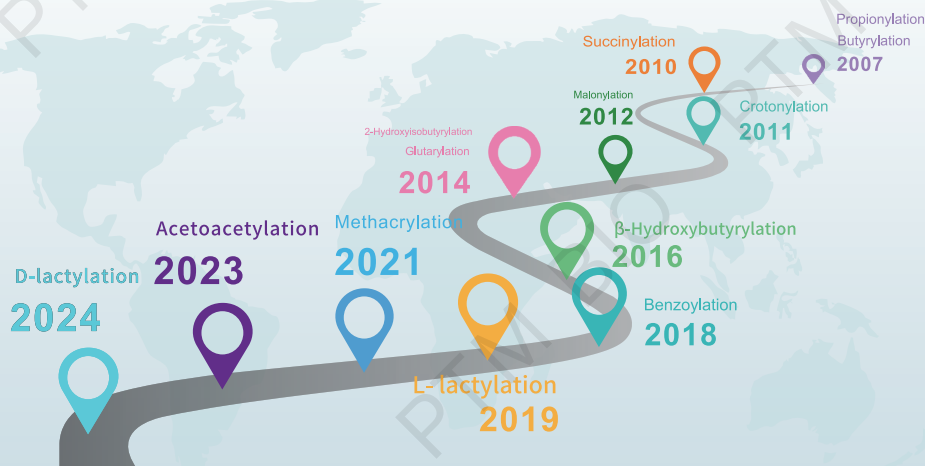
Novel acylation proteomics profiling reveals how metabolic states are translated into functional phenotypes—and uncovers disease mechanisms, biomarkers, and potential therapeutic targets.



The Expanding Landscape of Novel Lysine Acylation

Milestones in Metabolite-Driven PTM Discovery

Over the past two decades, novel lysine acylation has expanded from a small group of histone marks into a diverse family of metabolite-responsive post-translational modifications. These discoveries have revealed direct links among cellular metabolism, chromatin regulation, protein function, and disease biology—opening new opportunities for biomarker discovery and therapeutic research.

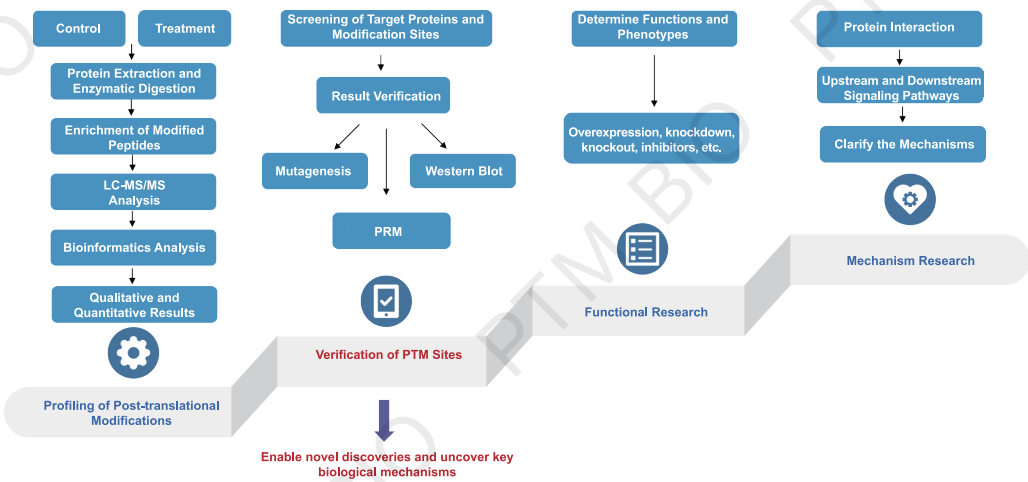


DISCOVER THE MODIFICATION • DECODE THE MECHANISM • ADVANCE THE SCIENCE

PTM Type	Biological Relevance
 Pyruvylation First reported in <i>Cell</i> , 2026	Driven by pyruvate, the end product of glycolysis, pyruvylation responds to changes in the metabolic microenvironment, including hyperglycemia and tumor-associated aerobic glycolysis. Emerging evidence suggests roles in antiviral immunity and potential relevance to tumor immune evasion, metabolic disorders, and severe infections.
 L-lactylation First reported in <i>Nature</i> , 2019	Closely linked to glycolysis and mitochondrial oxidative metabolism, L-lactylation helps translate metabolic state into protein and chromatin regulation. It has been implicated in tumor progression, inflammation, metabolic regulation, and cellular adaptation to hypoxia.
 D-lactylation First reported in <i>Nature Chemical Biology</i> , 2024	D-lactylation represents a distinct link between the glyoxalase pathway, immunometabolism, and protein regulation. Its potential roles are being explored in intestinal diseases, cancer, cardiovascular disease, and neurological disorders.
 Succinylation First reported in 2010	Widely involved in metabolic regulation. Many enzymes in central metabolism are succinylated, and this modification is closely associated with cancer, cardiovascular disease, and inflammation.
 Crotonylation Recognized as a major highlight in epigenetics by <i>Cell</i> , 2011	Regulates gene expression, stem cell differentiation, reproductive development, tumor metabolism, DNA damage repair, and other biological processes.
 β-Hydroxybutyrylation First reported in 2016	Closely linked to core cellular metabolism, including fatty acid oxidation. Involved in energy metabolism, DNA damage repair, and tumorigenesis.
 2-Hydroxyisobutyrylation First reported in 2014	Associated with amino acid biosynthesis and glycolysis. Involved in gene expression regulation, germ cell differentiation, and pathogenicity of plant-pathogenic fungi.
 Phosphorylation A classic and widely studied PTM	Regulates enzymatic activity and ligand–receptor interactions, playing important roles in signal transduction, development, differentiation, cancer progression, and stress responses.
 Acetylation A classic PTM with a long research history	Affects chromatin structure and gene expression, and participates in epigenetic regulation, signal transduction, metabolic regulation, immune response, tumorigenesis, and apoptosis.
 Methylation A classic PTM with a long research history	Regulates cancer, aging, neurodegenerative diseases, and other processes through epigenetic mechanisms, including gene expression control, protein function regulation, and RNA processing.
Malonylation First reported in 2012	Involved in cellular energy metabolism, metabolic disorders, immune regulation, and plant stress responses.
Benzoylation First reported in 2018	Participates in the regulation of signaling pathways, hormone secretion, epigenetic regulation, and metabolic control.
Glutarylation First reported in 2014	Regulates chromatin-related functions, including nucleosome assembly, gene expression, DNA damage repair, and cell cycle progression.
 Methacrylation First reported in 2021	An isomeric modification of crotonylation, with potential regulatory roles in epigenetics and cellular detoxification. It may also be associated with neurological and liver diseases.

Solutions for Novel Acylation Research

PTM BIO provides integrated solutions for novel acylation research, combining highly specific PTM antibodies, high-throughput PTM proteomics, and advanced bioinformatics.



Molecular Cancer

Deciphering a profiling based on multiple post-translational modifications functionally associated regulatory patterns and therapeutic opportunities in human hepatocellular carcinoma

PTM BIO Solutions Used:

Proteomics, Succinylation Proteomics, Lactylation Proteomics, β -Hydroxybutyrylation Proteomics, Crotonylation Proteomics, Phosphorylation Proteomics, Acetylation Proteomics, Ubiquitination Proteomics, Malonylation Proteomics, N-glycosylation Proteomics.

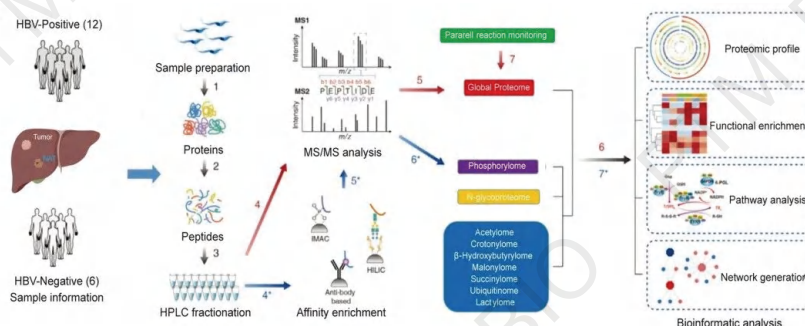
Research Overview

1. Proteomic and nine-PTM profiling of tumors and matched adjacent tissues from 18 HCC patients identified 7,637 proteins and 104,229 modification sites.

2. CYB5R3 K42 malonylation emerged as a feature of HBV-associated HCC, while phosphorylation and crotonylation were enriched in major oncogenic pathways.

3. Phosphorylation preferentially occurred in intrinsically disordered regions, whereas acylation sites were enriched in folded protein regions.

4. Coordinated phosphorylation and acylation of NCL regulated alternative RNA splicing, revealing a potential PTM-driven mechanism and therapeutic opportunity in HCC.



Signal Transduction and Targeted Therapy

Conversion of Ku80 K568 crotonylation to SUMOylation facilitates DNA non-homologous end joining and cancer radioresistance

PTM BIO Solutions Used:

Crotonylation Proteomics, Crotonylation and Acetylation Antibodies, Custom Antibodies.

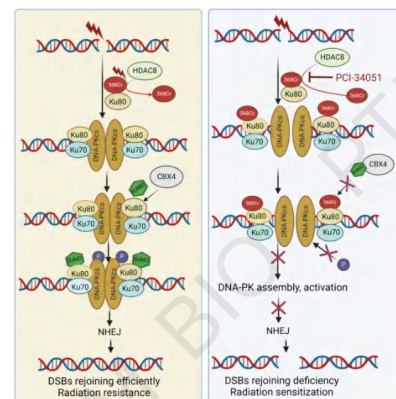
Research Overview

1. Quantitative crotonylation proteomics profiling identified 20,910 crotonylation sites across 3,844 proteins and revealed a rapid loss of Ku80 K568 crotonylation following irradiation.

2. PCAF and HDAC8 were identified as the crotonyltransferase and decrotonylase, respectively, that dynamically regulate Ku80 K568 crotonylation.

3. HDAC8-mediated decrotonylation enables CBX4-dependent SUMOylation at the same site, promoting DNA-PKcs activation and NHEJ-mediated DNA repair.

4. Disrupting this PTM switch impaired DNA double-strand break repair and sensitized tumor cells to radiotherapy and chemotherapy, highlighting a potential strategy for overcoming treatment resistance.



Nature Metabolism

Ketogenic diet reshapes cancer metabolism through lysine β -hydroxybutyrylation

PTM BIO Solutions Used:

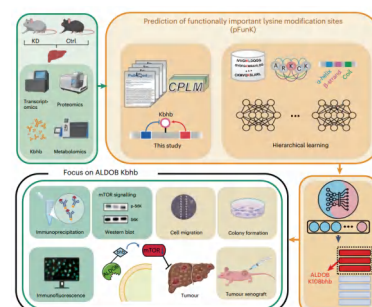
β -Hydroxybutyrylation Proteomics, Pan Antibodies, Custom Antibodies.

Research Overview

1. Multi-omics profiling of ketogenic diet-fed mouse livers identified 5,304 lysine β -hydroxybutyrylation (Kbhb) sites, including 3,946 previously unreported sites.

2. Kbhb remodeling was linked to glycolysis, the TCA cycle, fatty acid oxidation, and other metabolic pathways.

3. Ketogenic diet or β -OHB induced ALDOB K108bhb, suppressing ALDOB activity, glycolysis, mTOR signaling, and cancer cell proliferation.



Selected PTM BIO Collaborative Publications in Novel Protein Acylation

Title	Journal	PTM Type
Pyruvate is a natural suppressor of interferon signaling by inducing STAT1 protein pyruvylation	<i>Cell</i>	Pyruvylation
Long-term histone lactylation connects metabolic and epigenetic rewiring in innate immune memory	<i>Cell</i>	Lactylation
AARS1 and AARS2 sense L-lactate to regulate cGAS as global lysine lactyltransferases	<i>Nature</i>	Lactylation
Metabolic regulation of homologous recombination repair by MRE11 lactylation	<i>Cell</i>	Lactylation
Lysine catabolism reprograms tumour immunity through histone crotonylation	<i>Nature</i>	Crotonylation
Linking chromatin acylation mark-defined proteome and genome in living cells	<i>Cell</i>	Crotonylation
Erythroid mitochondrial retention triggers myeloid-dependent type I interferon in human SLE	<i>Cell</i>	Lactylation
The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination	<i>Cell</i>	Crotonylation
Metabolic regulation of gene expression by histone lactylation	<i>Nature</i>	Lactylation
Single-cell chromatin modification profiling reveals increased epigenetic variations with aging	<i>Cell</i>	Crotonylation
Kat2a coupled with the α -KGDH complex acts as a histone H3 succinyltransferase	<i>Nature</i>	Succinylation
Succinate is an inflammatory signal that induces IL-1 β through HIF-1 α	<i>Nature</i>	Succinylation
Identification of 67 histone marks and histone lysine crotonylation as a new type of histone modification	<i>Cell</i>	Crotonylation

The PTM BIO Advantage

01 Comprehensive PTM Profiling



Coverage of 28 PTM types, enabled by a large portfolio of validated PTM-specific antibodies.

02 High-Performance Proteomics



High-resolution, high-sensitivity mass spectrometry enables deep, accurate, and highly reproducible quantification.

03 Integrated Scientific Expertise



A unified workflow combining proteomics, PTM proteomics, and advanced bioinformatics, supported by experienced scientific teams.

04 Pioneering Innovation



Proprietary multi-omics technologies continuously push the boundaries of proteome depth and PTM site identification.

4,600+ Publications Supported | 100,000+ Samples Analyzed

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