MS+M_23 Conference Schedule

All activities will be held in the DeLuca Forum unless otherwise noted.

MONDAY, OCTOBER 2

4:00–6:30 pm Registration & Poster Hanging

6:30–7:15 pm John Rubinstein, University of Toronto

V-ATPase: The birth, life, death, and re-birth of a proton pump

7:30–9:30 pm Reception and Poster Session

TUESDAY, OCTOBER 3

MORNING SESSION 1: Soft Landing 1

9:00–9:25 am Liz Hecht, Consultant (formerly of Genentech)

Soft landing charge reduced proteins at atmosphere

9:30–9:55 am Stephan Rauschenbach, University of Oxford

Cryo-EM atomic structure determination from macromolecular samples fabricated by

native electrospray ion beam deposition (ESIBD)

10:00–10:25 am Michael Westphall, University of Wisconsin-Madison

Cryogenic soft landing improves structural preservation of protein complexes

10:30-11:00 am Break

MORNING SESSION 2: Native MS 1

11:00-11:25 am Carla Schmidt, Johannes Gutenberg University Mainz

A roadmap for SNARE complex assembly: Mass spectrometry uncovers intermediates and

off-pathway complexes

11:30–11:55 am Michael Marty, University of Arizona

Probing energetics of lipid binding to membrane proteins with native MS and mutant

cycles

12:00-2:00 pm Lunch

AFTERNOON SESSION 1: Cryo-EM 1

2:00–2:25 pm Yifan Cheng, University of California, San Francisco

Tagging endogenous proteins for structural studies

2:30–2:55 pm Liz Wright, University of Wisconsin-Madison

Recent developments in cryo-electron tomography

3:00–3:25 pm Mimi Ho, Columbia University

3:30–4:00pm Break

AFTERNOON SESSION 2: Structural MS

4:00–4:25 pm Brandon Ruotolo, University of Michigan

Native cyclic ion mobility-mass spectrometry: From accurate, high-resolution collision cross

sections to the collision induced unfolding of polydisperse protein complexes

4:30–4:55 pm Charlotte Uetrecht, University of Siegen

Flying viruses - mass spectrometry meets X-rays

5:00–5:25 pm Ruwan Kurulugama, Agilent

Microdroplet enzyme digestion, collision induced unfolding and drift tube and SLIM based

ion mobility-mass spectrometry for intact protein analysis

5:30-6:00 pm Break

AFTERNOON SESSION 3: Scanning Probe Microscopy

6:00–6:25 pm Wyatt Behn, McGill University

Single electron spectroscopy and ultrafast microscopy by AFM

6:30–6:55 pm Simon Scheuring, Cornell University

A pentameric TRPV3 channel with a dilated pore

7:00–7:25 pm Meni Wanunu, Northeastern University

Single-molecule proteomics: probing conformational changes, unfolding, and flossing

proteins through pores

EVENING

7:30–10:00 pm Dinner with Billiards, Bowling & Games

Union South Sett Recreation, 1308 W Dayton St; across the street from the Discovery

Building

WEDNESDAY, OCTOBER 4

MORNING SESSION 1: Soft Landing 2

9:00–9:25 am Kelvin Anggara, Max Planck Institute

Single molecule analysis of biomolecules by direct imaging

9:30–9:55 am Hannah Ochner, Cambridge University

Low-energy electron holography as a technique for imaging biomolecules: Theory and

experiment

10:00–10:25 am Zheng Ouyang, Tsinghua University

Enabling capability of mass spectrometry technologies for structural analysis

10:30-10:55 am Break

MORNING SESSION 2: Emerging Technologies

11:00-11:25 am Justin Benesch, University of Oxford

Super-resolved mass photometry reveals the dissociation pathways of individual molecules

11:30-11:55 am Albert Konijnenberg, Thermo Fisher Scientific

Direct single molecule imaging on a modified Q Exactive UHMR with electron holography

capability

12:00–12:25 pm Randall Goldsmith, University of Wisconsin Madison

Label-free observation of individual solution phase molecules and assessment of

conformation using optical microcavities

12:30–3:30 pm Lunch

AFTERNOON SESSION 1: Native MS 2

3:30–3:45 pm Vicki Wysocki, The Ohio State University

Electrons and surfaces: Complementary methods for characterizing protein complexes

3:45–4:00 pm Albert Heck, Utrecht University

Single molecule mass analysis: a next frontier in studying protein assemblies

4:00–4:25 pm Perdita Barran, University of Manchester

The use of mass spectrometry, light and landing to measure conformationally dynamic

proteins

4:30-4:55 pm Break

AFTERNOON SESSION 3: Student Travel Award Talks

5:00–5:10 pm Caroline Brown, Yale University

Capturing membrane snapshots: A quantitative proteome-wide guide for high-throughput spatially-resolved extraction of membrane proteins for structural/functional studies on

native membranes

Niklas Geue, The University of Manchester 5:15-5:25 pm Lessons from native ion mobility mass spectrometry applied to supramolecular complexes Marko Grabarics, University of Oxford 5:30-5:40 pm Real-space imaging of the atomic structure and conformation of individual cyclic oligosaccharides with noncontact atomic force microscopy Virginia James, University of Texas at Austin 5:45-5:55 pm Native mass spectrometry reveals binding interactions of SARS-CoV-2 PLpro with inhibitors and cellular targets 6:00-6:10 pm Leon (Yu-Fu) Lin, The Ohio State University Native mass spectrometry on a modified timsTOF Pro Dominik Saman, University of Oxford 6:15-6:25 pm Unveiling the complex dynamics of HspB1 and HspB5 assemblies through native mass spectrometry and mass photometry

EVENING

6:30–9:30 pm Dinner and Poster Session Continues

Posters will be removed after the session

THURSDAY, OCTOBER 5

A luggage room will be available for those needing to store their bags.

MORNING SESSION 1: Cryo-EM 2

9:00–9:25 am

David Taylor, University of Texas at Austin
Unraveling native structures using shotgun cryo-EM

9:30–9:55 am

Melanie Ohi, University of Michigan
Structural analysis of caveolea

10:00–10:25 am

Tim Grant, Morgridge Institute for Research
New cryo-EM methodologies for difficult samples

10:30-10:55 am Break

MORNING SESSION 2: Contributed Talks

11:00–11:25 am Mazdak Taghioskoui, Trace Matters Scientific
 Flexible ion guides for integrating mass spectrometry and microscopy platforms
 11:30–11:55 am Boris Krichel, University of Wisconsin-Madison

A comprehensive perspective of AMPK activation: phosphorylation, small molecule binding

and isoform specific allostery analyzed with native and top-down MS

12:00 Adjourn