

Accurate Quantitative Acetylproteomics Service by MtoZ Biolabs

Boston, Massachusetts Jan 5, 2025 ([IssueWire.com](https://www.issuewire.com)) - The [quantitative acetylproteomics service](#) provides precise, high-resolution analysis of protein acetylation modifications. Utilizing advanced mass spectrometry technologies, including high-resolution instruments such as the Q Exactive HF and Orbitrap, quantitative acetylproteomics service enables detailed characterization of acetylation patterns and their role in regulating protein function and dynamic biological processes. It is an essential tool for exploring the molecular mechanisms underlying cellular regulation and various physiological conditions.

Protein acetylation, first explored by Matthias Mann's laboratory in 2006, has since become a critical area of study due to its significant role in regulating cellular processes such as gene expression, metabolism, and disease progression. With advancements in mass spectrometry and labeling techniques, acetylproteomics has evolved into a powerful approach for investigating these modifications in greater depth. In line with these developments, **MtoZ Biolabs** offers comprehensive [quantitative acetylproteomics service](#) to support detailed analysis of acetylation dynamics in a variety of biological contexts.

Workflow of Quantitative Acetylproteomics Service

MtoZ Biolabs' professional platform ensures that each step, from sample preparation to data analysis, is executed with high quality. Below is the detailed workflow for our quantitative acetylproteomics service:

1. Sample Preparation and Protein Extraction

Initially, proteins are extracted from the provided biological samples using optimized extraction protocols. This process ensures high-quality protein yields from various types of biological samples, such as cells, tissues, and blood.

2. Protein Digestion and Peptide Labeling

MtoZ Biolabs performs protein digestion using multiple enzymes to ensure comprehensive fragmentation of the proteins and capture of acetylated peptides. Following digestion, peptide labeling is carried out using iTRAQ, TMT, or SILAC techniques to enhance the relative quantification accuracy across different samples.

3. Acetyl Peptide Enrichment

Since acetylated proteins typically exist in low abundance, **MtoZ Biolabs'** [quantitative acetylproteomics service](#) employs acetylation-specific antibodies for efficient enrichment of acetylated peptides. This step minimizes the interference from non-acetylated peptides, significantly enhancing the capture of acetylated peptides.

4. Liquid Chromatography-Mass Spectrometry (LC-MS/MS) Analysis

Enriched acetylated peptides are separated using a Nano-LC system before being analyzed by high-resolution mass spectrometry. These advanced mass spectrometers enable in-depth scanning of

acetylation modifications and provide highly accurate quantitative data for acetylation levels.

5. Data Quantification and Analysis

The mass spectrometry data is processed through **MtoZ Biolabs'** dedicated data analysis platform. Using specialized algorithms and comprehensive database searches, acetylated protein expression profiles and modification sites are accurately identified and quantified. The results reveal the differences in acetylation levels across samples and offer insights into the potential functional impacts of acetylation modifications on proteins.

Why Choose MtoZ Biolabs?

The CEO of MtoZ Biolabs said, "By integrating high-resolution mass spectrometry with advanced labeling techniques such as iTRAQ, TMT, and SILAC, we are able to perform precise and comprehensive investigations of acetylation modifications, which are crucial for elucidating cellular regulation and disease progression. Our quantitative acetylproteomics service is committed to providing researchers with efficient and accurate research tools." The core advantages of this service include:

1. High-Throughput Processing

We are capable of processing multiple samples concurrently, leveraging iTRAQ/TMT or SILAC labeling technologies to enhance the accuracy of inter-sample quantitative comparisons, thereby significantly increasing experimental efficiency.

2. Sensitive Protein Detection

By employing acetylation-specific antibodies to enrich acetylated peptides, coupled with a variety of enzyme digestion strategies, our quantitative acetylproteomics service enhances the sensitivity for detecting low-abundance acetylated proteins, surpassing the limitations of conventional methods.

3. Accurate Peptide Quantification

Utilizing a high-resolution Nano-LC-MS/MS system, **MtoZ Biolabs** provides highly accurate quantitative analysis of acetylated peptides, ensuring both high sensitivity and precision, and addressing the analytical challenges posed by complex sample matrices.

4. Comprehensive Data Analysis

MtoZ Biolabs offers expert data processing and bioinformatics analysis services, enabling researchers to gain deep insights into the dynamic changes of acetylation modifications, and providing precise data for advancing biological research and exploring disease mechanisms.

5. One-Time-Charge

Our pricing is transparent, no hidden fees or additional costs.

Applications

1. Gene Expression Regulation Research

Acetylation, as a critical regulatory mechanism of gene expression, modulates chromatin structure and transcriptional activity through the modification of histones and other nuclear proteins. [Mass spectrometry-based acetylproteomics solutions](#) enable researchers to elucidate the dynamic changes in gene expression under varying biological conditions, offering robust datasets and insights to advance epigenetic research.

2. Metabolic Research

Acetylation plays a fundamental role in the regulation of metabolic enzymes and pathways within cellular metabolism. **MtoZ Biolabs** provides large-scale quantitative analysis of acetylation levels in metabolism-associated proteins, uncovering molecular mechanisms underlying metabolic regulation.

3. Disease Mechanism Analysis

Dysregulated acetylation is frequently implicated in the pathogenesis and progression of numerous diseases, including cancer, neurodegenerative disorders, and inflammatory conditions. Quantitative acetyl-proteomics enables systematic exploration of aberrant acetylation patterns and their functional implications in disease, facilitating the identification of diagnostic biomarkers and therapeutic targets.

4. Drug Development and Target Validation

Acetylation is instrumental in modulating the functionality of drug targets. Using advanced high-throughput techniques, quantitative acetylproteomics service offered by MtoZ Biolabs support drug discovery efforts by identifying potential targets, assessing the effects of compounds on acetylation, and validating underlying mechanisms.

What Could Be Included in the Report?

1. Comprehensive Experimental Details

2. Materials, Instruments, and Methods

3. Total Ion Chromatogram & Quality Control Assessment (project-dependent)

4. Data Analysis, Preprocessing, and Estimation (project-dependent)

5. Bioinformatics Analysis

6. Raw Data Files

MtoZ Biolabs, an **integrated chromatography and mass spectrometry (MS) services provider**, provides advanced proteomics, metabolomics, and biopharmaceutical analysis services to researchers in biochemistry, biotechnology, and biopharmaceutical fields. Our ultimate aim is to provide more rapid, high-throughput, and cost-effective analysis, with exceptional data quality and minimal sample consumption.

We offer specialized [quantitative acetylproteomics service](#) designed to resolve challenges in your research projects, enhance the efficiency of your scientific investigations, and ensure a superior standard of technical support.

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