



Birgit Schilling, PhD
President

MESSAGE FROM THE PRESIDENT

Dear US HUPO members,

I hope you are all enjoying the summer. I am excited to launch this new, quarterly US HUPO Newsletter, a way for us to stay connected in between the annual conferences. Thank you again for those of you who were able to attend our 2022 conference in Charleston or our virtual synopsis, the "Best of US HUPO 2022". Check out all of our existing webinars - our virtual **US HUPO Global Campus** - plus up and coming events at <https://www.ushupo.org/Webinars> (Proteome Talks – 'Ask the Expert', and Early Career Research panel discussions). We are also recruiting new members for our Virtual Media Outreach (VMO) Committee and other working groups. If you like to get more involved in our activities, please email me directly or the US HUPO office at office@ushupo.org. We need your input on naming our newsletter! If you have an idea, please complete [this form](#) by August 15, 2022. We'll send out a Twitter poll to select the new name and the winner will receive a Chicago-themed welcome gift at the 2023 Annual Conference. See you all in Chicago in 2023 for our next annual conference !!

A handwritten signature in black ink that reads "Birgit Schilling".

Birgit Schilling



HIGH CALIBER SCIENCE... ONLY A CLICK AWAY!

The Best of US HUPO 2022 webinar will featured encore presentations from some of the most exciting research presented at the Conference:

- **Discovering the "Eagle Killer Living on Hydrilla; Aetokthonos hydrillicola"** - Presented by Susan Wilde, University of Georgia
- **Intelligent Data Acquisition for Multiplexed Single Cell Analysis** - Presented by Christopher Rose, Genentech
- **Elucidating the Structural Variations and O-Glycoform Heterogeneity of SARS-CoV-2 S-RBD Variants by Top-Down Mass Spectrometry** - Presented by David Roberts, University of Wisconsin at Madison
- **A Learned Embedding for Efficient Joint Analysis of Millions of Mass Spectra** - Presented by Wout Bittremieux, University of California, San Diego
- **Profiling the Diversity of Agonist Selective Effects on the Proximal Proteome Environment of GPCRs** - Presented by Ruth Huttenhain, University of California, San Francisco
- **Differences in Stromal Patterns from Breast Cancer Metastatic Lymph Between Black Women and White Women in the South Carolina Sea Islander Population** - Presented by Peggi Angel, Medical University of South Carolina

Watch the Webinar

MEET OUR 2022 ASSOCIATION AWARDEES

Congratulations to our 2022 awardees! Nominations for the 2023 awards will open in August 2022. Award winners present a lecture at the annual conference and receive \$2,500 and complimentary conference registration.

DONALD F. HUNT DISTINGUISHED CONTRIBUTION IN PROTEOMICS AWARD

Jonathan V. Sweedler

School of Chemical Sciences, The University of Illinois at Urbana-Champaign

Jonathan V. Sweedler is the James R. Eiszner Family Endowed Professor of Chemistry and Director of the School of Chemical Sciences at the University of Illinois at Urbana-Champaign. His overarching research emphasizes bioanalytical chemistry/measurement science technology development and the study of cell-cell signaling. He is recognized for creating innovative approaches for small-volume mass spectrometry (MS) and used these approaches to probe single cells for their proteins, peptides, and metabolites. Recent advances allow them to probe tens of thousands of cells for their chemical content and select specific cells for follow-up MS-based measurements. Together with their collaborators, they have interrogated the genome, transcriptome, and peptidome in a broad range of animals uncovered signaling molecules and pathways involved in diverse functions and behaviors and characterized neuropeptides in the honey bee, planarian, songbird, sea snail, and multiple mammalian species, as well as in individual cells and vesicles.

[Read More](#)



Jonathan V. Sweedler

CATHERINE E. COSTELLO LIFETIME ACHIEVEMENT IN PROTEOMICS AWARD

Catherine Fenselau

Johns Hopkins School of Medicine



Catherine Fenselau

When she joined the faculty of the Department of Pharmacology and Experimental Therapeutics at the Johns Hopkins School of Medicine in 1967, Catherine Fenselau (Cotter) was given the job description to develop and exploit mass spectrometry's new high mass, high-resolution capabilities across the spectrum of biomedical research. Peptide and protein analysis held her attention from the beginning. In 1982 the Hopkins laboratory published the first considerations of the isotopic complexities of protein molecular ion populations. In 1992 her team, now at UMBC, produced the first experimental measurement of the proton affinity of arginine, a major determinant of peptide fragmentation. Mass spectrometry and HPLC-based studies of protein acylation by carboxyl-linked glucuronides, stoichiometric metal ion flux in metallothionein, site-specific alkylation of metallothionein by therapeutic agents, modifications and processing of the HIV GAG protein, and many others positioned her to be an early contributor to the global post-genomic effort now known as proteomics.

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GILBERT S. OMENN COMPUTATIONAL PROTEOMICS AWARD

Eric Deutsch

Institute for Systems Biology

Dr. Eric Deutsch obtained his Ph.D. in Astrophysics from the University of Washington, and then moved to the Institute for Systems Biology where he is now a Principal Scientist focusing on Computational Proteomics. He currently leads the team that develops the Trans-Proteomic Pipeline (TPP), an open-source suite of software tools for processing proteomics mass spectrometry data. He also leads the team that develops PeptideAtlas, a resource that gathers publicly deposited proteomics data from around the world, reprocesses the data with the TPP, and provides the results as ensemble views of the observed proteome for many different species. Dr. Deutsch contributes to the development of minimum information standards and standardized data formats as co-chair of the HUPO Proteomics Standards Initiative (PSI) and chair of its mass spectrometry standards working group, which has produced such standards as mzML and the Universal Spectrum Identifier (USI). He is one of the leaders of the ProteomeXchange Consortium of proteomics repositories that aims to promote data sharing in the community. He is also chair of the HUPO Human Proteome Project (HPP) Knowledge Base Pillar and a member of the HPP Executive Committee and Biology/Disease focused HPP Executive Committee.

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Eric Deutsch

ROBERT J. COTTER NEW INVESTIGATOR AWARD

Stephanie M. Cologna
University of Illinois Chicago (UIC)



Stephanie M. Cologna

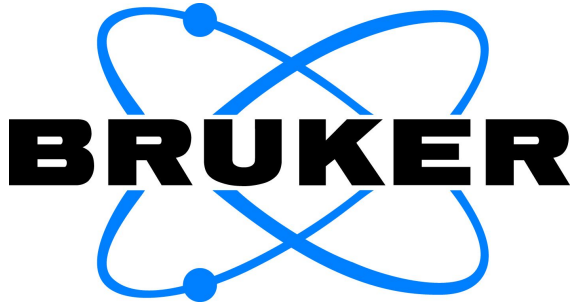
Stephanie M. Cologna is an Associate Professor of Chemistry at the University of Illinois Chicago (UIC). She received her B.S. in Chemistry from the University of Arizona followed by doctoral studies at Texas A&M University under the mentorship of David H. Russell. Dr. Cologna carried out post-doctoral training at the Eunice Kennedy Shriver, National Institute of Child Health and Human Development, National Institutes of Health. In 2015, Stephanie began her independent career at UIC. Her research program is focused on integrating mass spectrometry-based proteomics and lipidomics to understand neurodegeneration. A significant effort in her laboratory is focused on the fatal, lysosomal storage disorder, Niemann-Pick Type C.

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US HUPO

1300 SE Stark Street, Suite 307

Portland, OR 97214, USA

505.989.4876

www.ushupo.org | office@ushupo.org