

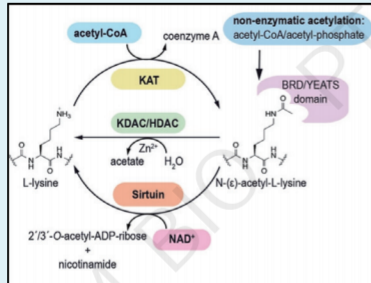


Decoding the Acetylome

*Comprehensive Acetylation Proteomics for Systems-Level
Biological Discovery*

Protein Acetylation: A Key Interface Between Metabolism and Signaling

Lysine acetylation is a dynamic, reversible modification found on histone and non-histone proteins. It is one of the best-characterized lysine acylations.

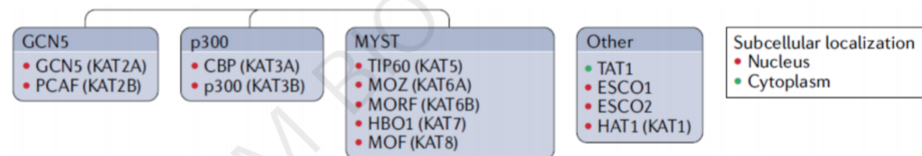


Protein acetylation is one of the most prevalent forms of protein acylation. In lysine acetylation, an acetyl group is added to the ϵ -amino group of lysine residues. Enzymatic lysine acetylation is catalyzed by lysine **acetyltransferases** (KATs; historically termed histone acetyltransferases, HATs), which use acetyl-CoA as the acetyl donor. Nonenzymatic acetylation can also occur under specific metabolic conditions. As a dynamic and reversible post-translational modification, lysine acetylation contributes to gene transcription, DNA damage repair, cell division, signal transduction, and other physiological and disease-associated processes.

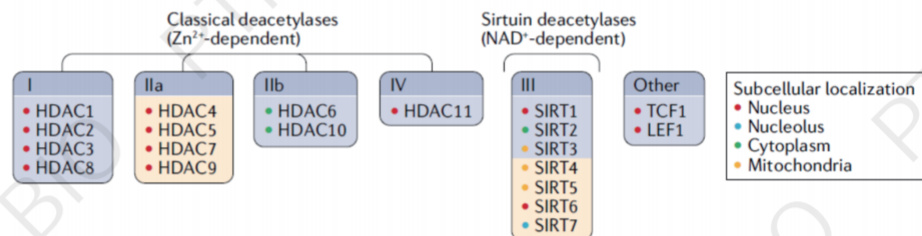
Writers, Readers, and Erasers: The Regulatory Machinery of Protein Acetylation

Post-translational modifications can be viewed as a molecular language governed by three fundamental processes: writing, reading, and erasing. Accordingly, proteins that install, recognize, and remove PTMs are referred to as **Writers**, **Readers**, and **Erasers**, respectively. Together, these regulatory proteins dynamically control protein acetylation and its downstream biological functions.

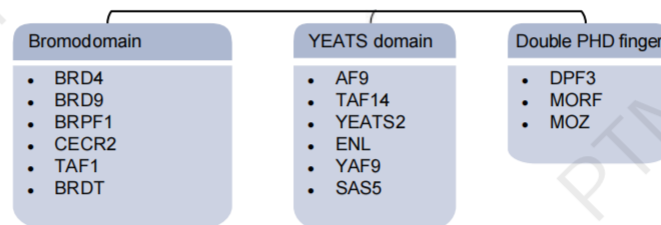
Writer Acetyltransferases



Eraser Deacetylases



Reader Acetylation Readers



PTM BIO Acetylation Proteomics Workflow



PTM BIO Acetylome Solutions

From sample to site, and from discovery to validation—supporting a complete research workflow.

Our Advantages

In-House Antibody Platform

A portfolio of pan-acetyllysine and site-specific antibodies for enrichment and orthogonal validation.

Integrated Proteome Analysis

Joint analysis of protein abundance and acetylation levels helps distinguish acetylation changes from changes in total protein abundance.

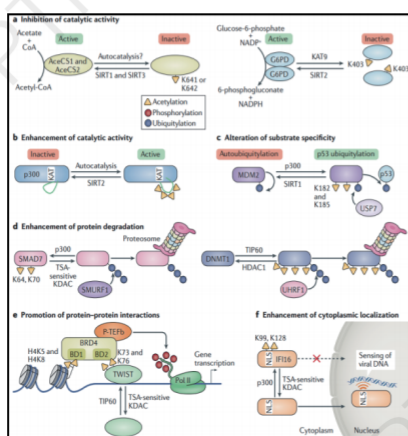
High-Sensitivity LC–MS/MS Analysis

Supports deep acetylated-peptide identification and quantitative acetylome profiling in complex samples.

Mechanistic Follow-Up and Validation

From candidate sites and regulatory enzymes to Western blotting, immunoprecipitation, and site-specific antibody validation.

Applications



- Protein Structure and Activity
- Protein–Protein Interactions
- Subcellular Localization
- Signal Transduction
- Transcriptional Regulation
- Protein Homeostasis

Landmark Research Highlights

1. Clinical Cohort Study

Cell

A proteogenomic portrait of lung squamous cell carcinoma

Samples: 108 tumor tissues and 99 adjacent non-tumor tissues

Technologies: Genomics, proteomics, ubiquitinomics, acetylomics, and phosphoproteomics

Key Findings: Identified candidate therapeutic vulnerabilities and proteomic features associated with clinical outcomes in lung squamous cell carcinoma.

2. PTM Landscape Profiling

Cell

Single-Cell Chromatin Modification Profiling Reveals Increased Epigenetic Variations with Aging

Samples: Primary human immune cells (PBMCs) from younger and older adults, including a twin cohort.

Technologies: Acetylomics, phosphoproteomics, ubiquitinomics, methylation proteomics, and crotonylation proteomics

Key Findings: Revealed dynamic chromatin modification changes across multiple immune cell types from individuals of different ages and established chromatin modification maps of immune cells across aging.

3. Multi-PTM Crosstalk

Molecular Cell

Dynamic Regulation of ME1 Phosphorylation and Acetylation Affects Lipid Metabolism and Colorectal Tumorigenesis

Samples: 31 paired colorectal cancer tissues

Key Findings: The balance between PGAM5-mediated phosphorylation of ME1 at S336 and ACAT1-mediated acetylation at K337 strongly influences NADPH production, lipid biosynthesis, and susceptibility to colorectal tumorigenesis.

4. Identification of Acylation Erasers

50 iScience

Open access

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SIRT1/SIRT3 are robust lysine deacetylases and SIRT1-mediated deacetylation regulates glycolysis

Samples: HepG2 cells

Technologies: Acetylomics and lactylation proteomics

Key Findings: Demonstrated that SIRT1 and SIRT3 function as erasers of lysine lactylation (Kla) on both histone and non-histone proteins, with distinct regulatory patterns and substrate specificities.

+ 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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