



Power

Vacuum

Communication

System

Scan

# PROTEOMICS

## PROTEOMICS BEYOND THE STATE-OF-THE-ART

Although genes have gotten much attention since the human genome project revolutionized modern genetics, proteins are the workhorses in biology. Proteins are derived from the information encoded in our genes, and approximately 12,000 different genes are active in a single human cell, producing more than 42,000 different proteins. Proteins give cells structure, convert metabolites and act as signals or transporters. They are the decisive players in life, and protein analysis is pivotal to understanding an organism's processes. Hence, researchers are generally interested in a comprehensive approach to analyzing proteins, their interactions, and modifications.

The Proteomics Facility was initially established in 2002 by Karl Mechtler, one of the leading experts in proteomics research today, and has been committed to providing access to cutting-edge MS technology and services ever since. The facility was one of the first to master protein sequencing from polyacrylamide gels using MS and pioneered the incorporation of NanoHPLC into the MS workflow, one of the most significant technical advances in MS technology.

NanoHPLC greatly improved the sensitivity of the MS-based protein analysis, and in 2019, the facility presented the world record in proteomics - identifying 2,800 proteins from one nanogram of human cell lysate. NanoHPLC also significantly improved the sample throughput of the facility and allowed for 24/7 MS runs without direct supervision by staff.

Since 2013, the proteomics facility has been operated as a joint venture of the VBCF, IMP, IMBA, GMI, and Max Perutz labs in an unprecedented inter-institutional concept. The equipment is maintained and provided for users as an instrument park but operated by two dedicated core facility teams employed by the partners. In this way, the facility supports all research groups at the VBC with a pool of advanced mass spectrometers as well as maintenance and quality control of the diverse LC-MS setups.

2023 saw organizational changes in the Proteomics Facility to secure high-quality services and accelerate our R&D efforts. The VBCF instrument park is now used by our newly formed Proteomics Tech hub - a VBC joint venture led by Karl - and the facility staff offering tailored services to their in-house user base. External users can access their offered services through the VBCF. Thus, the cutting-edge research infrastructure at VBCF and the experience and expertise of scientists provide the solid foundation for breakthrough discoveries at the Vienna BioCenter, one of Central Europe's most outstanding and prominent life sciences hubs.

## SERVICES AND METHODOLOGIES

The facility offers **liquid chromatography-mass spectrometry (LC-MS)** measurements for protein identification, characterization of posttranslational modifications, protein quantification and the respective data interpretation. The following types of analyses (and various combinations thereof) are available in our portfolio:

- Identification of gel-separated proteins
- Analysis of affinity-purified protein complexes (AP-MS)
- System-wide protein identification and label-free or TMT-based relative protein quantification
- System-wide identification and TMT-based relative quantification of post-translational modifications
- Label-free relative quantification of multiple target proteins in complex samples (targeted analysis using parallel reaction monitoring (PRM))
- Crosslinking-MS (XL-MS)
- Intact protein mass spectrometry
- Bioinformatic data analysis and interpretation

## EQUIPMENT

Since 2013, the mass spectrometers and nano-HPLCs have been integrated into the Vienna BioCenter Core Facilities (VBCF) and are operated by the Proteomics facility staff. The following instruments are available:

- Orbitrap Exploris 480 (Thermo Scientific)
- Orbitrap Eclipse (Thermo Scientific)
- TimsTOF HT (Bruker)
- Q-TOF Synapt G2 (Waters)



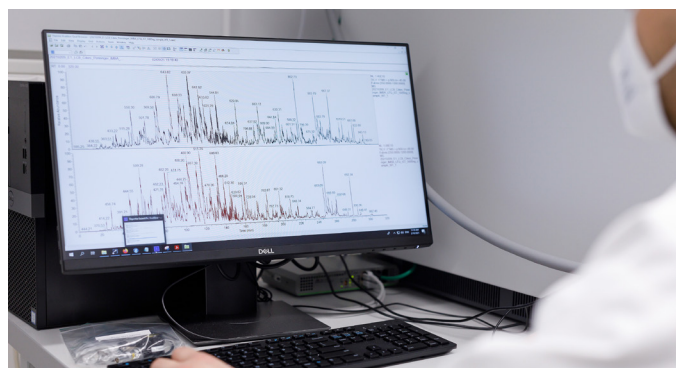
Orbitrap Eclipse coupled online to an Ultimate 3000 nano-HPLC



Peptides are ionized by electrospray ionization



MS instrument room, accommodating 8 mass spectrometers



MS chromatogram of a complex peptide mixture

## CONTACT

Proteomics

Vienna BioCenter Core Facilities [VBCF]

<https://www.viennabiocenter.org/vbcf/proteomics/>  
elisabeth.roitinger@imba.oeaw.ac.at, markus.hartl@maxperutzlabs.ac.at