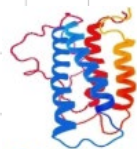


PROGRAM



CTDP

Consortium for Top-Down Proteomics

Bringing Proteoforms to Life™

2ND INTERNATIONAL TOP-DOWN PROTEOMICS SYMPOSIUM

October 3- 5, 2023

Northwestern University, Chicago, IL

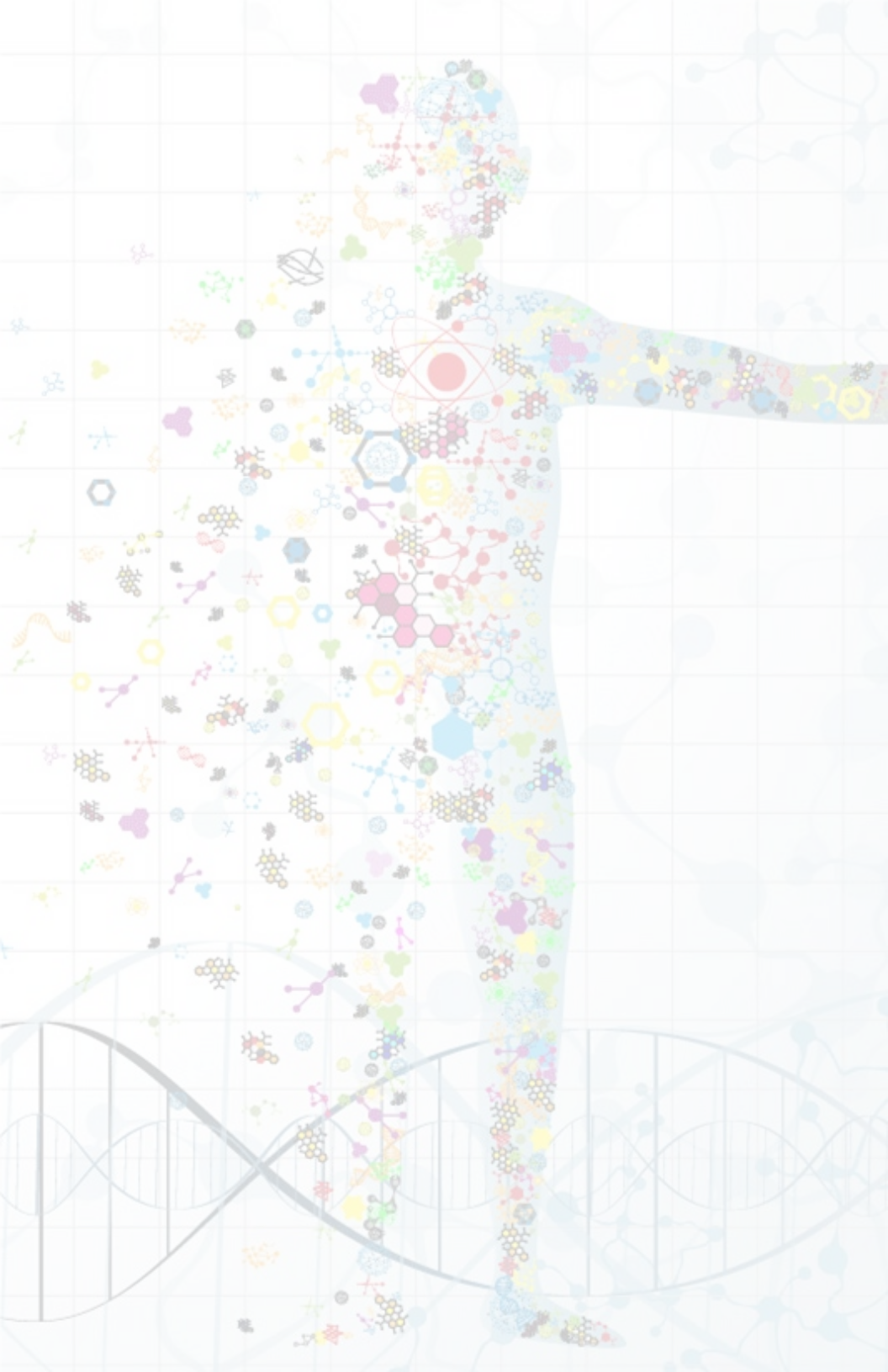
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Chemistry of Life
Processes Institute

Northwestern | PROTEOMICS



WELCOME ADDRESS

Dear Colleagues,

We would like to welcome you to the Second International Symposium on Top-Down Proteomics. The first Symposium held in Paris in 2019 was a resounding success, and we hope that you will find this meeting as productive and enjoyable.

The fields of top-down proteomics and proteoform biology continue to evolve at a rapid pace with advances in separations, analyzers, and data methods moving us into exciting application areas such as single cell and single molecule analysis, native top-down of complexes, and proteoform-specific imaging and clinical diagnostics. In addition, the advent of solutions for chip-based and non-MS analysis will help usher in a new era for rapid, broad-based research in proteoform discovery and screening.

This Symposium will host world leaders presenting their latest findings in the development of technology, as well as applications across the spectrum of life science research – from basic proteoform biology to biopharmaceutical development and clinical diagnostics. Additionally, we will host a series of round table discussions to engage all the participants. These discussions will examine the art and science of proteoform discovery, next-generation proteomics and proteoform sequencing, and the clinical value of proteoforms.

There will also be a round table on the Human Proteoform Project where the community can lend its ideas and help advance this exciting endeavor. We would like to thank the Scientific Committee that has put together this wonderful program as well as the Organizing Committee that has made all of this possible. And finally, we thank all of our sponsors and exhibitors who are an essential part of this community and an important engine in the growth and success of top-down proteomics.

We hope you enjoy the meeting and thank you for your participation.

Sincerely yours,

Paul Danis, PhD

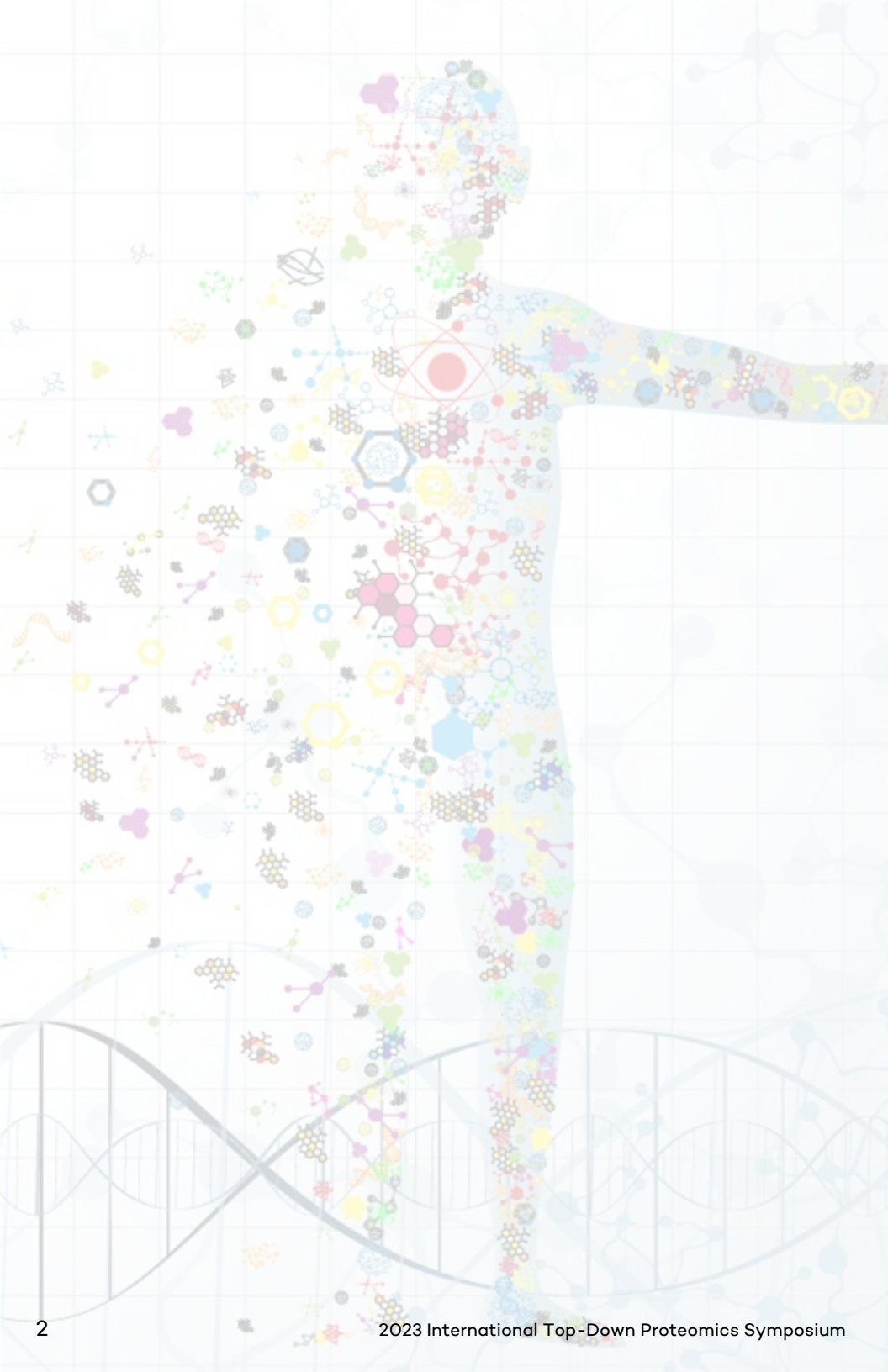
CEO, Consortium for Top-Down Proteomics



Neil Kelleher, PhD

President, Consortium for Top-Down Proteomics Board of Directors
Director, Chemistry of Life Processes Institute and Northwestern Proteomics,
Northwestern University





SCIENTIFIC AND SOCIAL PROGRAM

Please use the QR code below to view digital copies of the Scientific Program, Speaker Abstracts and Poster Abstracts.



SCHEDULE

TUESDAY, OCTOBER 3

REGISTRATION OPENS

9:00 am Northwestern Medicine's Prentice Women's Hospital
3rd Floor Harris Atrium | 250 E Superior St., Chicago IL

10:30 am **Early Career Researchers Session** (Prentice Hospital
3rd Floor, Room M)
This in-person and online session is targeted to early
career researchers and requires pre-registration. The
session will include discussion and Q&A with **Luca
Fornelli, PhD**, University of Oklahoma; **Kyowon Jeong, PhD**,
University of Tuebingen; and **Neil L. Kelleher, PhD**,
Northwestern University, followed by lunch (included) from
11:30 am-12:30 pm.

INSTALLATION OF POSTERS & EXHIBITOR TABLES – Harris Atrium

12:00 pm

WELCOME AND OPENING – Room L

1:00 pm **Milan Mrksich, PhD**, Northwestern University
Neil L. Kelleher, PhD, Northwestern University

SESSION 1: NEW FRONTIERS IN PROTEOMICS – ENTERING THE PROTEOFORM ERA

Session Chair: **Luca Fornelli, PhD**, University of Oklahoma

1:10 pm *New Frontiers in Proteomics: Proteoforms, Proteoform
Families, and the Human Proteoform Project (1)*
Lloyd M. Smith, PhD, University of Wisconsin – Madison

1:45 pm *Ultrasensitive Methods for Hypotheses–Driven Protein
Discovery and Validation (2)*
David R. Walt, PhD, Harvard Medical School

2:20 pm *A Systems Biology Approach to Discovery of Clinically Actionable Protein Isoforms* (3)
Gloria M. Sheynkman, PhD, University of Virginia School of Medicine

2:45 pm *A Word from the Consortium for Top-Down Proteomics* (4)
Paul O. Danis, PhD, Consortium for Top-Down Proteomics

2:50 pm Coffee Break

SESSION 2: ADVANCING MASS SPECTROMETRY TECHNOLOGIES FOR PROTEOFORM ANALYSIS

Session Chair: **Si Wu, PhD**, University of Alabama

3:15 pm *Recent Advances in Mass Spectrometry of Proteoforms* (5)
Joseph A. Loo, PhD, University of California, Los Angeles

3:50 pm *Lessons from Navigating the Ion Activation Network of the Omnitrap Platform Applied to Top-Down Mass Spectrometry* (6)
Dimitris Papanastasiou, PhD, Fasmatech

4:15 pm *Capillary Electrophoresis-Mass Spectrometry for Proteoforms and Protein Complexes* (7)
Liangliang Sun, PhD, Michigan State University

4:40 pm *Top Double-Down and Middle-Down Characterization of Proteoforms Using TIMS-UVPD-TIMS-Q-ECD-TOF MS/MS* (8)
Francisco A. Fernandez-Lima, PhD, Florida International University

5:00 pm And now a word from our sponsors!
Bruker
Thermo Fisher Scientific

ROUND TABLE 1: THE ART AND SCIENCE OF PROTEOFORM DISCOVERY

5:20 pm Moderator: **Hartmut Schlüter, PhD**, University Medical Center Hamburg-Eppendorf

Panelists:

Luca Fornelli, PhD, The University of Oklahoma

Rohan Thakur, PhD, Bruker

Si Wu, PhD, The University of Alabama

Vlad Zabrouskov, PhD, Thermo Fisher Scientific

POSTER SESSION & COCKTAILS/HORS D'OEUVRES – Harris Atrium

6:00 pm Harris Atrium

WEDNESDAY, OCTOBER 4

SESSION 3: EMERGING PROTEOMIC PLATFORMS

Session Chair: **Kyowon Jeong, PhD**, University of Tuebingen

9:00 am *Towards Long-Read Single-Molecule Protein Sequencing on an Array of Unfoldase-Coupled Nanopores (9)*
Jeffrey Nivala, PhD, University of Washington

9:35 am *Miniaturized Quantitative Low-Input (Nano)-Top-Down Proteomics Reveals Information About Proteoforms Not Accessible Via Bottom-Up Proteomics (10)*
Andreas Tholey, PhD, Kiel University

9:55 am And now a word from our sponsors!
Quantum-Si

10:05 am Coffee Break

10:35 am *Sampling the Proteome by Mass Spectrometry Versus Emerging Single Molecule Counting Methods* (11)
Michael MacCoss, PhD, University of Washington

11:05 am And now a word from our sponsors!
Nautilus Biotechnology

ROUND TABLE 2: NEXT-GENERATION PROTEOMICS AND SINGLE-MOLECULE PROTEOFORM SEQUENCING

11:15 am Moderator: **Lloyd Smith, PhD**, University of Wisconsin - Madison

Panelists:

Michael MacCoss, PhD, University of Washington

Parag Mallick, PhD, Nautilus Biotechnology

Gloria Sheynkman, PhD, University of Virginia

Kenneth Skinner, PhD, QuantumSi

LUNCH & POSTER SESSION – Harris Atrium

12:00 pm

SESSION 4: MAPPING SPATIAL AND SINGLE-CELL PROTEOFORM LANDSCAPES

Session Chair: **Julea Vlassakis, PhD**, Rice University

1:30 pm *Single-cell omics: Precision microanalytical tools designed to profile proteoforms* (12)
Amy E. Herr, PhD, University of California, Berkeley

2:05 pm *Toward Single-cell Proteoforms and Proteoform Imaging* (13)
Ljiljana Pasa-Tolic, PhD, Pacific Northwest National Laboratory

2:35 pm *Digitizing Proteoform Biology with Single Molecule Mass Spectrometry* (14)
Neil Kelleher, PhD, Northwestern University

3:05 pm Coffee Break

SESSION 5: DEFINING FUNCTIONS OF PROTEOFORMS AND THEIR COMPLEXES

Session Chair: **Bryon Drown, PhD**, Purdue University

- 3:35 pm *Functionalizing Proteoforms* (15)
Dave Hill, PhD, Harvard University
- 4:10 pm *Elevated Pressure CID in Tandem-Trapped Ion Mobility Spectrometry (Tandem-TIMS-CID) for Structural Characterization of Protein Complexes* (16)
Fanny C Liu, PhD, Florida State University
- 4:30 pm *Chemical proteomic strategies to discovery proteoform-specific small-molecule probes* (17)
Ben Cravatt, PhD, The Scripps Research Institute
- 4:55 pm *Direct Determination Of Membrane Protein Complexes From Cellular Membranes Through Native Top-Down MS* (18)
Wonhyeuk Jung, PhD, Yale University

ROUND TABLE 3: THE HUMAN PROTEOFORM PROJECT

5:15 pm Moderator: **Neil L. Kelleher, PhD**, Northwestern University

Panelists:

Alexandra Naba, PhD, University of Illinois at Chicago
Douglas Sheeley, ScD, Office of Strategic Coordination - the Common Fund, the National Institutes of Health
Marta Vilaseca, PhD, Institute for Research in Biomedicine
David R. Walt, PhD, Harvard Medical School

COCKTAILS AND DINNER AT WOODWIND RESTAURANT

7:00 – Registration includes cocktails and dinner at
11:00 pm Woodwind Restaurant located at 259 E. Erie St., 18th Floor, just a few minutes walk from Prentice.

SESSION 6: PROTEOFORMS AS DRIVERS OF CLINICAL RESEARCH

Session Chair: **Marta Vilaseca, PhD**, IRB Barcelona

9:00 am *Top-Down Proteomics for Cardiac Precision Medicine and Clinical Diagnosis (19)*

Ying Ge, PhD, University of Wisconsin-Madison

9:35 am *The Importance of Proteoform-Level Knowledge in Biomedical Research (20)*

Julia Chamot-Rooke, PhD, Institute Pasteur

10:00 am *Top-Down Protein Analysis for Accurate Identification Of Hemoglobin Variants Using Capillary Electrophoresis-High-Resolution Mass Spectrometry (21)*

Ruben Luo, PhD, Stanford University

10:20 am Coffee Break

10:45 am *Accelerating Disease Marker Identification and Drug Discovery by Clinical Proteoformics (22)*

Hartmut Schlüter, PhD, University Medical Center Hamburg-Eppendorf

CLOSING DAY LECTURE

11:05 am *Cleavage of Histone H2A During Embryonic Stem Cell Differentiation Destabilizes Nucleosomes to Counteract Gene Activation (23)*

Benjamin A. Garcia, PhD, Washington University

ROUND TABLE 4: THE CLINICAL VALUE OF PROTEOFORMS

11:40 am Moderator: **Ying Ge, PhD**, University of Wisconsin-Madison

Panelists:

Josh Levitsky, MD, Northwestern Medicine

Wendy Sandoval, PhD, Genentech

Chris Shuford, PhD, LabCorp

Julea Vlassakis, PhD, Rice University

FINAL REMARKS

12:25 pm **Neil L. Kelleher, PhD**, Northwestern University

12:30 pm Symposium Close

SOCIAL PROGRAM

Cocktails and Dinner at Woodwind Restaurant Wednesday, October 4, 7–11 p.m.



Registration includes cocktails and dinner at Woodwind restaurant located just a few blocks from Prentice Hospital. The restaurant can be accessed via inside walkways (see yellow path on the provided map), or outdoors by taking the elevators down to the main entrance on Fairbanks Court, exit right (south), walk 2.5 short blocks to Erie St., and turn right. Enter the Northwestern Lavin Family Pavilion on Erie Street and take the elevator to the 18th floor.



ORGANIZATIONAL COMMITTEE

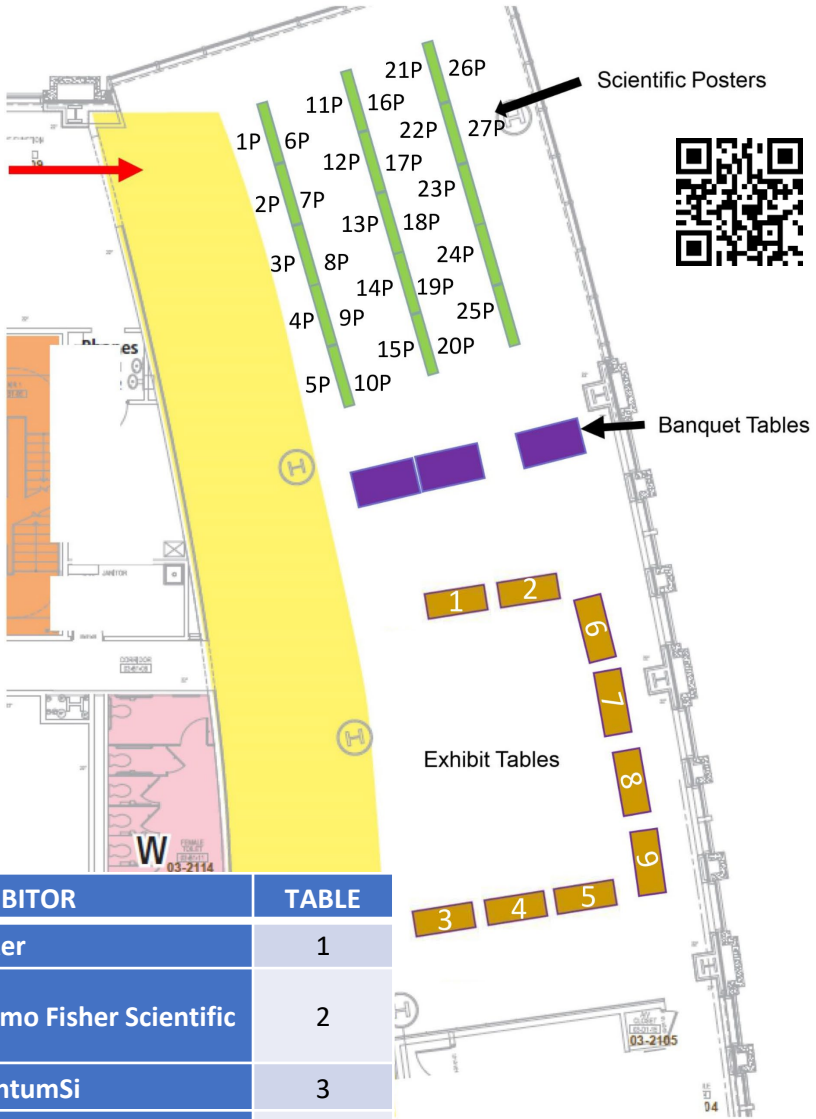
- Michael Caldwell, PhD, Northwestern University
- Julia Chamot-Rooke, PhD, Institut Pasteur
- Paul Danis, PhD, Consortium for Top-Down Proteomics
- Penelope Johnson, CMP, Northwestern University
- Sheila M. Judge, PhD, Northwestern University
- Neil L Kelleher, PhD, Northwestern University (Chair)
- Lisa La Vallee, MS, Northwestern University (Lead Organizer)

SCIENTIFIC PROGRAMMING COMMITTEE

- Michael Caldwell, PhD, Northwestern University
- Julia Chamot-Rooke, PhD, Institut Pasteur
- Paul Danis, PhD, Consortium for Top-Down Proteomics
- Ying Ge, PhD, University of Wisconsin-Madison
- Neil L Kelleher, PhD, Northwestern University (Chair)
- Joseph A. Loo, PhD, University of California, Los Angeles
- Ljiljana Pasa-Tolic, PhD, Pacific Northwestern National Laboratory
- Hartmut Schlüter, PhD, Universität Hamburg
- Gloria Sheynkman, PhD, University of Virginia
- Lloyd M. Smith, PhD, University of Wisconsin-Madison

POSTERS AND EXHIBITORS

HARRIS ATRIUM FLOOR MAP



EXHIBITOR	TABLE
Bruker	1
Thermo Fisher Scientific	2
QuantumSi	3
Sciex	4
Covaris	5
Seer	6
ZefSci	7
CMP Scientific Corp	8
Affiniseq	9

Posters

Poster # Location	Title	Presenter
1P	CONNECTING PROTEOFORMS TO STRUCTURE WITH CLINIC	Ian K Webb
2P	SYSTEMATIC OPTIMIZATION OF ELECTRON-ACTIVATED DISSOCIATION FOR TOP-DOWN TARGETED PROTEIN SEQUENCING	David Colquhoun
3P	QUANTUM-SI PLATINUM TM PROTEIN SEQUENCING REVEALS PEPTIDES MISSED IN DEFAULT MASS SPECTROMETRY DATABASE SEARCHES	Kenneth Skinner
4P	FALSE DISCOVERY RATE ESTIMATION IN SPECTRAL DECONVOLUTION IN TOP-DOWN PROTEOMICS	Kyowon Jeong
5P	PATIENT-SPECIFIC ISOFORM CHARACTERIZATION VIA SPLICE- AND VARIANT-AWARE LONG-READ PROTEOGENOMICS	David Wissel
6P	ACHIEVING HIGHER PRODUCTIVITY IN CELL LINE OPTIMIZATION BY A STREAMLINED MIDDLE-DOWN WORKFLOW	Michael Poltash
7P	INFLUENCE OF SAMPLE PREPARATION AND PROTEOFORM SEPARATION FOR IN-DEPTH TOP-DOWN PROTEOMICS	Philipp T. Kaulich
8P	TOP-DOWN PROTEOMIC IDENTIFICATION OF PLASMID-ENCODED PROTEINS FROM PATHOGENIC BACTERIA USING MALDI-TOF-TOF MASS SPECTROMETRY	Clifton K. Fagerquist
9P	2D-GELC-FAIMS-MS WORKFLOW FOR IN-DEPTH MIDDLE-DOWN PROTEOMICS	Nobuaki Takemori
10P	COLLOIDAL ASSEMBLIES FOR ON-CHIP PROTEIN SEPARATION AND TRANSFER FOR TOP-DOWN MS ANALYSIS	Tanushree Dutta
11P	ADVANCING EXD-BASED TOP-DOWN ORBITRAP ANALYSIS OF GLYCOPROTEINS BY ACQUISITION AND PROCESSING OF TRANSIENTS AND FULL PROFILE MASS SPECTRA	Yury Tsybin
12P	ASSESSMENT OF LABELED PURIFIED PROTEINS WITH TOP-DOWN PROTEOMICS	John J.H. Shin
13P	CHARACTERIZATION OF PATIENT SERUM MONOCLONAL PROTEINS BY BIOLAYER INTERFEROMETRY COUPLED WITH HIGH-RESOLUTION MASS SPECTROMETRY	Priscilla S.-W. Yeung
14P	QUADRUPOLE ISOLATION AND CHARACTERIZATION OF SPECIFIC PROTEOFORMS AND PROTEIN COMPLEXES AT A HIGH M/Z RANGE USING ORBITRAP ASCEND	Rafael D Melani
15P	TOP-DOWN CHARACTERIZATION OF NATIVE MONOCLONAL ANTIBODIES OBTAINED WITH ELECTRON CAPTURE DISSOCIATION ON Q-ToF INSTRUMENTS	John Sausen

Posters Cont'd.

16P	INFORMATICS OF INDIVIDUAL ION MASS SPECTROMETRY ENABLES SINGLE CELL TOPDOWN PROTEOMICS	Michael A. R. Hollas
17P	COMPARISON OF SINGLE MOLECULE PROTEIN SEQENCING AND TOP-DOWN PROTEOMICS	Danielle Tullman-Ercek
18P	PROTEOFORM IDENTIFICATIONS IN HUMAN TISSUE USING INTACT MASS, CYSTEINE COUNTING VIA ISOTOPIC CHEMICAL LABELING, AND A PROTEOFORM ATLAS	Brian L. Frey
19P	PTM-FOCUSED TOP-DOWN PROTEOFORM ANALYSIS	Bryon Drown
20P	TOP-DOWN PROTEOMICS PLATFORM ENABLED BY PHOTOCLEAVABLE SURFACTANT AZO FOR THE COMPREHENSIVE CHARACTERIZATION OF ENDOGENOUS PHOSPHOLAMBAN	Holden Rogers
21P	ADVANCING TOP-DOWN PROTEIN ANALYSIS BY INTEGRATED TANDEM-TIMS-UVPD-PASEF AND TIME-RESOLVED TANDEM-TIMS APPROACHES.	Christian Bleiholder
22P	CHARACTERIZING HISTONE AND HISTONE-MODIFYING PROTEINS FROM THE GREEN MICROALGA CHLAMYDOMONAS REINARDTHII BY TOP-DOWN MASS SPECTROMETRY	James J. Pesavento
23P	DIFFERENTIAL INTERROGATION OF PROTEOFORMS ACROSS THE DYNAMIC RANGE OF PLASMA PROTEOME BY NANOPARTICLES USING A MODIFIED PROTEOGRAPH WORKFLOW	Che-Fan Huang
24P	COMPARING ALGORITHMS FOR PROTEOFORM IDENTIFICATION IN TOP-DOWN PROTEOMICS	Megan S. Gant
25P	A NEW SPE TIPS METHOD BASED ON AN INNOVATIVE SORBENT FOR FAST AND EFFICIENT PEPTIDE FRACTIONATION IN PROTEOMIC STUDIES	Mana Shafaei
26P	PROTEOFORM ATLASING: PAST, PRESENT, AND FUTURE	Ryan T. Fellers
27P	AUTOMATED WORKFLOW FOR HIGHLY-SENSITIVE FRAGMENTATION IN ONCOPROTEOMICS USING THE SAMPLESTREAM PLATFORM AND INDIVIDUAL ION MASS SPECTROMETRY	Raveena Gupta



Use QR Code
to view
abstracts

GENERAL INFORMATION

CONTACTS

General Inquiries:

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773.319.8011

Catering, Evening Program:

Penelope Johnson*

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847.528.2631

Early Career Researcher Session:

Ryan Fellers

ryan.fellers@northwestern.edu

217.273.1331

Poster Session Inquiries:

Jody Hirsh

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Sponsor Inquiries:

Sheila Judge*

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Speaker Inquiries:

Mike Caldwell

michael.caldwell@northwestern.edu

443.915.3704

**Can also provide answers to general inquiries.*

GENERAL INFORMATION AND INSTRUCTIONS

CHECK-IN

When you enter Northwestern's Women's Prentice Hospital, please take the elevator up to the third floor and proceed to the check-in table at the entrance of Harris Atrium. Your name tag will serve as proof of payment and enable access to the symposium, refreshments, lunch, cocktail party, and dinner at Woodwind Restaurant.

EARLY CAREER RESEARCHER SESSION

This session will take place in Room M located on the third floor of Prentice near the Harris Atrium.

SYMPOSIUM

All invited scientific talks, roundtable discussions, and sponsor presentations will take place in Room L North and South adjacent to the Harris Atrium.

POSTER SESSIONS

The poster sessions will take place in the Harris Atrium during the Oct. 3 cocktail party and the Oct. 4 lunch period. Set up begins at 12:00 p.m. on Oct. 3. Please check the program for your poster number and find the matching number on the poster boards to display your poster in the right place. Push pins will be provided.

MEALS

Coffee breaks, lunch, and the cocktail party on Oct. 3 will be served in the Harris Atrium. Cocktails and dinner on Oct 4. are at Woodwind Restaurant at 7:00 p.m. located on Northwestern's downtown campus (see map). Access is limited to registered participants.

EXHIBITORS

Exhibitor tables are in the Harris Atrium. Set up begins at 11:00 a.m. on Oct 3. Please check for your company's name displayed on the tables.

PRESENTERS

Speakers, your slide decks are due to Mike Caldwell, Michael.Caldwell@northwestern.edu, at least 24 hours in advance of your talk.

HOTEL AND VENUE MAP & PARKING

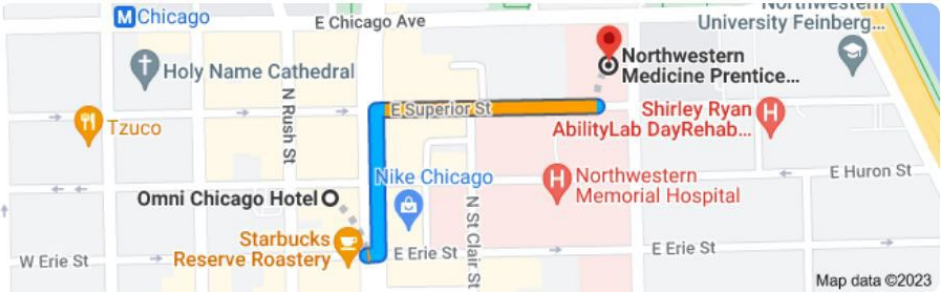
Symposium Venue:

Northwestern Medicine Prentice Women's Hospital

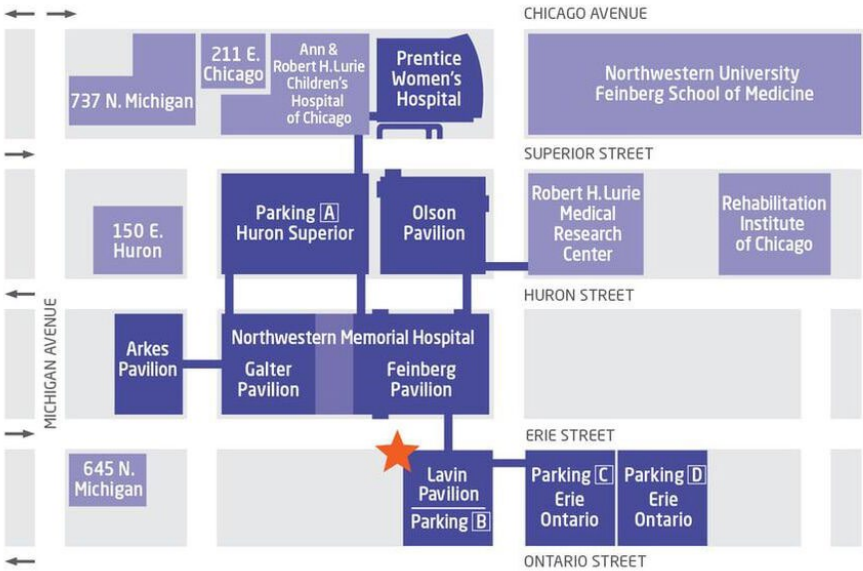
250 E Superior St, 3rd Floor, Harris Atrium & Room L, Chicago, IL

Omni Hotel

676 Michigan Ave, Chicago, IL



UNIVERSITY PARKING LOTS



PRENTICE THIRD FLOOR MAP

The scientific program will take place in L North and L South. The Early Career Session will be held in Room M. Refreshments will be served in the Harris Family Atrium where poster sessions and sponsor tables are located.



Prentice Women's Hospital Third Floor Conference Center Map



- Stairs
- Elevator
- Escalator
- Women's restroom
- Men's restroom

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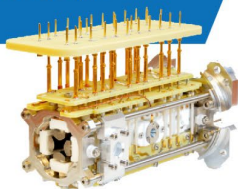
The Protein Sequencing Company™





2nd International Top-Down Proteomics Symposium

Session 2: Advancing Mass Spectrometry Technologies for Proteoform Analysis on October 3 at 3:50 pm



Lessons From Navigating the Ion Activation Network Of The Omnitrap Platform Applied To Top-Down Mass Spectrometry

Dimitris Papanastasiou Fasmatech Science & Technology – A Bruker Company

Session 2: Advancing Mass Spectrometry Technologies for Proteoform Analysis on October 3 at 5:00 pm



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Michael Greig, Bruker

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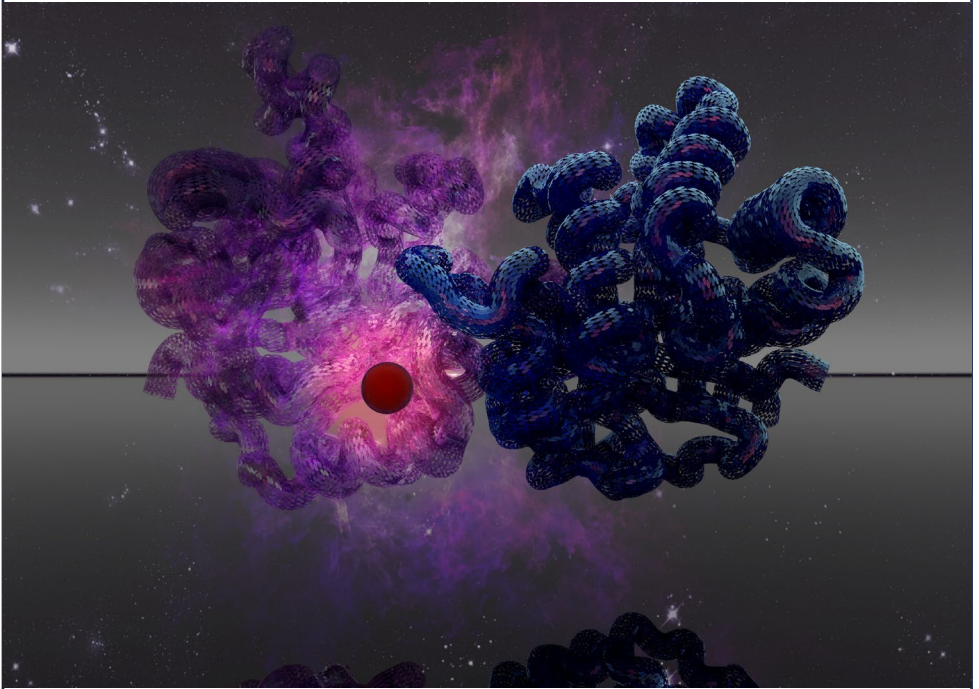
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