

Details

Analytics Core Facility Essen (ACE)

The Analytics Core Facility Essen (ACE) is a central facility of the Center of Medical Biotechnology (ZMB) and of the Faculty of Biology of the University Duisburg-Essen. It offers access to state-of-the-art mass spectrometry-based proteomics for internal and external users. The modern technical equipment of the ACE allows us to provide a wide variety of different "bottom-up" and "top-down" proteomics methods. Furthermore, we also develop innovative solutions for project-specific demands. The service comprises all aspects of mass spectrometry-based proteomics, starting from technical advice and project planning, sample preparation and analysis to data analysis, data management and interpretation of results.

Address: Universitätsstrasse 2

45117 Essen Nordrhein-Westfalen Deutschland **To website**

Host Institution

Universität Duisburg-Essen

Universitätsstraße 2 45117 Essen Nordrhein-Westfalen Deutschland

https://www.uni-due.de/

Zentrum für Medizinische Biotechnologie (ZMB)

Universitätsstraße 2 45117 Essen Nordrhein-Westfalen Deutschland

https://www.uni-due.de/zmb/

Scientific Domain

Primary Subjects:

Biology

Secondary Subjects:

- Medicine
- Chemistry

Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

Scientific Services

The Analytics Core Facility Essen (ACE) offers the following services for internal and external users: (1.) Recording of mass spectra in the direct injection mode with the ESI ionization technique and optionally exact mass determination. (2.) UHPLC/HPLC-MS measurements (ESI) (3.) Mass determination of intact proteins or protein complexes (denaturing or native) (4.) Mass spectrometry-based protein identification of affinity purified proteins or complex full proteome samples either in a qualitative or quantitative fashion (either by label-free quantification or by using tandem mass tags (TMT) (5.) Identification and optionally quantification of post-translational modifications (e.g. phosphorylation, ubiquitination, methylation) (6.) Analysis of crosslinked proteins (CrossLinking-MS) (7.) Basic data analysis and delivery of the overview spectra or initial results (8.) For all proteomics projects: scientific data interpretation by ACE staff members.

- Orbitrap Fusion Lumos mass spectrometer
- Exactive PLUS EMR mass spectrometer
- LTQ-XL mass spectrometer
- Triversa nanomate ion source
- Ultimate 3000 HPLC
- Vanquish Neo UHPLC
- Evosep One HPLC
- Kingfisher Apex sample preparation robot
- Typhoon FLA 9000 fluorescent scanner

Keywords

- proteomics
- label-free quantification (LFQ) MS
- AQUA
- cross-linking MS
- reaction control of chemical reactions
- Tandem Mass Tags (TMT)
- Native MS
- AE/AP-MS

Networks

CRC 1430: Molecular Mechanisms of Cell State Transitions https://www.uni-due.de/crc1430/

Users per annum

Internal Users: 70
External Users in total: 10
External Users: 1

External Users in the EU: 8
External Users outside of EU: 1