

# TDP SYMPOSIUM 2025

26–28 August  
University of  
Hamburg

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3<sup>RD</sup> INTERNATIONAL  
TOP-DOWN PROTEOMICS  
SYMPOSIUM





We are delighted to welcome you to this year's symposium at the University of Hamburg. Over the coming days, you will have the opportunity to engage with leading experts, exchange ideas, and explore new perspectives in our field. We wish you an inspiring, productive, and enjoyable time with us in Hamburg.

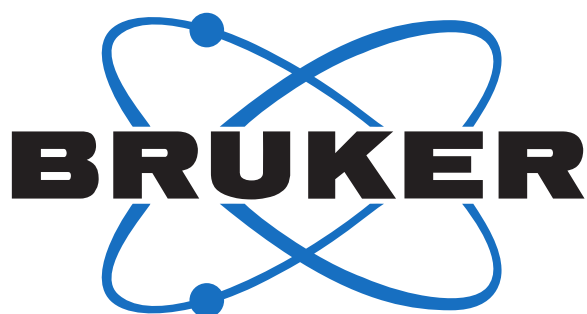


### Acknowledgement of Sponsors

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We extend our heartfelt thanks to our sponsors for their generous support, which has made this event possible. Their commitment helps us bring together outstanding speakers, foster scientific exchange, and create a memorable experience for all participants.

#### Platinum Sponsor



#### Gold Sponsors

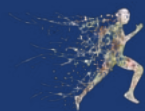


#### Silver Sponsors

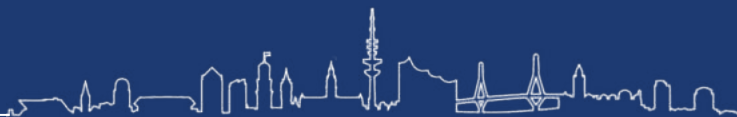


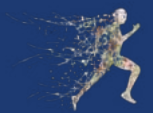
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We are proud to present an exceptional line-up of distinguished experts and thought leaders from around the world. Each of our keynote and featured speakers brings unique insights, groundbreaking research, and inspiring perspectives to this year's symposium.



**Julia Chamot-Rooke**  
Institut Pasteur, France



**Juan Antonio Vizcaino**  
EMBL-EBI, PRIDE, Great Britain



**Ying Ge**  
University of Wisconsin-Madison, USA



**Nobuaki Takemori**  
Ehime University, School of Medicine, Japan



**Michal Sharon**  
Weizmann Institute of Science, Israel



**Manfred Wuhrer**  
Leiden University, Netherlands



**Ljiljana Paša-Tolić**  
Pacific Northwest National Laboratory (PNNL), USA



**Lloyd Smith**  
University of Wisconsin-Madison, USA



**Albert Heck**  
Utrecht University, Netherlands



**Neil Kelleher**  
Northwestern University, USA



**Joseph A. Loo**  
University of California, USA



**Charlotte Uetrecht**  
CSSB Centre for Structural Systems Biology, Germany



**Ole Nørregaard Jensen**  
University of Southern Denmark, Denmark



**Guinevere Lageveen-Kammeijer**  
University of Groningen, Netherlands



**Jeffrey Agar**  
Northeastern University, Bouvé College of Health Sciences, USA



**Dimitris Papanastasiou**  
Fasmatech, Greece



**Paul Danis**  
Consortium for Top-Down Proteomics, USA



**Yury O. Tsybin**  
Spectroswiss, Switzerland



**Kyowon Jeong**  
Universität Tübingen, Germany



**Mowei Zhou**  
Zhejiang University, China







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9:00 AM

## Short Course 1: Top-Down Proteomics

**Session** | **Location:** Lecture Hall F, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

9:00 – 9:30 AM **Proteoforms - Introduction (Hartmut Schlüter)**

9:30 – 10:00 AM

**Analysis of proteoforms in tissues - Sampling and homogenization (Hartmut Schlüter)**

10:00 – 10:30 AM **Sample preparation for top-down proteomics (Andreas Tholey)**

10:30 – 11:00 AM **Coffee Break**

11:00 – 11:30 AM

**Liquid chromatography for proteoform fractionation (Hartmut Schlüter)**

11:30 AM – 12:00 PM **Concepts and implications for TD/MD MS (Yuri Tsybin)**

12:00 – 1:30 PM **Lunch**

1:30 – 2:15 PM

**Data processing - concepts and implications for TD/MD MS (Yuri Tsybin)**

2:15 – 3:00 PM

**Mass spectrometry of intact proteins & Fragmentation of proteoforms (Bente Siebels & Maria Riedner)**

3:00 – 3:30 PM **Coffee Break**

3:30 – 5:00 PM

**Charge Detection for Deep Proteoform Characterization (Neil Kelleher)**

5:00 PM





8:30 AM	<b>Short Course 1: Top-Down Proteomics</b> <b>Session   Location:</b> Lecture Hall F, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg
	8:30 – 9:15 AM <b>Biotherapeutics - Analysis of therapeutic proteins (Yuri Tsybin)</b>
	9:15 – 10:00 AM <b>Bioinformatics - spectral deconvolution (Kyowon Jeong)</b>
	10:00 – 10:30 AM <b>Coffee Break</b>
	10:30 – 11:15 AM <b>Bioinformatics of TD/MD MS: use of FLASHApp (Kyowon Jeong, Tom Müller)</b>
	11:15 AM – 12:00 PM <b>Adapting de novo sequence inference to top-down proteomics (David Tabb)</b>
12:00 PM	
12:00 PM	<b>Check-in</b> <b>Session   Location:</b> Audimax
6:00 PM	
1:00 PM	<b>ECR Meeting (Hybrid)</b> <b>Session   Location:</b> Lecture Hall F, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg
	<b>Description</b> On-site moderators: Mowei Zhou, Kyowon Jeong, Philipp Kaulich, Boris Krichl Program: 1. Trivia games 2. Introduction to the ECR committee 3. Interlaboratory initiatives of the current ECR (Quantitative, high-throughput TDP: Kellye, Data analysis for Native TDP: Corrine, Ion Mobility TDP: Fabio) 4. Online resource for TDP TopDownVerse <a href="https://topdownverse.netlify.app/">https://topdownverse.netlify.app/</a> : Bryon 5. Online presentation series introducing upper-level graduate students: Kellye
2:30 PM	
3:15 PM	<b>Welcome Session</b> <b>Session   Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg
3:30 PM	
3:30 PM	<b>New Frontiers in Life Sciences - Entering the Proteoform Era</b> <b>Session   Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg
	3:30 – 3:55 PM <b>New Frontiers in Proteomics - Proteoforms, Proteoform Families, and the Human Proteoform Project</b> <b>Speaker</b> Lloyd Smith
	3:55 – 4:20 PM <b>Digitizing Proteoform Biology with Single Molecule &amp; Single Cell Mass Spectrometry</b>





5:10 PM

**Speaker**

Neil Kelleher

4:20 – 4:45 PM

**Revealing Functional Proteoforms by Native Top-Down Proteomics****Speaker**

Joseph Loo

4:45 – 5:10 PM

**Touching upon the millions of hidden treasures in the plasma proteome****Speaker**

Albert Heck

5:10 PM

**Round Table Discussion****Session | Location:** Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg**Description**

Why do we need a 'Mars-shot project' for proteoform research?

Moderators: Guinevere Lageveen-Kammeijer, Manfred Wuhrer

Participants:

Rohan Thakur – Bruker

Jake Melby – AstraZeneca

Max Kraner – NovoNordisk

Alexander Makarov – Thermo

Andreas Huhmer – Nautilus

Michal Sharon (Weizmann Institute of Science)

Neil Kelleher (Northwestern University)

6:10 PM

6:15 PM

**Welcome Reception****Session | Location:** Audimax

9:00 PM

6:30 – 6:45 PM

**Nautilus: Flash Talk**





8:30 AM

## New Tools for Proteoform Analysis

**Session** | **Location:** Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

8:30 – 8:50 AM

### Advances in hardware design and function of the new timsOmni MS platform

**Speaker**

Dimitris Papanastasiou

8:50 – 9:10 AM

### Top-down sequencing of intact, modified proteins by timsTOF technology with new multi-modal fragmentation capabilities

**Speaker**

Ole Nørregaard Jensen

9:10 – 9:30 AM

### Sensitive Top-down Analysis using Spray-capillary-based CE-MS approaches

**Speaker**

Si Wu

9:30 – 9:45 AM

### Combining advanced fragmentation techniques and spectral simplification for deep proteoform interrogation

**Speaker**

Luca Fornelli

9:45 – 10:00 AM

### Mass-Invariant Log-Transformed Mass Spectra Enable De Novo Sequencing and Internal Calibration of Intact Proteins

**Speaker**

Lissa C. Anderson

10:00 AM

10:00 AM

## Coffee Break

**Break** | **Location:** Audimax

10:30 AM

10:30 AM

## Lightning Talks

**Session** | **Location:** Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

10:35 – 10:40 AM

### Properties, Origin, and Reproducibility of Truncated Proteoforms Across Top-Down Proteomic Studies

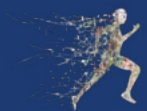
**Speaker**

Philipp T. Kaulich

10:40 – 10:45 AM

### Novel bridged hybrid monolithic columns combined with mass spectrometry for top-down proteomic analysis



**Speaker**

Yu Liang

10:45 – 10:50 AM

**Spatial Phosphoproteomic Profiling of Murine Heart Reveals Region-Specific Functions via TiO<sub>2</sub> Enrichment Optimized for Laser-Capture Microdissected Samples****Speaker**

Dan Zhao

10:50 – 10:55 AM

**FLASHApp: Interactive Data Analysis and Visualization for Top-Down Proteomics****Speaker**

Tom David Müller

10:55 – 11:00 AM

**Metabolomics and proteomics reveal the inhibitory effect of *Lactobacillus crispatus* on cervical cancer****Speaker**

Lingyan Zhong

11:00 – 11:05 AM

**SEC-complex-down approaches with functional O<sub>2</sub>-affinity assay: Correlation between the higher order structure of bird hemoglobin homologues and their function.****Speaker**

Léa Letissier

11:05 – 11:10 AM

**Multi-dimensional High-Throughput Molecular Glue Screening via Gas Phase Affinity Selection Native Mass Spectrometry and Cryo-EM Analysis****Speaker**

Amanda Lee

11:10 – 11:15 AM

**Legionella effector AnkX puts the brakes on IMPDH2 filaments****Speaker**

Marietta Sandkamp-Kaspers

11:15 – 11:20 AM

**Top-Down Mass Spectrometry of a Clinical Antibody Light Chain Using the Omnitrap-Orbitrap-Booster Platform****Speaker**

Marie Yammine

11:20 – 11:25 AM

**X-ray spectroscopy meets native mass spectrometry: probing gas-phase protein complexes****Speaker**

Jocky Chun Kui Kung

11:25 – 11:30 AM

**A prototype TIMS-FT-ICR MS instrument capable of deep characterisation of complex samples and biomolecules**

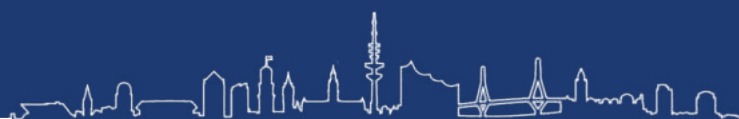


	<p><b>Speaker</b> Christopher Wootton</p>
	<p>11:30 - 11:35 AM</p> <p><b>Pin-pointing phosphorylation-dependent Pin1 binding to a cytoskeletal protein altered in Alzheimer's Disease using structural mass spectrometry</b></p> <p><b>Speaker</b> Nikolas Brooks</p>
	<p>11:35 - 11:40 AM</p> <p><b>Enhancing Drug-Payload Localization in Antibody-Drug Conjugates with a Middle-Down Approach Utilizing Proton Transfer Charge Reduction on an Orbitrap Ascend BioPharma Tribrid Mass Spectrometer</b></p> <p><b>Speaker</b> Rachel Grady</p>
	<p>11:40 - 11:45 AM</p> <p><b>Digital Membrane Chromatography — A New Way to Rapid Antibody Purification for Top-Down MS</b></p> <p><b>Speaker</b> Kilian Müller</p>
12:00 PM	
12:00 PM	<p><b>Lunch Seminar (Agilent Technologies)</b></p> <p><b>Break</b>   <b>Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg</p>
1:00 PM	
1:00 PM	<p><b>Poster Session 1</b></p> <p><b>Poster Session</b>   <b>Location:</b> Audimax</p>
1:45 PM	
1:45 PM	<p><b>Native MS &amp; Protein Complexes</b></p> <p><b>Session</b>   <b>Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg</p>
	<p>1:45 - 2:05 PM</p> <p><b>Uncovering the unique properties of circulating proteasomes: A mass spectrometry perspective</b></p> <p><b>Speaker</b> Michal Sharon</p>
	<p>2:05 - 2:25 PM</p> <p><b>Flying viruses - mass spectrometry meets X-rays</b></p> <p><b>Speaker</b> Charlotte Uetrecht</p>
	<p>2:25 - 2:40 PM</p> <p><b>Filling the Structural Knowledge Gap in Protein Design via Native Mass Spectrometry</b></p> <p><b>Speaker</b> Mowei Zhou</p>
2:40 PM	
2:40 PM	<p><b>Coffee Break</b></p> <p><b>Break</b>   <b>Location:</b> Audimax</p>
3:10 PM	





3:10 PM	<b>Databases &amp; Bioinformatics</b> <b>Session</b>   <b>Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg
	3:10 – 3:30 PM <b>Replacing “OR” Logic and Mass Accuracy with “AND/OR” Logic and Mass Resolving Power, as the Basis for Peak Assignment in Top-Down Mass Spectrometry Data.</b> <b>Speaker</b> Jeffrey Agar
	3:30 – 3:50 PM <b>Advancing Top- and Middle-Down Antibody Analysis Using Simulated FTMS Datasets</b> <b>Speaker</b> Yury Tsybin
	3:50 – 4:05 PM <b>Computational methods in top-down proteomics to address challenges in proteoform analysis</b> <b>Speaker</b> Kyowon Jeong
	4:05 – 4:20 PM <b>TDAuditor assesses deconvolution quality for the Blood Proteoform Atlas</b> <b>Speaker</b> David Tabb
	4:20 – 4:40 PM <b>The Implementation of Open Science Practices Can Enable A Faster Development Of Top-Down Proteomics</b> <b>Speaker</b> Juan Antonio Vizcaino
4:40 PM	
4:40 PM	<b>Break</b> <b>Break</b>
4:50 PM	
4:50 PM	<b>Minimum Information Describing A Proteoform (MIDAP) Proteoform Atlas Compendium System (PACS)</b> <b>Session</b>   <b>Location:</b> Lecture Hall A, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg
6:00 PM	
7:00 PM	<b>Conference Dinner</b> <b>Break</b>   <b>Location:</b> Museum Ship Rickmer Rickmers, Bei den St. Pauli-Landungsbrücken 1a 20459 Hamburg
11:00 PM	







8:30 AM

## Sample Preparation & Separation Technologies

**Session** | **Location:** Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

8:30 – 8:50 AM

### Enabling High-Throughput Proteoform Analysis via Gel-Based Sample Pre-Fractionation with PEPPI-SP3

**Speaker**

Nobuaki Takemori

8:50 – 9:05 AM

### Characterization of proteoforms of intact proteins by CE-MS and LC-CE-MS

**Speaker**

Christian Neusüß

9:05 – 9:20 AM

### Impact of sample preparation methods on proteoform identification by top-down proteomics

**Speaker**

Andreas Tholey

9:20 – 9:35 AM

### Proteoforms in Tissues - Approaching Their Native Composition with Nano- and Pico-Second Infrared Laser Systems

**Speaker**

Hartmut Schlüter

9:35 – 9:50 AM

### Comparison of RP-LC with CE for histone analysis

**Speaker**

Ansgar Poetsch

9:50 AM

9:50 AM

## Coffee Break

**Break** | **Location:** Audimax

10:20 AM

10:20 AM

## New approaches for proteoform analysis

**Session** | **Location:** Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

10:20 – 10:40 AM

### Advances in Orbitrap mass spectrometry for top-down analysis

**Speaker**

Alexander Makarov

10:40 – 11:00 AM

### Exploring Spatial Top-Down Proteomics

**Speaker**

Ljiljana Paša-Tolić

11:00 – 11:15 AM

### Exploring the effects of isotope depletion on proteins by native mass spectrometry and cryogenic electron microscopy







	<p><b>Speaker</b> Anjusha Mathew</p>
	<p>11:15 – 11:30 AM</p> <p><b>Discovering the ‘negative’ side of the proteomic landscape with top-down mass spectrometry</b></p> <p><b>Speaker</b> Cynthia Nagy</p>
	<p>11:30 – 11:45 AM</p> <p><b>Glycoproteomics Based on Deep Learning and Data Independent Acquisition</b></p> <p><b>Speaker</b> Liang Qiao</p>
	<p>11:45 AM – 12:00 PM</p> <p><b>High resolving power meets proton transfer charge reduction: unlocking new depths in intact protein characterization</b></p> <p><b>Speaker</b> Rafael D. Melani</p>
12:00 PM	
12:00 PM	<p><b>Lunch Seminar (Bruker Daltonics)</b></p> <p><b>Break</b>   <b>Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg</p>
1:00 PM	
1:00 PM	<p><b>Poster Session 2</b></p> <p><b>Poster Session</b>   <b>Location:</b> Audimax</p>
1:45 PM	
1:45 PM	<p><b>Biomedical Applications</b></p> <p><b>Session</b>   <b>Location:</b> Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg</p>
	<p>1:45 – 2:05 PM</p> <p><b>Top-Down Proteomics of the Heart: Decoding Cardiac Proteoforms for Precision Medicine</b></p> <p><b>Speaker</b> Ying Ge</p>
	<p>2:05 – 2:25 PM</p> <p><b>Dissecting the Proteoform Landscape of Prostate-Specific Antigen: Intact, Bottom-Up, and Glycomic Perspectives</b></p> <p><b>Speaker</b> Guinevere Lageveen-Kammeijer</p>
	<p>2:25 – 2:40 PM</p> <p><b>Spatial Phosphoproteomic Profiling Reveals Regional Functional Heterogeneity in the Murine Heart</b></p> <p><b>Speaker</b> Ling Lin</p>
	<p>2:40 – 2:55 PM</p> <p><b>Spatially Resolved Proteoform Mapping in Alzheimer’s Disease Brain Tissues</b></p> <p><b>Speaker</b> Yue Sun</p>





2:55 – 3:10 PM

### Top-down Proteomics Deciphers Cardiac Proteoform Landscape in Phospholamban R14del Cardiomyopathy for Precision Medicine

#### Speaker

Holden Rogers

3:10 – 3:25 PM

### MALDI MS-Based Rapid Antimicrobial Susceptibility Prediction

#### Speaker

Jia Yi

3:25 PM

3:25 PM

### Coffee Break

Break | Location: Audimax

3:55 PM

3:55 PM

## Biopharmaceutical & Therapeutic Proteins

Session | Location: Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

3:55 – 4:15 PM

### Deciphering Biotherapeutic Biotransformations with Top-Down Mass Spectrometry

#### Speaker

Julia Chamot-Rooke

4:15 – 4:35 PM

### Functional and structural characterization of antibodies by native-mode affinity separation-, middle-up, and top-down mass spectrometry

#### Speaker

Manfred Wuhrer

4:35 – 4:50 PM

### AiDA Accelerates Top-Down and Middle-Down MS Data Analysis Across Multiple Antibody Variants

#### Speaker

Francois Griaud

4:50 – 5:05 PM

### Enhanced usage of top-down data for de novo sequencing of antibodies

#### Speaker

Kira Vyatkina

5:05 – 5:20 PM

### Mass spectrometric ITEM-FOUR analysis reveals coding single nucleotide polymorphisms in human cardiac troponin T that evade detection by sandwich ELISAs which use monoclonal antibodies M7 and M11.7 from the Elecsys Troponin T® assay

#### Speaker

Michael Glocker

5:20 PM

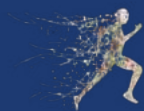
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### Poster Awards and Farewell

Break | Location: Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

5:50 PM





8:45 AM

4:45 PM

9:00 AM

2:00 PM

**Bruker Factory Tour**  
Session

**Short Course 2: Dissecting the impact of deconvolution on top-down identification**  
Session | Location: Lecture Hall F, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

9:00 – 10:30 AM

Assessing the degree of variation among deconvolution engines (David Tabb, Tom Müller, Kyowon Jeong)

10:30 – 11:00 AM

Coffee Break

11:00 AM – 1:00 PM

Detecting deconvolution impact on identifications (David Tabb, Tom Müller, Kyowon Jeong)

1:00 – 2:00 PM

Lunch





## Breaking The Bonds: Agilent ExD cell and ExD Viewer for comprehensive top-down protein characterization



**Join Agilent for our lunch seminar at 3rd Top-Down Proteomics Symposium**

**Wed, Aug 27, 12:00 - 1:00 pm CEST**

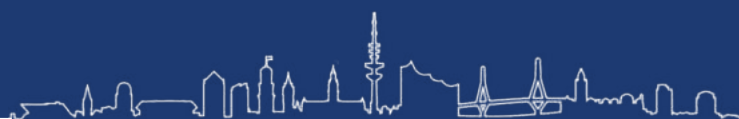
Location: University of Hamburg, Von-Melle-Park 6, Lecture Hall D

The whole is more than the sum of its parts - a truth that top-down analysis consistently reinforces.

In this lunch seminar we will cover key applications of the Agilent ExD cell as well as a live demonstration of the Agilent ExDViewer software for the analysis and visualization of top-down fragmentation spectra. A variety of examples will be presented - from the comprehensive characterization of multiple GLP-1 analogs, differentiation of isobaric Leu/Ile residues in ubiquitin, and phospho-site detection in the Bcl-xL protein, to the characterization of mAb subunits initiated by microdroplet reactions - where the exceptionally high efficiency of the ExD cell was invaluable for generating impactful analytical results.

The seminar will conclude with a live demonstration of ExDViewer, highlighting the importance of isotopic fidelity in highly charged fragments, as well as other capabilities of ExDViewer.

**Register here!**





## Join the Bruker Lunch Seminar at the 3<sup>rd</sup> International Top-Down Proteomics Symposium – Hamburg

**Thu, Aug 28, 12:00 - 1:00 pm CEST**

Location: University of Hamburg, Von-Melle-Park 6, Lecture Hall D

Discover the latest advancements in **Top-Down Proteomics** during our exclusive **Bruker Lunch Seminar** at the University of Hamburg, Von-Melle-Park 5, Lecture Hall A in Hamburg, Germany. This session will feature groundbreaking research and showcase the capabilities of the new **timsOmni™ technology**, delivering a deep leap forward in **proteoform sequencing** and **advanced structural elucidation**, alongside the trusted performance of **Bruker's MRMS platform**.

### Speakers



#### Top-down Antibody analysis using the Bruker timsOmni™ instrument

Albert Heck, Ph.D., Distinguished Faculty Professor of Chemistry and Pharmaceutical Sciences, Utrecht University and Scientific Director, Netherlands Proteomics Center, Utrecht, Netherlands



#### A Hybrid Proteomics Approach Captures the Extent and Dynamics of Phosphorylation of AMP-activated kinase Complex

Boris Krichel, Ph.D., Postdoctoral Fellow, Centre for Structural Systems Biology CSSB, Hamburg, Germany

### Visit the Bruker Daltonics Factory in Bremen

We are excited to invite you to a special behind-the-scenes tour of the Bruker Daltonics headquarters, where innovation in mass spectrometry and proteomics comes to life.

#### What to expect:

- A guided tour of our state-of-the-art mass spectrometer production
- Insights into the development of cutting-edge technologies like timsOmni™ and MRMS
- A relaxed networking lunch with fellow symposium attendees

#### Event Details:

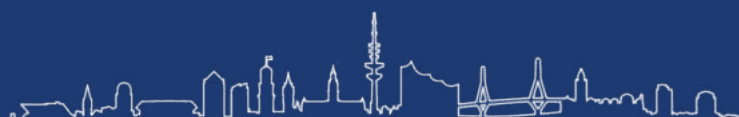
- Date: **Friday, August 29, 2025, 8:45 am CEST**
- Departure: Morning bus transfer from Von-Melle-Park 4, 20146 Hamburg, Germany
- Return: Early afternoon transfer back to Hamburg
- Lunch: Light refreshments and lunch included

Register here!

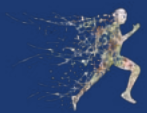


The tour is free of charge! Seats are limited and available on a first-come, first-served basis. Register now to secure your place on this exclusive tour!

Please note that due to potential traffic disruptions, delays in the bus transfer may occur, and fixed arrival times cannot be guaranteed—please take this into account when planning your onward travel.







## Conference Dinner aboard the Rickmer Rickmers: An unforgettable maritime evening on Hamburg's most famous museum ship

**Wed, Aug 27, 7:00 - 11:00 pm CEST**

Location: Museum Ship Rickmer Rickmers, Bei den St. Pauli Landungsbrücken, Ponton 1a, 20459 Hamburg

Step aboard the legendary three-masted barque Rickmer Rickmers – a historic vessel built in 1896 and now an iconic museum ship moored at Hamburg's Landungsbrücken. Enjoy a unique blend of maritime history, harbour views, and fine cuisine in an extraordinary setting.



### Getting There

On Foot from the Conference Venue:

- approx. 40-minute walk

By Public Transport:

- U3 subway line to Landungsbrücken (exit toward the Elbe). The Rickmer Rickmers is located directly at Ponton 1a.

Parking:

- Public parking garages nearby, e.g., "Parkhaus Hafentor" (approx. 5 min walk).



### Did you know?

The Rickmer Rickmers sailed under three different national flags – German, Portuguese, and British – before returning to Hamburg as a museum in 1983.





Hamburg, Germany's second-largest city, is a bustling port city known for its maritime history, modern architecture, and diverse cultural scene. Here are a few things to explore while you're in Hamburg.

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### Elbphilharmonie

A modern architectural marvel, the Elbphilharmonie combines striking design with world-class acoustics and offers panoramic views over Hamburg and the Elbe River.



### Jungfernstieg / Binnenalster

Hamburg boasts a variety of shopping areas, such as Mönckebergstraße and the Jungfernstieg by the scenic Binnenalster, and offers a lively culinary scene featuring everything from fresh seafood to international specialties.



### Miniatur Wunderland

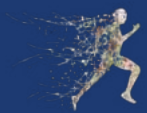
Home to the world's largest model railway, this extraordinary exhibition enchants visitors of all ages with its meticulously crafted miniature worlds, from bustling cities to breathtaking natural landscapes, all brought to life with remarkable detail and creativity.



### Planten un Blomen

This lush urban park in the heart of Hamburg invites visitors to relax among vibrant gardens, themed landscapes, and tranquil green spaces. A highlight is the magical water light concerts, where fountains dance in sync with music and colorful lights, creating an unforgettable evening experience held **daily** starting at **10:00 PM**.





We thank the Scientific and Organizing Committees for their expertise and dedication in shaping the programme and ensuring the success of this symposium.

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The map below provides a general overview of the University of Hamburg campus, showing the main buildings (53 & 51) used during the symposium. Use it to get a sense of the campus layout before exploring.







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