PROTEOMICS CORE FACILITY
SAHLGRENSKA ACADEMY

Proteomics and glycomics to support clinical research, planetary and systems biology

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Proteomics Core Facility, SciLifeLab and BioMS infrastructures

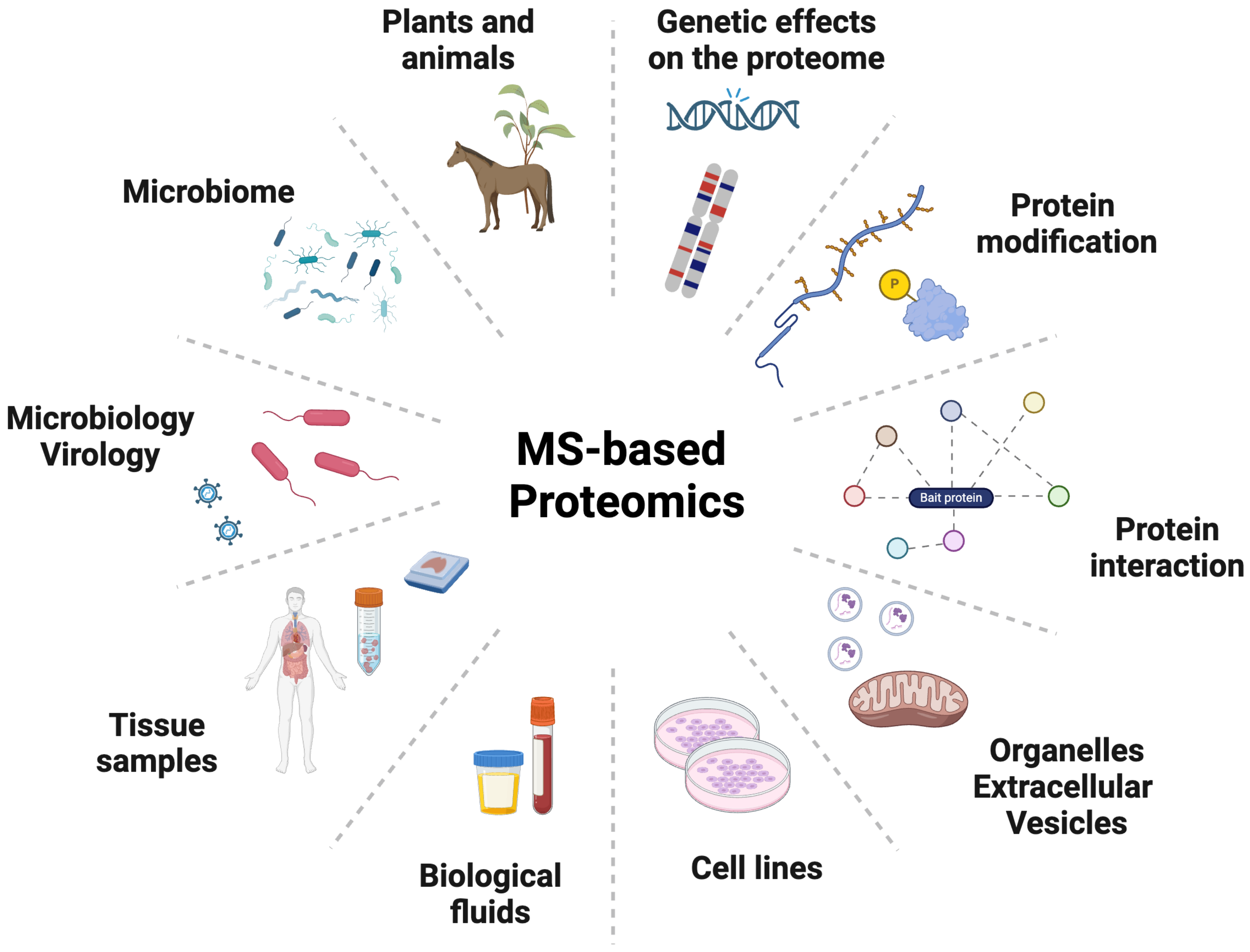
Background

Mass spectrometry (MS)–based proteomics and glycomics enables comprehensive and quantitative analysis of proteins and glycosylation in virtually **any biological material or species** with an available protein sequence database. MS is a versatile technology for global and detailed profiling, pathway analysis, investigation of protein networks, and characterization of post-translational modifications.

Integrated Research Support

We provide end-to-end support for projects:

- Study design and experimental planning
- Customized analytical workflows
- Data processing
- Statistical analysis and bioinformatics



Research fields span **basic research**, **clinical proteomics**, **biomarker discovery**, **microbiology**, **plant biology**, and many other life-science disciplines.

Applications, Technology and Workflow

Research Questions & Applications

Clinical Proteomics and Precision Medicine

- Biomarker discovery or protein panel for diagnosis
- Monitoring stage of disease or response to treatment
- Molecular mechanisms and disease-associated pathways
- Identification of drug targets

Fundamental Biological Research

- Cellular responses to internal and external stimuli
- Networks and interaction analysis (co-interacting proteins)
- Secretome profiling
- Extracellular vesicles
- Post translational modifications or other modifications

Qualitative analysis

- Global protein identification
- Sequence of expressed protein
- Assessment of sample purity (protein, organelles, isolates)
- Characterization of protein e.g. phosphorylation, endogenous cleavage site, drug–protein adduct binding

Glycoproteomics & Glycomics

- Global and targeted analysis of glycoproteins and glycans
- Characterization of released glycans
- Identification of glycoproteins carrying specific glycans
- Determination of glycan structures and attachment sites
- Multiple enrichment strategies and ionization techniques for tailored glycoproteomic and glycomic analysis.

Global Quantitative Proteomics

Tandem Mass Tag (TMT)

- Multiplexed, low technical variability in quantification
- Accurate comparison across 10–50 samples
- Typically, 6,000–9,000 quantified proteins per experiment

Label Free Data Independent Acquisition (LFQ DIA)

- Ideal for large scale clinical studies (50–1,000+ samples)
- High throughput, automated sample preparation
- Analysis using Orbitrap Astral or timsTOF HT
- Protein coverage:
  - 8,000–11,000 proteins in fresh frozen tissue
  - 4,000–6,000 proteins in FFPE samples

Plasma Proteomics

Biognosys P2 Enrichment System

- Global plasma profiling
- Automated sample preparation enable large scale studies
- Quantification of approximately 4,500–7,000 proteins, depending on disease context

Targeted Proteomics – ProteomEdge

- Targeted protein panels enabling absolute quantification using isotopically labelled internal standards.
- Available panels: ApoEdge18, ComplementEdge81, LiverEdge39, ThromboEdge11, DiscoveryEdge176

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https://www.scilifelab.se, Glycoproteomics and MS Proteomics