# APPLICATION OF MASS SPECTROMETRY IN CLINICAL BIOCHEMISTRY: IDENTIFICATION OF NOVEL METABOLIC PATHWAYS

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**Abstract:** *This study examines the role of mass spectrometry (MS) technology in clinical biochemistry, with particular emphasis on its application in the identification of novel metabolic pathways. In contemporary biomedical research, metabolomic analyses enable the acquisition of comprehensive information regarding the physiological and pathological states of the organism. MS-based analytical approaches allow detailed profiling of metabolites, through which previously uncharacterized biochemical pathways can be elucidated. The findings of this study demonstrate that mass spectrometry represents a powerful tool not only for clinical diagnostics but also for the discovery of novel biomarkers and for advancing the understanding of the molecular mechanisms underlying various diseases.*

**Keywords**: *mass spectrometry, clinical biochemistry, metabolomics, biomarker, metabolic pathway, medical diagnostics.*

## INTRODUCTION

In clinical biochemistry, advanced analytical technologies—particularly mass spectrometry (MS)—are widely employed to investigate the molecular basis of various diseases. Mass spectrometry is an analytical technique based on the measurement of the mass-to-charge (m/z) ratio of ions, enabling highly sensitive and specific detection of metabolites, proteins, lipids, and other biomolecules. In recent years, MS has become a cornerstone of metabolomics research, facilitating the identification of novel metabolic pathways, the early detection of metabolic disorders, and the advancement of personalized medicine. Its ability to generate comprehensive metabolic profiles has significantly enhanced our understanding of disease-related biochemical alterations at the molecular level.

**Research Methodology.** This study employed gas chromatography–mass spectrometry (GC–MS) and liquid chromatography–mass spectrometry (LC–

MS) techniques for metabolomic analysis. Metabolites derived from clinical samples, specifically blood plasma and urine, were analyzed.

Sample preparation: Biological fluids were deproteinized and subjected to methanol-based extraction to isolate low-molecular-weight metabolites.

Instrumental analysis: Metabolites were analyzed using an LC–MS system, allowing precise determination of their mass-to-charge (m/z) ratios.

Data processing: Mass spectrometric data were processed using the MetaboAnalyst software platform, and metabolite identification was performed with reference to the Human Metabolome Database (HMDB).

Statistical analysis: Principal component analysis (PCA) was applied to identify metabolic differences between healthy and pathological groups, enabling the mapping and interpretation of previously uncharacterized metabolic pathways.

**Results and Discussion.** Mass spectrometric analyses revealed several previously uncharacterized metabolic pathways associated with specific disease states. In particular, novel intermediate metabolites related to amino acid metabolism, lipid oxidation, and energy metabolism were identified. The concentrations of these metabolites exhibited significant alterations across different pathological conditions, indicating their potential relevance to disease-specific metabolic dysregulation.

Furthermore, when mass spectrometry–derived metabolomic data were integrated with genomic and proteomic datasets using an integrative metabolomics approach, a more comprehensive map of biochemical processes in the human organism was constructed. Such multidimensional integration enhances diagnostic accuracy in clinical analysis, supports the development of individualized therapeutic strategies, and improves the early detection of disease.

**Conclusion.** Mass spectrometry is emerging as a pivotal tool in clinical biochemistry, not only for the detection and quantification of known metabolites but also for the discovery of novel metabolic pathways, the elucidation of disease-related molecular mechanisms, and the identification of new biomarkers. Integrated MS-based metabolomic analyses provide a robust foundation for personalized diagnostic and therapeutic approaches in modern medicine. Future advancements in mass spectrometry, particularly increased automation and enhanced analytical resolution, are expected to further expand its application and impact in routine clinical practice.

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