



2026 Wisconsin Human Proteomics Symposium

EMPOWERING THE NEXT GENERATION OF SCIENTISTS

Madison, WI | August 5-6, 2026





Welcome Letter

Dear all,

It is our great pleasure to welcome you to the 2026 Wisconsin Human Proteomics Symposium! We are delighted to host this year's symposium at the University of Wisconsin–Madison Health Sciences Learning Center (with virtual participation available via Zoom) and to bring together trainees, faculty, clinicians, staff scientists, and industry researchers who share a passion for advancing human proteomics.

The theme of this year's symposium, **Empowering the Next Generation of Scientists**, reflects our commitment to fostering scientific excellence, mentorship, and career development while highlighting cutting-edge advances in proteomics. We hope this symposium will provide an inspiring forum for exchanging ideas, forging new collaborations, and supporting the next generation of leaders in our field.

This year's program features two keynote lectures by internationally recognized leaders, presentations from outstanding early-career faculty, Rising Star oral presentations, a poster session, sponsor exhibits, and abundant opportunities for networking. The symposium will showcase exciting advances in mass spectrometry-based proteomics, top-down proteomics, native mass spectrometry, mass spectrometry imaging, and complementary multi-omics approaches, with applications spanning cardiovascular disease, cancer, neurodegenerative disorders, lung disease, and many other areas of biomedical research. A new highlight this year is our **Career Development Workshop (hosted virtually via Zoom)**, which will bring together scientists from academia, industry, and national laboratories to share career insights and participate in an interactive panel discussion. Together with our Rising Star Competition, this workshop underscores our commitment to mentoring trainees and supporting scientists at every stage of their careers.

We extend our sincere gratitude to our generous sponsors, whose partnership has been instrumental in making this symposium possible. We are also deeply grateful to our keynote and invited speakers for sharing their expertise and to all participants for contributing their enthusiasm, ideas, and scientific excellence. Special thanks go to our organizing committee, trainee organizing committee, staff, and volunteers for their dedication and hard work in planning this event.

Whether you are joining us in person or virtually, we hope you enjoy a stimulating and rewarding symposium filled with exciting science, meaningful discussions, and new collaborations. For those visiting Madison, we encourage you to take some time to explore our beautiful campus, enjoy the city's vibrant atmosphere, and experience Wisconsin's renowned hospitality.

Thank you for being part of the 2026 Wisconsin Human Proteomics Symposium. We wish you an enjoyable, productive, and inspiring meeting!

Sincerely,

Symposium organizing committee



Allan Brasier, MD
Honorary Symposium Chair



Ying Ge, PhD



Lingjun Li, PhD



Judith Simcox, PhD



2026 Wisconsin Human Proteomics Symposium

"EMPOWERING THE NEXT GENERATION OF SCIENTISTS"

August 6, 2026 | UW-Madison Health Sciences
Learning Center

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2026 Wisconsin Human Proteomics Symposium

EMPOWERING THE NEXT GENERATION OF SCIENTISTS

August 5-6, 2026 | Join us virtually or in-person at the
UW-Madison Health Sciences Learning Center



DAY 1 | Aug. 5 (Virtual Only in Zoom)

Career Development Workshop

Chairs: Mallory Wilson and Claire Boos
(9:30-11:00 am, [Zoom Link](#))

9:30 – 9:45 am	<i>Introduction</i>
9:45 – 10:10 am	Split into breakout rooms for prescreened questions
10:10 – 10:30am	Moderated breakout discussions with live audience questions
10:30– 11:00 am	Networking with panelists in individual breakout rooms
	Breakout Room 1: Academic & Clinical Frontiers Panelists • Emma Guiberson, Assistant Professor of Chemistry, Middlebury College • Che-Fan Huang, Incoming Assistant Professor of Chemistry, Texas A&M University • Corinne Lutomski, Incoming Assistant Professor of Chemistry, University of California, San Francisco (UCSF) • Morgan Mann, Assistant Director of Newborn Screening and Assistant Professor of Pediatrics, UW–Madison School of Medicine and Public Health Moderators: Jericha Mill, Margaret Robinson, Kendra Selby, Tina Dang, Hsin-Ju (Ruby) Chan Breakout Room 2: Industry & Government Sectors Panelists • Savannah Snyder, Regional Sales Manager, Bruker • Lisa Jenkins, Senior Associate Scientist, National Cancer Institute (NCI) • M. Violet Lee, Senior Principal Scientist, Genentech • Jennifer Lofland, Senior Medical Director, U.S. Medical Affairs, Incyte Moderators: Will Leiter, Sarah Lofland, Claire Boos, Anna Grace Towler, Jiahao Zhang Main Breakout Room / Participant Support Facilitators: Mallory Wilson, Isabella (Bella) Clemmer IT Support: Matthew Fischer Andrew Perciaccante

DAY 2 | August 6

Scientific Symposium

(HSLC 1306, Virtual option available in [Zoom](#))

8:30am – 5:00pm	Conference Registration	HSLC Atrium
Session I Chair: Ying Ge, PhD		
9:00–9:10 am	Welcome and Opening Remarks Allan Brasier, MD Senior Associate Dean Clinical and Translational Research, School of Medicine and Public Health University of Wisconsin - Madison	
9:10–10:00 am (45 min Presentation, 5 min Q/A)	Keynote Speaker Joseph Loo, PhD University of California-Los Angeles <i>“Impacting Structural Biology and Disease Research with Native Top-Down Proteomics”</i>	
10:00 –10:20 am (17 min Presentation, 3 min Q/A) 10:20– 10:40 am (17 min Presentation, 3 min Q/A)	Amy Weeks, PhD University of Wisconsin - Madison <i>“New enzyme chemistry to decipher post-translational modification function using MS-based proteomics”</i> Francisco Alvarado, PhD University of Wisconsin - Madison <i>“Ryanodine receptor 2 regulation in the healthy and diseased heart: a new look at an old problem”</i>	
10:40 – 11:00am	Coffee Break	HSLC Atrium
Session II Chair: Zicheng Jin, PhD, DABCC		
11:00 –11:20 am (17 min Presentation, 3 min Q/A) 11:20– 11:40 am (17 min Presentation, 3 min Q/A) 11:40– 12:00 pm (17 min Presentation, 3 min Q/A)	Stefani Thomas, PhD, DABCC, NRCC University of Minnesota <i>“Predictive biomarkers of PARP inhibitor resistance in ovarian cancer”</i> Wei Wei, PhD University of Wisconsin – Madison <i>“Deorphanizing Biochemical Pathways of Nutrient Metabolism”</i> Rachel Turn, PhD University of Wisconsin – Madison <i>“Time-Resolved Proteomics Maps Stepwise Primary Cilia Assembly and GPCR Trafficking”</i>	

12:05 – 1:00pm	Lunch, Sponsor Exhibit and Networking	HSLC Atrium
<u>Rising Star Session</u> Chair: Judith Simcox, PhD 1:00 pm – 3:00 pm Each finalist will give a 10 min presentation plus 2 min Q&A.		
Fanny Caroline Liu, PhD Research Faculty, Bleiholder Lab, Florida State University <i>“Beyond Ensemble Measurements: Resolving Antigen Binding and Conformational Heterogeneity in Multispecific Antibodies”</i> Benjamin Minkoff, PhD Senior Scientist, Sussman Lab, University of Wisconsin – Madison <i>“Paired structural proteomic and phosphoproteomic analysis of CDK7 inhibition in fibrolamellar carcinoma patient-derived organoid models”</i> John Shuster MD-PhD Student, Simcox Lab, University of Wisconsin – Madison <i>“Optimization of Oxylin Quantification using Bio-Inert Chromatography Systems and Mass Spectrometry”</i> Claire Boos Graduate Student (6th year), Smith Lab, University of Wisconsin – Madison <i>“The Proteoform Landscape of HIV-1 Virions”</i> Angel E. Ibarra Graduate Student (6th year), Li Lab, University of Wisconsin – Madison <i>“Building a Quantitative Neuropeptidomic Toolkit”</i> Hsin-Ju (Ruby) Chan Graduate Student (5th year), Ge Lab, University of Wisconsin – Madison <i>“Resolving the Complex Human Cardiac Proteome by Gel-Based Prefractionation and Top-Down Proteomics”</i> Margaret Robinson Graduate Student (5th year), Coon Lab, University of Wisconsin – Madison <i>“Proteome-wide QTL mapping enables gene-protein-phenotype network construction in a genetically diverse MASLD mouse model”</i> Vu Ngoc Huong Tran Graduate Student (5th year), Li Lab, University of Wisconsin – Madison <i>“Quantitative Neuropeptidomics Reveals Spinal Cord Neurochemical Signatures of Disease-Modifying Osteoarthritis Drugs”</i> Jiahao Zhang Graduate Student (4th year), Li Lab, University of Wisconsin – Madison <i>“Integrated Lipidomics and Subcellular Proteomics Reveal Trans Fat-Induced Hepatic Organelle Remodeling”</i> Andrew J. Perciaccante Graduate Student (4th year), Ge Lab, University of Wisconsin – Madison <i>“Integrated Multiomics Enabled by Sequential Extraction for Comprehensive Molecular Profiling of Small Extracellular Vesicles”</i>		

3:00 – 3:10pm	Break	HSLC Atrium
Session III Chair: Lingjun Li, PhD		
3:10– 3:45 pm (30 min Presentation, 5 min Q/A)	<u>Keynote Speaker II</u> <i>Amanda Hummon, PhD</i> The Ohio State University <i>“Spatial SILAC—Developing Isotopic Zip Codes”</i>	
3:45 – 3:53 pm (8 min Presentation)	Gold Sponsor Presentation <i>Shashank Jain, PhD.</i> Waters Corporation <i>“Enabling deep proteome coverage at ultra-high throughput using stepped-quadrupole DIA on a novel MRT benchtop MS”</i>	
3:53 - 4:00 pm	Award Ceremony	
4:00 – 5:30pm	Poster Session, Exhibits, and Reception	HSLC Atrium
5:30pm	Closing Remarks	HSLC Atrium



Keynote Speakers

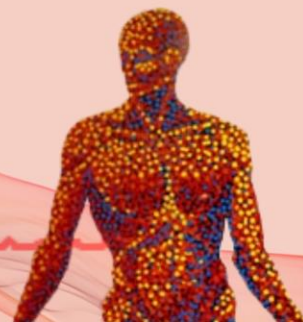
Joseph Loo, Ph.D.

**Professor, Department of Chemistry and Biochemistry
Professor, Department of Biological Chemistry
University of California-Los Angeles**



Joseph A. Loo, Ph.D. is Professor of Chemistry and Biochemistry, and Biological Chemistry (David Geffen School of Medicine at UCLA) at the University of California, Los Angeles. He is also a member of UCLA/Dept. of Energy Institute for Genomics and Proteomics and the UCLA Molecular Biology Institute. He received his Ph.D. in chemistry working with Professor Fred McLafferty at Cornell University, and he was a postdoctoral fellow and Senior Research Scientist at Pacific Northwest National Laboratory with Dr. Richard Smith. Prior to UCLA, Dr. Loo was an Associate Research Fellow and Mass Spectrometry Group Leader at Parke-Davis Pharmaceutical Research/Pfizer. His group uses and develops novel methods based on mass spectrometry (MS), proteomics, and protein chemistry strategies, including top-down MS, native MS, ion mobility, and label-free quantification, to characterize proteins and protein complexes (and their post-translational modifications). He has published over 380 papers and book chapters.

He has held leadership and advisory positions with scientific organizations, including the American Society for Mass Spectrometry (ASMS), the US Human Proteome Organization (US HUPO), and the Consortium for Top-Down Proteomics; he was the Editor-in-Chief of the *Journal of the American Society for Mass Spectrometry* (2016-2022). He was the President of ASMS (and he will transition to the Past-President role in July 2026). His research has been supported by the US National Institutes of Health (NIH), the US National Science Foundation (NSF), the US Department of Energy (DOE), and the US Department of Defense (DOD).



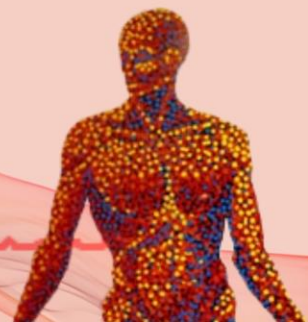
ABSTRACT OF KEYNOTE PRESENTATION

Impacting Structural Biology and Disease Research with Native Top-Down Proteomics

Native mass spectrometry (nMS) measures proteins and complexes that are functionally relevant to biology. Top-down proteomics (TDP), i.e., fragmentation of the gas-phase protein, reveals identification, sequence, and proteoform information. TDP can be used to characterize monoclonal antibodies (mAbs) and antibody-drug conjugates (ADCs), important biotherapeutics with large size (~150 kDa) and high structural complexity that require extensive sequence and structure characterization. Moreover, native top-down proteomics (nTDP) could be ideal for understanding how proteins interact with other proteins (and ligands and cofactors), identifying unknown proteoforms, and gaining information on their function at near physiological conditions.

We apply these MS tools to address questions related to the growing problem of neurodegenerative diseases (ND's). Alzheimer's disease is clearly becoming a national health crisis affecting people worldwide; other NDs such as Parkinson's disease, Huntington's disease, and many others add to the growing healthcare issue for future generations. Amyloid proteins can misfold into insoluble protein aggregates, including highly ordered fibrils that are hallmarks of various neurodegenerative and systemic diseases. Prior to fibril formation, these proteins populate a range of intermediate states and oligomer sizes, some of which are more toxic than others. Oligomers are dynamic and heterogeneous, varying in stoichiometry, population, and conformation, making them difficult to characterize using traditional biochemical and analytical techniques. Native/top-down MS can be applied to study these factors involved in NDs.

We are developing a nTDP workflow without on-line chromatographic separation to address a number of other projects. Understanding the human host-pathogen interface is key to combating antimicrobial resistance. For secretomes of model Gram+ pathogenic bacteria, *Corynebacterium diphtheriae*, a single direct infusion revealed more than 370 unique protein masses. We identify more than 70 proteoforms, including novel virulence factors and complexoforms reaching 300 kDa. A functional proteomics platform was developed to allow us to understand how they acquire iron during infection that opens new avenues for targeting iron metabolism in pathogens.



Amanda Hummon, Ph.D

**Professor, Department of Chemistry and Biochemistry
Comprehensive Cancer Center
The Ohio State University**



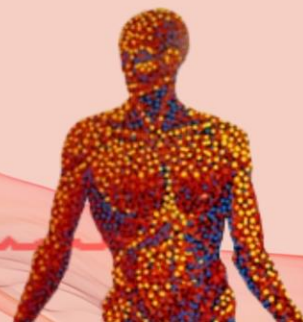
Amanda Hummon earned her A.B. in chemistry at Cornell University and her Ph.D. in analytical chemistry at the University of Illinois, in the laboratory of Prof. Jonathan V. Sweedler. She completed her postdoctoral work at the National Cancer Institute. She is currently a Professor in the Department of Chemistry and Biochemistry and the Comprehensive Cancer Center at The Ohio State University. She is the Director of the Mass Spectrometry and Proteomics Facility at Ohio State. Her laboratory develops mass spectrometric methods to explore cancer tissues, cell cultures, and organoids, with a focus on mass spectrometry imaging and proteomics. She has been recognized with an NSF CAREER award, the American Chemical Society Rising Star Award and the Presidential Early Career Award for Scientists and Engineers (PECASE). In 2021,

she completed a Fulbright Scholar Award in the Laboratory of Ron Heeren in Maastricht, the Netherlands.

ABSTRACT OF KEYNOTE PRESENTATION

Spatial SILAC—Developing Isotopic Zip Codes

Three-dimensional cell cultures are attractive models for biological research. They combine the flexibility of cell culture with some of the spatial and molecular complexity of tissue. For example, colon cancer cell lines form spheroids, in vitro mimics of poorly vascularized tumors. The spheroids are composed of a central necrotic core, a middle quiescent layer and an outer proliferative layer of cells, like a rapidly growing colon tumor. Our laboratory has characterized the distribution of endogenous proteins via MALDI imaging mass spectrometry in colon spheroids and determined that the molecular gradients correlate with the pathophysiological changes in the structure. We have developed Spatial SILAC, a method to selectively label the cells in the distinct chemical microenvironments in the spheroids and assess the proteomic changes in response to drug treatment. In this presentation, the spatially localized proteomic changes in response to the multiple kinase inhibitor Regorafenib will be described. In brief, the cellular response to Regorafenib treatment is significantly affected by the location of the cells and the chemical microenvironment.



Invited Speakers

Amy Weeks, PhD



Amy Weeks is an Assistant Professor of Biochemistry at the University of Wisconsin-Madison. She received her S.B. in Chemistry from the Massachusetts Institute of Technology and earned her Ph.D. in Chemistry at the University of California, Berkeley under the mentorship of Prof. Michelle Chang. She completed postdoctoral studies in the laboratory of Prof. James Wells at the University of California, San Francisco. Her research group engineers enzymatic tools for mapping biological signals across space and time in living cells. Using these tools, the lab seeks to provide an

integrated view of cellular signaling to advance biological discovery and development of therapeutics for human disease.

New enzyme chemistry to decipher post-translational modification function using MS-based proteomics

Spatial organization and temporal dynamics are essential properties of cellular signaling. Post-translational modifications (PTMs) to proteins relay biological signals by exerting precise spatiotemporal control over protein function, localization, and lifetime. The Weeks lab is focused on developing new chemical and enzymatic tools for PTM proteomics with subcellular spatial and temporal resolution. We develop chemical probes and genetically targetable, PTM-selective proximity labeling enzymes to covalently tag post-translationally modified proteins in specific subcellular locations, enabling their enrichment and analysis with mass spectrometry-based proteomics experiments. We focus on two pervasive PTMs, proteolysis and phosphorylation, both of which play critical roles in myriad biological signaling pathways relevant to human health and disease. Our technologies are broadly applicable to a wide variety of protease and kinase signaling pathways and provide an integrated view of cellular signaling with implications for both fundamental biological discovery and therapeutic innovation.

Stefani Thomas, PhD, DABCC, NRCC



Born and raised in Los Angeles, CA, Stefani earned her BA in Biological Sciences with a Minor in Music from Dartmouth College and her PhD in Pharmaceutical Sciences from the University of Southern California. After completing a research postdoctoral fellowship in the lab of Dr. Robert Cotter at Johns Hopkins, Stefani joined the Center for Biomarker Discovery and Translation at Johns Hopkins where she conducted mass spectrometry-based clinical proteomics research. She then completed a Clinical Chemistry

postdoctoral fellowship at Johns Hopkins and earned board certification from the National Registry of Certified Chemists and the American Board of Clinical Chemistry. At the University of Minnesota, Stefani is an Assistant Professor in the Department of Laboratory Medicine and Pathology, a faculty investigator at the Advanced Research and Diagnostic Laboratory (ARDL), and the Associate Medical Director of the M Health Fairview West Bank Laboratory. Research in the Thomas Lab focuses on applying mass spectrometry-based clinical proteomics methods for cancer biomarker development. Stefani has >80 publications and she is the 2026 recipient of the Bereman Award for Clinical Science Innovation.

Predictive biomarkers of PARP inhibitor resistance in ovarian cancer

Ovarian cancer is the second deadliest gynecological cancer globally with a 46% 5-year survival rate. Drug resistance is a common feature of patients treated with chemotherapy and targeted therapies, including PARP inhibitors (PARPi), with most patients developing resistance with a median progression-free survival of 7-15 months. The mechanisms driving drug resistance are unclear. To identify candidate predictive protein biomarkers of PARPi treatment, we applied an *in vitro* approach utilizing a panel of ovarian cancer cell lines with acquired resistance to the PARPi niraparib. Sensitivity to niraparib was measured using Sulforhodamine B assay, and cell survival was assessed via clonogenic assay. DNA damage response was analyzed by measuring γ -H2AX, and RAD51, and apoptosis was assessed via cleaved-PARP expression using Western blotting. TMT-based global proteomic analysis was conducted, followed by PRM-based targeted mass spectrometry to verify the proteins of interest with differential relative abundance in the sensitive vs. resistant cell lines. Mitochondrial translation and mitotic catastrophe-related cell cycle aberrations were identified as biological processes associated with acquired resistance to niraparib. Seahorse assay and flow cytometry analyses were conducted to elucidate the functional mechanisms driving the acquired resistance. The results from our study will inform future drug combination development efforts to overcome acquired resistance to PARPi therapy among ovarian cancer patients.

Francisco Alvarado, PharmD, PhD

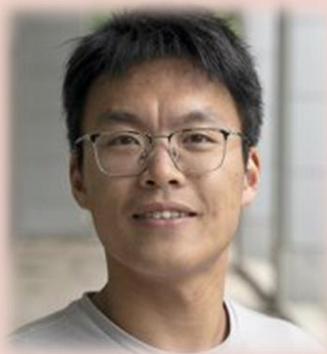


Dr. Alvarado obtained a PharmD degree from the University of Costa Rica in 2009 and an PhD in Molecular and Integrative Physiology from the University of Michigan in 2017. He joined the faculty of the University of Wisconsin-Madison in 2022. The long-term goal of the Alvarado Lab is to understand the mechanisms of heart disease and to develop safe and effective treatments that improve the life of patients. Our primary interest is the regulation of cardiac ion channels with emphasis on diseases arising from their dysfunction, especially calcium-dependent arrhythmias and structural cardiomyopathies. Calcium is required for heart function in a process called excitation-contraction coupling; yet, dysregulation of calcium

homeostasis is known to participate in heart disease. We apply state-of-the art imaging, electrophysiology and cell biology tools to understand how mutations affecting proteins involved in excitation-contraction coupling, such as ryanodine receptor 2, the major intracellular calcium channel in the heart, participate in the development of disease and, therefore, can be targets for drug development.

Ryanodine receptor 2 regulation in the healthy and diseased heart: a new look at an old problem

The adrenergic or “fight-or-flight” response is a fundamental mechanism that controls cardiac function during physical and emotional stress. It involves an increase in heart rate (chronotropy), contractile force (inotropy) and relaxation velocity (lusitropy), mediated by carefully orchestrated intracellular calcium cycling. The underlying mechanisms have been extensively studied, but the relative contribution of specific molecular players is debated. Multiple proteins are phosphorylated by protein kinase A (PKA) during the adrenergic response, most notably Rad, a regulator of voltage-gated calcium channels, phospholamban (PLB), a regulator of intracellular calcium uptake, and ryanodine receptor 2 (RyR2), the major calcium release channel in the heart. We are systematically evaluating the relative contribution of these PKA targets to different aspects of the fight-or-flight response. Ablation of three major phosphorylation sites in RyR2 (RyR2-TPM) did not affect the major features of the adrenergic response. Removing phosphorylation sites in Rad (4SA-Rad) or PLB (PLB-DM), however, blunts the adrenergic response. Using mass spectrometry, we demonstrate that basal phosphorylation of PLB in mouse hearts is high but provides enough dynamic range to regulate protein function. Targeting phosphorylation sites in both proteins (4SA-Rad/PLB-DM or Rad/PLB) completely abrogates the expected changes in intracellular Ca^{2+} handling following adrenergic stimulation. Rad/PLB myocytes and hearts completely lack the normal positive inotropic and lusitropic responses. A key observation is that phosphorylation of RyR2 is preserved in the Rad/PLB model, as measured using western blotting. We aim to develop mass spectrometry methodologies to assess RyR2 phosphorylation. These results settle a long-standing argument in the field by demonstrating that RyR2 phosphorylation does not meaningfully contribute to modulating global calcium. Dysregulation of the cardiac adrenergic response is implicated in numerous pathologies, including cardiac arrhythmias, hypertrophy and heart failure. Knowledge of these mechanisms is critical to both understanding the underlying molecular mechanisms and developing new therapeutic strategies for these conditions.



Wei Wei, PhD

Dr. Wei Wei is an Assistant Professor in the Department of Biochemistry at the University of Wisconsin–Madison, where his laboratory seeks to uncover the molecular logic by which nutrients and circulating signals control mammalian physiology. His research integrates biochemistry, chemical biology, mass spectrometry, metabolomics, proteomics, and physiology to discover how diet-derived and endogenous small molecules shape metabolic health, obesity, diabetes, exercise adaptation, and aging. He earned his B.S. in Biomedical Sciences from

Zhejiang University and his Ph.D. in Cell, Molecular, and Organismal Biology from Stanford University, followed by postdoctoral training in metabolism and physiology at Stanford School of Medicine. Dr. Wei has pioneered technologies for studying interorgan communication in vivo. During his Ph.D., he developed cell type-specific secretome profiling by combining secretory-pathway proximity biotinylation with quantitative proteomics, enabling circulating proteins to be traced back to their cellular origins in living animals. This work generated organism-wide maps of exercise-regulated secreted proteins and identified candidate exerkines that may mediate the beneficial effects of exercise on obesity, diabetes, and metabolic adaptation. As a postdoctoral fellow, he expanded into metabolomics, isotope tracing, and enzymology, discovering that the BMI-associated orphan enzyme PTER hydrolyzes N-acetyltaurine, a taurine-derived metabolite that regulates feeding, obesity, and glucose homeostasis. At UW–Madison, the Wei laboratory investigates how noncanonical nutrients and secreted proteins form hidden communication networks that coordinate systemic physiology. By combining technology development with mechanistic biochemistry and animal physiology, his group aims to define new molecular pathways linking nutrient metabolism to interorgan signaling, metabolic disease, and healthy aging.

Deorphanizing Biochemical Pathways of Nutrient Metabolism

Taurine is a conditionally essential nutrient and one of the most abundant amino-acid-like metabolites in humans. In endogenous taurine metabolism, dedicated enzymes mediate taurine biosynthesis from cysteine and regulate the downstream metabolism of secondary taurine metabolites. One such metabolite is N-acetyltaurine, whose levels are dynamically regulated by physiological and nutritional stimuli that alter taurine or acetate flux, including endurance exercise, dietary taurine supplementation, and alcohol consumption. However, the enzymes that control N-acetyltaurine metabolism, the transporters that distribute it, and the physiological functions of N-acetyltaurine itself have remained poorly understood. Here, we show that the body mass index-associated orphan enzyme phosphotriesterase-related protein (PTER) is the principal mammalian N-acetyltaurine hydrolase. In vitro, PTER catalyzes the hydrolysis of N-acetyltaurine to taurine and acetate with high selectivity. Genetic ablation of Pter in mice causes complete loss of tissue N-acetyltaurine hydrolysis activity and a systemic increase in N-acetyltaurine levels. Following stimuli that elevate taurine availability, Pter knockout mice exhibit reduced food intake, resistance to diet-induced obesity, and improved glucose homeostasis. Administration of N-acetyltaurine to obese wild-type mice similarly reduces food intake and body weight in a GFRAL-dependent manner. We further developed a PTER-selective inhibitor that suppresses feeding and obesity in mice, demonstrating the translational potential of pharmacologically engaging this pathway for the treatment of metabolic disease. Extending beyond this work, we have begun to solve additional pieces of the biochemical puzzle of taurine acetylation by identifying a taurine acetylase, an N-acetyltaurine transporter, and additional nutrient-derived metabolites controlled by PTER. Together, these studies define a new pathway of secondary taurine metabolism and reveal a nutrient-metabolite signaling axis that regulates energy balance, obesity, and metabolic health.



Rachel Turn, PhD

Rachel Turn, PhD, joined UW Madison School of Veterinary Medicine as an assistant professor in the Comparative Biosciences Department in July 2026. She recently completed her postdoctoral fellowship with Dr. Peter Jackson at Stanford University, studying the mechanisms underlying transient signaling events in key biological and physiological contexts. She received her PhD in Biochemistry, Cell, and Developmental Biology from Emory University with Dr. Richard Kahn and her BA in Biology from Harriet L. Wilkes Honors College of Florida Atlantic University. Dr. Turn's research investigates the mechanisms by which cells interpret and

integrate environmental cues to drive cell type and tissue-specific responses, spanning contexts from primary ciliary signaling to stem cell differentiation. She developed Synchronized Temporal-spatial Analysis via Microscopy and Proteomics (STAMP), an innovative approach that unites time-resolved imaging and mass spectrometry data in homogeneous tissue culture systems to interrogate novel, critical transient changes missed by other approaches. She established time-resolved mass spectrometry methods in functionally homogeneous cell populations, distinguishing molecular dynamics intrinsic to a defined cellular function from confounding heterogeneity, thereby revealing underlying regulatory mechanisms. This platform has yielded several recent publications and provides the foundation for her independent research program, centered on defining universal versus fate-specific molecular determinants licensing cell-cycle exit and lineage commitment. Her work has been recognized both nationally and internationally, and she is currently supported by the NIH Pathway to Independence Award (K99/R00). Beyond her research, Dr. Turn is committed to service and mentorship both in her local and global research community. She serves on the MBoC Early Career Editorial Board and has chaired sessions and workshops through US HUPO, ASCB, FASEB Cilia, and Small GTPase symposia. She is also dedicated to training the next generation of scientists, including through outreach with the Science Small Groups program, mentoring community college students transitioning into STEM careers.

Time-Resolved Proteomics Maps Stepwise Primary Cilia Assembly and GPCR Trafficking

Primary cilia are critical cellular antennae that form in most quiescent, human cells. Housing a subset of tissue-specific membrane-bound receptors including GPCRs, these organelles face the extracellular space to sense diverse environmental cues (e.g., metabolites, morphogens, neurotransmitters). When disrupted, severe pathologies arise, including developmental disorders, diabetes, Parkinson's disease, and cancers. Studying mechanisms driving primary cilia signaling in health versus disease comes with challenges. Because primary cilia are miniscule (only 1/10,000th total cell volume), the proteins and associated post-translational modifications (PTMs) that regulate them are low copy number. Furthermore, signals coordinating primary cilia function are transient and context-specific. Finally, because primary cilia are typically studied in heterogeneous cell populations forming primary cilia at different times, it is difficult to deconvolve molecular mechanisms regulating ciliary signaling in time and space. Therefore, we developed Synchronized Temporal-spatial Analysis via Microscopy and Proteomics (STAMP), a platform that integrates time-resolved proteomics and imaging to capture dynamic signals driving ciliary function. Here, we focus on key mechanisms governing GPCR entry and exit from primary cilia. We employed G₀-synchronized STAMP in retinal pigment epithelial cells to track the temporal-spatial proteomic and phosphoproteomic landscape of GPCR entry in newly-formed primary cilia as cells transition into G₀, resolving stage-specific recruitment and regulation with live and fixed cell imaging. Furthermore, we employed time-resolved temperature block-STAMP to synchronize ciliary GPCR entry and exit in fully-formed cilia and track intermediate steps via microscopy. Using membrane AP-MS coupled with AlphaFold and a Structure Based Prediction Omics Classifier (SPOC), we captured step-wise intermediates reflecting transient mechanisms governing ciliary GPCR traffic. Together, these data establish a temporally-resolved proteomic framework for ciliary signaling, revealing novel intermediate steps governing GPCR traffic in forming and fully-formed cilia. This work highlights the power of integrating synchronization strategies with mass spectrometry to resolve rapid, spatially-restricted signaling events in diverse biological contexts.

Shashank Jain, MS, PhD,

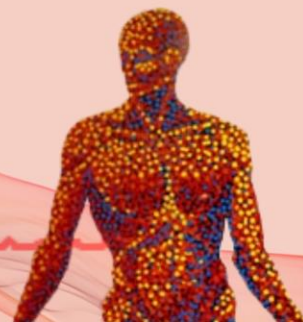
XMRT Business Development Manager, America, Waters Corporation



Shashank Jain is the Business Development Manager for Xevo™ MRT at Waters Corporation, supporting the strategic adoption of next-generation Xevo MRT high-resolution mass spectrometry platform across Americas. He has over 10 years of experience in analytical instrumentation, spanning field service, product specialization, and strategic sales in mass spectrometry. Shashank holds a Ph.D. in Analytical Chemistry from the University of Vermont where he focused on building TOF mass spec for atmospheric aerosol research and M.S. in Analytical Chemistry from Western Michigan University.

Title: Enabling deep proteome coverage at ultra-high throughput using stepped-quadrupole DIA on a novel MRT benchtop MS

Evaluating complex proteomes requires acquisition strategies that maintain high selectivity, quantitative robustness, and consistent performance across wide dynamic ranges. Stepped-quadrupole DIA enhances precursor isolation efficiency and reduces spectral interference, supporting higher-confidence peptide and protein identification in challenging matrices. To further improve analytical depth, a new benchtop mass spectrometer incorporating advanced MRT technology provides a 20-fold increase in MS/MS sensitivity relative to previous iterations of the technology. Leveraging this enhanced sensitivity, we assess overall workflow performance through ultrafast chromatographic gradients, protein identification depth, and quantitation accuracy in mixed-proteome benchmarks. Together, these evaluations establish the capability of combining stepped-quadrupole DIA with next-generation MRT instrumentation to deliver deeper, faster, and more reliable analysis of highly complex proteomes. Tryptic digests of a K562 human kidney cell line were analyzed using stepped-quadrupole DIA on a novel benchtop MRT mass spectrometer. To assess sensitivity and identification depth, a loading series (5, 50, 100, 250, and 500 ng on-column) was evaluated, with replicate injections acquired at each loading. High-throughput performance was tested using the Evosep™ Eno configuration operating up to 500 samples per day (SPD) with a cycle time of 2.9 minutes. Quantitative accuracy was assessed using a defined mixed-proteome benchmark comprising human, yeast, and E. coli components at controlled ratios. Qualitative and quantitative data were processed using DIA-NN and PEAKS® Studio. Additional review was conducted with Skyline.



Career Workshop Panelists

Emma Guiberson, PhD



Emma is starting her third year as an Assistant Professor at Middlebury College after completing her PhD at Vanderbilt University in 2022 and a postdoctoral fellowship at Stanford University. Her dual interest in research on the analytical chemistry/microbiology interface, and the education of the next generation of chemists led her to pursue a career at a small liberal arts college. She is passionate about science education and communication, as well as undergraduate research that benefits both students and human health. She is excited to share more about the PUI academic experience, navigating the job market, and what a career balanced in teaching and research looks like during the 2026 HPP Symposium Career Panel.

Che-Fan (Jeffrey) Huang, PhD



Dr. Che-Fan (Jeffrey) Huang is an Assistant Professor of Chemistry at Texas A&M University. His research develops top-down proteomics and mass spectrometry approaches to define proteoforms as functional molecular units, with applications in biomarker discovery and the study of human disease and cellular signaling. He earned his Ph.D. at Northwestern University (2021), where he combined surface engineering and MALDI mass spectrometry to investigate phosphatase biology, and completed postdoctoral training in top-down proteomics at Northwestern's Proteomics Center of Excellence (2026). Originally from Taiwan, Dr. Huang received his B.S. and M.S. from National Taiwan University, where his interest in proteomics began.

Lisa Jenkins, PhD



Dr. Lisa Jenkins is currently a Senior Associate Scientist at the Center for Cancer Research, National Cancer Institute. An alumnus of the University of Georgia, Dr. Jenkins currently heads the CCR Mass Spectrometry Resource where she leads a team collaborating with NCI investigators to advance cancer research. She also helps train and mentor young scientists in protein chemistry and mass spectrometry approaches. She looks forward to sharing her experience working at the National Institutes of Health, as well as any other insights she can offer.

M. Violet Lee, PhD



Dr. M. Violet Lee is a Senior Principal Scientist at Genentech, a Member of the Roche Group. She earned her M.S. in Chemistry from the University of Illinois at Urbana-Champaign, where she studied ribosomally and non-ribosomally synthesized natural products. She went on to obtain her Ph.D. in Chemistry from the University of Wisconsin-Madison (2011), employing a systems biology approach that combined quantitative proteomics and transcriptomics to study osmotic stress. In 2013, Dr. Lee joined the BioAnalytical Sciences Department at Genentech. Her group is responsible for developing and implementing immunoaffinity mass spectrometry-based PK assays, characterizing ADC ADME, quantifying associated catabolites, and assessing the potential immunogenicity of biotherapeutics. Her work supports projects ranging from late-stage research through the clinical development of ADCs and novel large molecule modalities. Dr. Lee is deeply passionate about workplace mentorship. She has dedicated much of her career to fostering talent and guiding emerging professionals in the pharma and biotech space. As an alumnus of UW-Madison, she looks forward to sharing her insights on supporting the growth and development of early-in-career scientists during the 2026 HPP Symposium Career Panel.

Jennifer Lofland, PhD, PharmD, MPH



Jennifer H. Lofland is currently a Senior Medical Director at Incyte. An alumnus of Johns Hopkins University (2004), Jennifer has dedicated much of her career to helping to improve the lives of individuals with immunological diseases. She considers herself a life-long learner and looks forward to sharing her insights on career transitions from academia to industry and how to maintain work-life balance during the 2026 HPP Symposium Career Panel.

Corinne Lutomski, PhD



Corinne Lutomski is currently a Senior Research Associate at the University of Oxford and incoming Assistant Professor at the University of California, San Francisco. An alumnus of Indiana University, 2019, Corinne has dedicated much of her career to fostering talent and guiding emerging professionals in academia. She is deeply passionate about workplace mentorship and looks forward to sharing her insights on navigating career transitions post-PhD, and perseverance in science during the 2026 HPP Symposium Career Panel.

Morgan Mann, PhD, DABCC



Morgan Mann is currently the Assistant Director of Newborn Screening at the Wisconsin State Laboratory of Hygiene, and an Assistant Professor (CHS) in the Department of Pediatrics at the University of Wisconsin – Madison. Morgan earned his Ph.D. at UW – Madison prior to completing a Clinical Chemistry Fellowship at Stanford University and the University of California San Francisco. His professional interests involve the use of high-resolution mass spectrometry and other innovative technologies to streamline medical diagnostics and address emerging challenges to our healthcare systems.

Savannah Snyder, PhD



Savannah Snyder is currently a Technical Sales Manager at Bruker Biosystems managing the Central US Sales Team. She is an alumna of The Chrys Wesdemiotis Lab at The University of Akron, graduating the Summer of 2020. Savannah has dedicated much of her career to fostering talent and guiding emerging professionals in the analytical chemistry space. She is deeply passionate about workplace mentorship and looks forward to sharing her insights on moving from Academia to Industry, career steppingstones, and work travel during the 2026 HPP Symposium Career Panel.

This career panel brings together professionals from diverse sectors to share the unique experiences and insights that shaped their paths. Designed to spark career discovery, the session offers attendees a firsthand look at the wide variety of roles and opportunities available after higher level -omics training. Following the career discussion, an interactive Q&A and networking segment will allow participants to connect directly with panelists and build valuable professional relationships.

Rising Star Finalists

Fanny Caroline Liu, Florida State University

Benjamin Minkoff, University of Wisconsin–Madison

John Shuster, University of Wisconsin–Madison

Angel Ibarra, University of Wisconsin–Madison

Claire Boos, University of Wisconsin–Madison

Hsin-Ju (Ruby) Chan, University of Wisconsin–Madison

Margaret Robinson, University of Wisconsin–Madison

Vu Ngoc Huong Tran, University of Wisconsin–Madison

Jiahao Zhang, University of Wisconsin–Madison

Andrew Perciaccante, University of Wisconsin–Madison

Honorable Mention

Him Shrestha, St. Jude Children's Research Hospital

Jenifer Qin, University of Wisconsin–Madison

Riley Rowland, University of Wisconsin–Madison

Austin Stram, University of Wisconsin–Madison

Alexander Nassar, University of Wisconsin–Madison

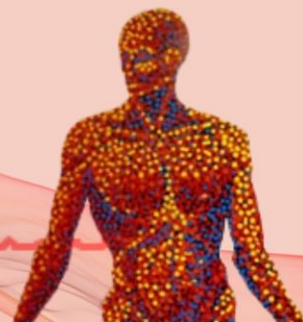
Zhimin Ma, University of Wisconsin–Madison

Bella Clemmer, University of Wisconsin–Madison

Matthew Fischer, University of Wisconsin–Madison

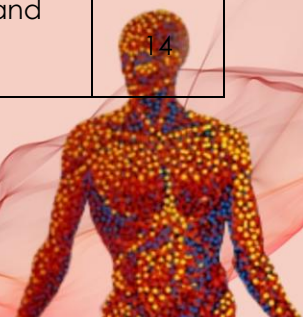
Anna Grace Towler, University of Wisconsin–Madison

Carstyn Joiner, University of Wisconsin–Madison

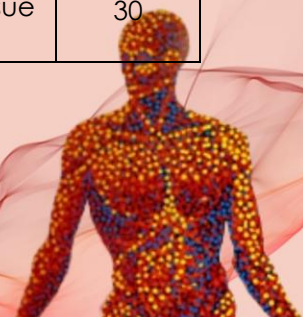


SUMMARY OF POSTER SESSION ABSTRACTS (Listed alphabetically by last name)

Last Name	First Name	Institution	Title	Poster #
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Bukhman	Yury	University of Wisconsin - Madison	Comparative Analysis of Human and Mouse Eosinophil Proteomes	2
Chen	Li-Yu	University of Wisconsin - Madison	Single-shot Multi-omic Analysis with an Intelligent Ion Source and Micropillar Array Columns	3
Clemmer	Bella	University of Wisconsin - Madison	High-Sensitivity Top-Down Proteomics of Phospholamban Proteoforms from Biopsy-Equivalent Cardiac Tissue	4
Del Mundo	Zachary	University of Wisconsin - Madison	Accessible IMAC Strategies for Discovery of Endogenous Phosphorylated Neuropeptides in Crustacean Neural Tissues and Hemolymph	5
Du	Joanne	University of Wisconsin - Madison	Rapid complexomics with native gel-mass spectrometry	6
Fischer	Matthew	University of Wisconsin - Madison	Deep Proteoform Mapping in Human Heart Enabled by Top-Down Proteomics with Online Multidimensional Liquid Chromatography and Machine Learning	7
Gao	Zhan	University of Wisconsin - Madison	A Reference Compendium of Human Cardiac Histone Proteoforms	8
Guiráo	Thauany Nantes	University of São Paulo/ University of Wisconsin - Madison	Leptin in Patients with Acute Leukemia: Associations with Body Composition and Systemic Inflammation	9
Hansell	Andrew	Beckman Institute for Advanced Science and Technology	A Bottom-Up Proteomics Workflow for Characterizing Exercise-Associated Changes in the Extracellular Vesicle Proteome During Aging	10
Huang	Kaichen (Zane)	University of Wisconsin - Madison	Comparative Proteomic Analysis of Keratinocytes Expressing Individual Human Versus Mouse Papillomavirus Oncogenes	11
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Johnson	Emily	University of Wisconsin - Madison	Global Profiling of Deamidation Susceptibility and Isoaspartate Formation via PIMT-Mediated Labeling	13
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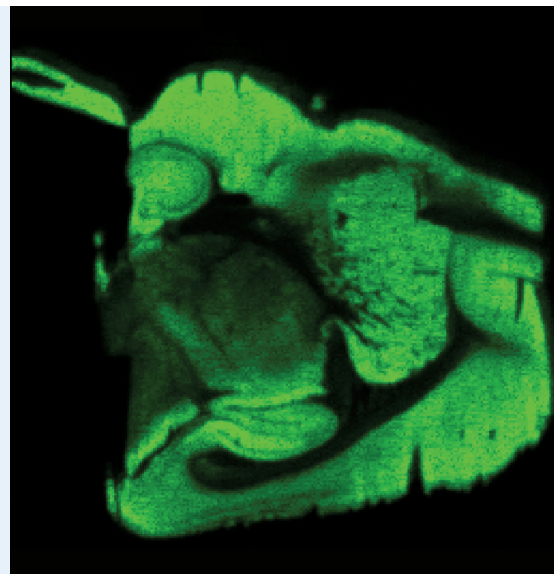
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Acknowledgements

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School of Medicine and Public Health Human Proteomics Program



The UW SMPH Human Proteomics Program (HPP), established in 2006 through support from the SMPH Wisconsin Partnership Program, is dedicated to addressing the needs of researchers and clinicians at UW-Madison in the rapidly growing field of proteomics and metabolomics. Proteomics and metabolomics enable researchers to obtain real-time information on a person's physiological status leading to an in-depth understanding of the causes of diseases, which has great potential for precision medicine.



Mission

The overall mission of the University of Wisconsin-Madison Human Proteomics Program is to develop cutting-edge technologies in proteomics and metabolomics for basic/translational/clinical research to improve the health of the citizens of Wisconsin, the nation, and the world through a program of research collaboration and education.

Goals

Provide advanced proteomic and metabolomic capabilities featuring state-of-the-art, ultra-high resolution mass spectrometry, top-down proteomics, native mass spectrometry, and multi-omics.

Provide new opportunities to catalyze basic, translational, and clinical research collaborations for understanding the basis of human health and diseases, discovering novel biomarkers for diagnosis, and identifying new molecular targets for treatment of human diseases.

Establish educational programs to inform investigators and the public about proteomics and metabolomics, and its potential use for biomedical research and public health. Provide hands-on training to users in proteomics and metabolomics.

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