

Available Focus Technologies

Glycomics and Glycoproteomics

Lipidomics

Protein Structure

Targeted Proteomics

Proteogenomics

Chemical Proteomics

Quantitative Clinical Proteomics

Large Scale Quantitative Proteomics

Learn More About our Focus Technologies

The aim of BioMS is to facilitate MS-based research of national importance, to address biological mass spectrometric applications in life science. In this brochure you can get an overview of the usage areas for our focus technologies.

Examples of application areas for our technologies:

- Biomarker discovery
- Disease mechanism studies
- Environmental studies
- Clinical analysis
- Bacteriology
- Plant breeding
- Cancer research
- Neurology

BioMS – the Swedish National Infrastructure for Biological Mass Spectrometry – is a nationally distributed infrastructure for biological mass spectrometry and proteomics, enabling the cutting-edge mass spectrometry and related advanced technology platforms to be part of research projects across Sweden. Each node offers specialized analytical techniques and experimental knowledge to meet the Swedish life science community demands. Biological mass spectrometry is an indispensable tool for molecular researchers in biology, medicine and beyond.

BioMS is a cooperation between Lund University, Chalmers University of Technology, University of Gothenburg and Karolinska Institutet, funded by the Swedish Research Council and the participating universities.



LUND
UNIVERSITY



UNIVERSITY OF
GOTHENBURG



Karolinska
Institutet



CHALMERS



Swedish
Research
Council



Photo: Tobias Ohlsson / KI

Adding Cutting-Edge Mass Spectrometry to Your Research Project

BioMS
Swedish National
Infrastructure for Biological
Mass Spectrometry



Glycomics and Glycoproteomics

Glycosylation is among the most complex and diverse modification of proteins and lipids found in all forms of biological life, and advanced mass spectrometry is central in the analysis of these structures. Analogous to proteomics, glycoproteomics is based on advanced mass spectrometry technologies that has evolved as the method of choice for global or directed analysis of glycoproteins and proteoglycans in biological tissue.



Chemical Proteomics

Chemical proteomics includes a powerful set of complementary, mass spectrometry (MS)-based approaches for identifying the key proteins relevant for producing the phenotypic effects of a treatment with a molecule of a potential new drug, including discovery of protein direct and indirect targets as well as mechanism of action in a proteome-wide manner.



Lipidomics

Lipidomics is categorized as a subgroup of metabolomics, and has been defined as "the system-level analysis and characterization of lipids and their interacting moieties". For accurate and comprehensive lipid characterization using mass spectrometry several approaches might be taken.



Protein Structure Analysis

Structural and dynamic analysis of proteins is an emerging field of biological mass spectrometry and complements information which can be obtained by NMR, cryo-EM and other technologies. With the development of Biological MS instruments, software and methods it is now possible to obtain detailed information about disordered protein regions, folding, protein-protein interactions, and protein small molecule interactions.



Proteogenomics

A new exciting field in biological mass spectrometry is currently emerging that combines proteomics information with sample specific genomic and transcriptomics information. It is called proteogenomics and is used to discover novel protein coding regions/genes and provide protein level-evidence confirming a protein coding potential of a gene, thereby improving genome annotation.



Learn more about our technologies, get in contact with us, and make a project application at [Bioms.se](https://bioms.se)

Large Scale Quantitative Proteomics

Global quantitative proteomics is a powerful strategy to analyse and understand protein changes in biopsies, cells, body fluid or other biological material. It can provide critical insights in the global protein expression underlying the molecular mechanisms of biological processes and dynamics.



Targeted Proteomics

Targeted Proteomics is a very powerful technique for simultaneous determination of protein abundance for a selected set of proteins. The technique is based on proteolytic degradation of proteins and high performance liquid chromatography coupled to an MS instrument. Tandem MS experiments are automatically scheduled for a selection of predefined peptides, enabling accurate quantification of the protein concentration in the sample.



Quantitative Clinical Peptidomics

Quantitative targeted proteomics is a highly sensitive and selective method which can be used for quantitation of selected proteins/peptides in complex biological samples such as cerebrospinal fluid. By adding an isotopic labelled version (e.g., ^{13}C and/or ^{15}N) of the peptide of interest prior to any sample preparation, absolute quantification can be obtained.

