

## Details

### Core Facility Mass Spectrometric Proteomics (CF-MSP-UKE)

The Core Facility Mass Spectrometric Proteomics is a scientific group who is using established cutting edge glycome, protein and proteome analysis strategies and is also developing and establishing novel strategies for the analysis of proteins and proteomes. These methods are made available for research institutes in the greater Hamburg and Schleswig-Holstein area. The Main focus is on the identification of purified proteins and the application of mass spectrometric based strategies for the differential quantitative proteomics to answer scientific questions. This includes consulting for experimental design and sample preparation, the application of mass spectrometric methods for glycan and protein identification and quantification and the interpretation of mass spectrometric data.

**Address:** N27 Campus Forschung, Martinstraße 52  
20246 Hamburg  
Hamburg  
Deutschland  
[To website](#)

### Host Institution

**Universitätsklinik Hamburg-Eppendorf (UKE), Medizinische Fakultät der Universität Hamburg**  
Martinstraße 52  
20246 Hamburg  
Hamburg  
Deutschland  
<https://www.unitag.uni-hamburg.de/fakultaeten/medizin.html>

### Scientific Domain

**Primary Subjects:**

- Biology
- Medicine

**Secondary Subjects:**

- Agriculture, Forestry, Horticulture and Veterinary Medicine
- Chemistry
- Physics

### Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

### Scientific Services

The services offered by the Core Facility of Mass Spectrometric Proteomics includes basic services such as the identification of purified proteins out of a gel matrix or in solution. For scientific cooperations the following methods are offered: - Quantitative differential glycome and proteome analysis in a label-free approach (MS1 based [LFQ], Data Independent Mass Spectrometry [DIA]); - Quantitative differential proteome analysis with labeling (SILAC, TMT); - Chromatographic enrichment / fractionation of biomolecules (pH dependent reversed phase Chromatography, Strong Cation/Anion Exchange Chromatography, Displacement Chromatography); - Mass spectrometry of intact proteins; - Mass spectrometric imaging; - Statistics of MS data; - Interpretation of the results of the MS analysis including gene ontology analysis and text-mining aiming the generation of new hypothesis. Additionally, tailored procedures of experiments, data processing and interpretation routes are being developed and discussed in close collaboration with each collaboration partner.

### Scientific Equipment

- Orbitrap-Tandem Mass Spectrometer (QExactive, Thermo)
- Orbitrap-Tribrid Mass Spectrometer (Fusion, Thermo)

- MALDI Time of Flight Mass Spectrometer (RapiFlex, Bruker)
- Quadrupol Time of Flight Mass Spectrometer (QToF Premier, Waters)
- Triple Quadrupole Mass Spectrometer (Agilent, 6430)
- UPLC (NanoAcquity, Waters)
- UPLC (Acquity, Waters)
- 2 x UPLC (Dionex Ultimate 3000, Thermo)
- HPLC with UV/Vis Detector (1100 Series, Agilent)
- 3 x HPLC Systeme for Protein Purification (GE-Healthcare; 1 x ÄKTA Explorer; 2 x Purifier)
- MALDI Matrix Sprayer (SunCollect, SunChrom)
- 1D & 2D Gelelektrophoresis
- Gel-Free System for Isoelectric Focusing (OFF-Gel, Agilent)

## Keywords

- Proteomics
- Data-dependent Mass Spectrometry (DDA)
- Data-independent Mass Spectrometry (DIA)
- Differential Quantive Proteomics
- SILAC
- TMT
- Top-Down mass spectrometry of proteins
- Chromatographic protein purification
- Liquid Chromatography
- Electro spray ionization (ESI)
- Matrix-assisted Laser Desorption/Ionization (MALDI)
- 1D & 2D Gelelektrophoresis
- Label-Free Quantification
- Proteoform analysis
- Glycomics

## Networks

**Virtual Center for Mass Spectrometry Hamburg / Schleswig Holstein (CMS-HH/SH)**  
<https://www.cms-hhsh.de/>

## Users per annum

**Internal Users:** 100  
**External Users in total:** 20  
**External Users:** 17  
**External Users in the EU:** 2  
**External Users outside of EU:** 1