

Overview

The symposium will focus on top-down proteomics, the analysis of intact proteins and protein complexes using high-resolution mass spectrometry. Top-down proteomics is an emerging technology offering an unprecedented level of accuracy in detecting differentially modified intact proteins (proteoforms) or associated complexes. The term proteoform designates all of the different molecular forms in which the protein product of a single gene can be found, encompassing all forms of genetic variation, alternative splicing of RNA transcripts, and posttranslational modifications (PTMs).

Over the last decade, significant progress has been made to advance top-down proteomics (both in denaturing and native conditions). As a result, interest in top-down proteomics has grown considerably, and several studies have already showcased the potential of this disruptive technique for the unraveling of disease mechanisms and discovery of new biomarkers.

In this program, world-leading experts in top-down proteomics will present the most advanced technologies and approaches.

The symposium will cover a wide range of topics, including:

- New frontiers in proteomics
- Emerging technologies and platforms for proteoform analysis
- Integrating data types for proteoform analysis in complex systems
- Proteoforms as actionable drivers of biological and clinical research
- Functional roles for proteoforms, PTMs and their complexes
- Applications for proteomics in life sciences and human health

- Applications for proteomics in biopharmaceuticals, life sciences and human health
- Applications of top-down proteomics in single-cell analysis

Additionally, we will engage attendees in discussions on the future directions, challenges, and opportunities for top-down proteomics. In addition to notable scientists, the meeting will also attract younger researchers who are building their careers and are looking to interact with leaders in the field.

The symposium will explore the state of the art of the proteome wide analysis of proteoforms. It showcases advances, challenges, and applications in life sciences and health in basic science and industry.

The symposium examines state-of-the-art proteome-wide proteoform analysis, highlighting advances, challenges, and applications in life sciences and health, benefiting both basic science and industry.

Organizers

- Hartmut Schlüter, Prof., Head of the Section Mass Spectrometry and Proteomics, University Medical Center Hamburg-Eppendorf (UKE)
- Andreas Tholey, Prof., Institute for Experimental Medicine; Head of the Section Systematic Proteomics and Bioanalytics, University of Kiel, Germany
- Neil L. Kelleher, Prof., Director, Chemistry of Life Processes Institute and Director, Northwestern Proteomics, Northwestern University, Evanston, IL; USA.
- Charlotte Uetrecht, Prof., Head of the Institute of Chemistry and Metabolomics, University of Lübeck
- Board of directors of the Consortium for Top-Down Proteomics (CTDP) (https://ctdp.org/about-the-consortium/board-of-directors/)

Location

The Conference venue will be the University of Hamburg which conveniently located in the heart of Hamburg close to the station Dammtor. The journey from Hamburg airport to the University of Hamburg and the city center takes approximately 30 minutes.

Delegate and student fees

Fees will cover coffee breaks, the poster session/cocktail party on Tuesday, lunch on Wednesday and registration for the conference.

	Early	Late
Student	200	250
Regular delegate	400	500
Industry	800	1000

Optional: Conference dinner

Sponsorship

We are seeking sponsors in the fields of mass spectrometry, proteomics, informatics, and related technologies and services to help support the conference and build the community.

Several opportunities are available. *Please contact:*

Christian Schulz

(Teamlead congress management, Operations & Services)

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