Preliminary Program

Tuesday, August 26

11:00 **Registration opens**

Atrium in front of Lecture Hall Phil A

13:00-15:00 **Early Career Researchers meeting**
Room 1 beside Lecture Hall Phil A

13:00-15:00 **Installation of Posters opens**

Atrium in front of Lecture Hall Phil A

15:15 **Welcome and Opening** Lecture Hall Phil A

Neil L. Kelleher, Northwestern University, Chicago; USA

Preliminary Program

Hartmut Schlüter, Hamburg University, Hamburg; Germany

Paul Danis, Consortium for Top-Down Proteomics, Cambridge; USA

15:30

New Frontiers in Life Sciences – Entering the Proteoform Era

Lloyd Smith:

New frontiers in proteomics - proteoforms, proteoform families, and the human proteoform project

University of Wisconsin-Madison, Madison; USA

Neil L. Kelleher:

Digitizing Proteoform Biology with Single Molecule & Single Cell Mass Spectrometry

Northwestern University, Chicago; USA

Joseph A Loo:

Revealing Functional Proteoforms by Native Top-Down Proteomics

UCLA, Los Angeles; USA

Round Table: **Why do we need proteoform-centric research in life sciences**

17:00-18:00 Moderator: N.N.

Panel List: N.N.

18:00-21:00 **Poster session, cocktails & finger food**

Atrium in front of Lecture Hall Phil A

Preliminary Program

Wednesday, August 27

Sessions in Lecture Hall Phil A

8:30 **New Tools for Proteoform Analysis**

Dimitris Papanastasiou:

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

Fasmatech Science and Technology, Athens; Greece

Ole Nørregaard Jensen:

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

University of Southern Denmark (SDU), Odense; Denmark

Ljiljana Paša-Tolić:

Spatial top-down proteomics (preliminary title)

Pacific Northwest National Laboratory (PNNL), Richland; USA

Hartmut Schlüter:

Nanosecond & Picosecond Infrared laser systems for getting closer to the original proteoform composition in tissues

Hamburg University, Hamburg; Germany

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10:00-10:20 Break

Preliminary Program

10:20 **Sample Preparation & Separation Technologies**

Yu Liang:

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

Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Dalian; China

Nobuaki Takemori:

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

Ehime University School of Medicine, Matsuyama; Japan

Andreas Tholey:

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

Christian-Albrechts-Universität, Kiel; Germany

Christian Neusüss:

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

Aalen University, Aalen; Germany

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12:00-13:00 Lunch

13:00-14:00 **Poster-Session**

Preliminary Program

14:00 Biopharmaceutical & Therapeutic Proteins

Albert Heck:

Touching upon the millions of hidden treasures in the plasma proteome

Utrecht University, Utrecht, Netherlands

Julia Chamot-Rooke:

Monitoring mAb proteoforms blood plasma (preliminary title)

Institut Pasteur, Paris; France

Manfred Wuhrer:

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

Leiden University, Leiden; Netherlands

Yury Tsybin:

Top-Down and Middle-Down Mass Spectrometry of Antibodies (preliminary title)

Spectroswiss, Lausanne; Switzerland

Francois Griaud:

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

*Analytical Characterization, Biologics Analytical Development, Technical Research & Development, **Novartis Pharma** AG, Basel, Switzerland*

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16:00-16:20 Break

Preliminary Program

16:20 **Native MS & Protein Complexes**

Michal Sharon:

Uncovering the unique properties of circulating proteasomes: A mass spectrometry perspective

Weizmann Institute of Science, Rehovot; Israel

Mowei Zhou:

Filling the Structural Knowledge Gap in Protein Design via Native Mass Spectrometry

Zhejiang University, Hangzhou; China

Charlotte Uetrecht:

Flying viruses – mass spectrometry meets X-rays

University of Lübeck, CSSB Centre for Structural Systems Biology, Deutsches Elektronen *Synchrotron DESY, Lübeck & Hamburg; Germany*

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20:00 **Conference Dinner**

Rick Rickmers: *Museum Ship*: https://www.rickmer-rickmers.de/

Preliminary Program

Thursday, August 28

Sessions in Lecture Hall Phil A

8:30 **Databases & Bioinformatics**

Jeffrey Agar:

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

Northeastern University, Bouvé College of Health Sciences, Boston; *USA*

Kyowon Jeong:

Computational methods in top-down proteomics to address challenges in proteoform analysis

Eberhard Karls University, Tübingen; Germany

David Tabb:

TDAuditor assesses deconvolution quality for the Blood Proteoform Atlas

Groningen University, Groningen; Netherlands

Juan Antonio Vizcaino:

The Implementation of Open Science Practices Can Enable A Faster Development Of Top-Down Proteomics

EMBL-EBI, Hinxton; *Great Britain*

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10:00 Break

Preliminary Program

10:20 **Posttranslational modifications**

Liang Qiao:

Analysis of glycoproteins

Fudan University, Shanghai; China

Yue Sun:

Spatially Resolved Proteoform Mapping in Alzheimer's Disease Brain Tissues

Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Dalian; China

Holden Rogers:

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

University of Wisconsin-Madison, Madison; USA

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12:00-13:00 Lunch

13:00-14:00 **Poster-Session**

14:00 **Proteoform Related Topics**

Anjusha Mathew:

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

Maastricht Multi-Modal Molecular Imaging (M4i) Institute, Maastricht University, 6229 ER Maastricht, Netherlands.

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15:30-15:50 Break

15:50 **Biomedical Applications**

Michael Glocker:

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

University of Rostock, Rostock; Germany

Guinivere Lageveen-Kammeijer:

Dissecting the Proteoform Landscape of Prostate-Specific Antigen: Intact, Bottom-Up, and Glycomic Perspectives

Groningen University, Groningen; Netherlands

Ying Ge:

Top-Down Proteomics of the Heart: Decoding Cardiac Proteoforms for Precision Medicine

University of Wisconsin-Madison, Madison; USA

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17:50-18:00 **Final Remarks**

18:00 **Symposium close**

Preliminary **Program**

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