

### Parabola of Neon (1913)

Featured on the cover is an early 20th century parabola mass spectrograph. The early mass spectrometers, pioneered by J. J. Thomson, used electric and magnetic fields to disperse ion populations on photographic plates. Depending on their masses, the ions were dispersed along parabolic lines with those of the highest energy landing in the center and those with the least extending to the outermost edges. Positive ions are imaged on the upper half of the parabola while negative ions are deflected to the bottom half. Note that Ne produces two lines in the spectrum. Francis Aston, a former Thomson student, concluded from these data that stable elements also must have isotopes. These observations won Aston the Nobel Prize in Chemistry in 1922.

Grayson, M.A. <u>Measuring Mass: From Positive Rays to Proteins.</u> **2002**. Chemical Heritage Press, Philadelphia.

# Welcome to the 2nd Annual North American Mass Spectrometry Summer School

We are proud to assemble world-leading experts in mass spectrometry for this second annual mass spectrometry summer school. We aim for you to experience an engaging and inspiring program covering the fundamentals of mass spectrometry and how to apply this tool to study biology. Also infused in the course are several workshops aimed to promote professional development. We encourage you to actively engage in discussion during all lectures, workshops, and events.

This summer school is made possible through generous funding from the National Science Foundation (Plant Genome Research Program, Grant No. 1546742), the National Institutes of Health National Center for Quantitative Biology of Complex Systems (P41 GM108538), and the Morgridge Institute for Research. We thank Promega and Thermo Fisher Scientific for sponsoring refreshments.

### **Organized by:**



Joshua Coon



Evgenia Shishkova



Laura Van Toll

### **Sponsored by:**













### **Traveling to meeting venue**

#### **TAXI SERVICE**

The city of Madison has taxi services.

Green cab: 608-255-1234 Union cab: 608-242-2000 RIDESHARE SERVICES

Lyft and Uber operate in Madison.

### Registration

Registration will start at 5:30 pm on July 21. The registration table will be located on the rooftop of the Pyle Center (702 Langdon Street, Madison, WI). Registration will also continue on Monday morning starting at 8:00 am outside of the H.F. DeLuca Forum on the 1st floor of the Discovery Building (330 N Orchard Street, Madison, WI).

### **Meeting Sessions and Location**

Most meeting sessions will take place in or around the H.F. DeLuca Forum located on the 1st floor of the Discovery Building. Workshops sessions will also take place in the Orchard Room on the 3rd floor.

### **Badges**

For catering purposes, please make sure that you wear your conference badges throughout the conference. Replacement badges are available at the registration desk.

### **Speakers**

Presenters are reminded to be in the H.F. DeLuca Forum no later than 15 minutes before the start of the session to preload presentation. An A/V specialist will be available to assist with the transition.

#### **Poster Sessions**

Posters should be created to fit on a 4ft x 4ft poster board. Poster sessions will take place in the Main Court. Posters should be hung Monday, July 22nd from 8:00 to 8:30 am. Poster should remain hung until end of Tuesday.

### Poster Session 1

Odd-Numbered Posters Monday, July 21 5:00-6:00 pm

### **Poster Session 2**

Even-Numbered Posters Monday, July 21 6:00-7:00 pm

#### **Twitter**

### #MassSpecMadison2019

Please use this #Hashtag when tweeting about the conference.

#### YouTube

#### **NCQBCS**

Subscribe to our YouTube channel to view the presentations after the meeting.

#### Wi-Fi

Go to **Settings** and select: **Discovery-Guest** or **Towncenter** 

Open a browser - Enter the following address in the search bar:

http://discovery.wisc.edu

You will be redirected to a wireless authentication page - Scroll to the bottom of the page and click **Accept**.

NOTE: Summer School presentations will be video recorded and made available to the participants about a week after the program ends. By participating in the program you consent to possible inclusion in conference photographs and videos.

# MAP 1st Floor, Discovery Building

### N. Orchard Street 韋



## MAP Campus

Discovery Building
330 N. Orchard Street

Madison, WI 53715

🖒 Pyle Center

702 Langdon Street Madison, WI 53706

Parking Ramps

State Street

Memorial Union Terrace

800 Langdon Street Madison, WI 53706

Union South

1308 W. Dayton Street Madison, WI 53715

HotelRed
1501 Monroe Street
Madison, WI 53711

Lowell Center Inn
610 Langdon Street

Graduate Madison 601 Langdon Street Madison, WI 53703

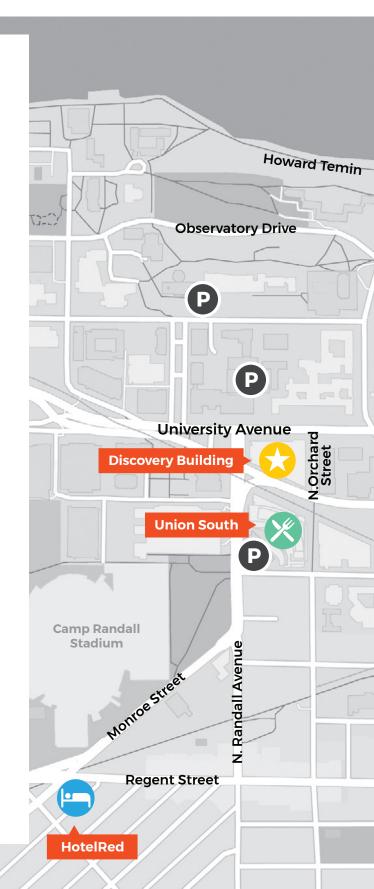
Madison, WI 53703

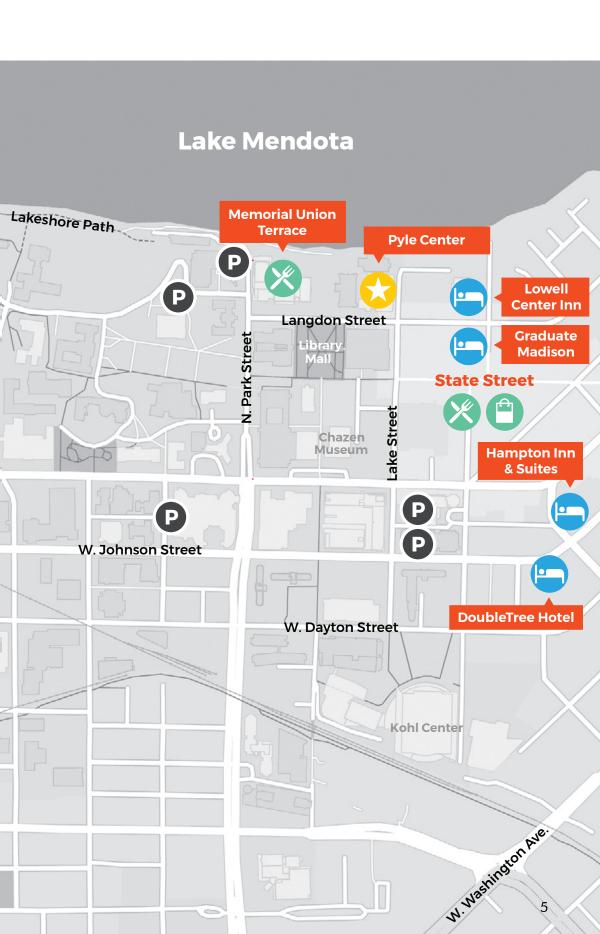
Hampton Inn & Suites Madison/Downtown

> 440 W. Johnson Street Madison, WI 53703

Doubletree Hotel
525 W. Johnson Street

525 W. Johnson Stree Madison, WI 53703





# **Refreshment Sponsor**



### **Promega**

Promega offers a wide range of products to accelerate your mass spectrometry research. From reagents to reference standards and cellular lysates, our tools allow you to monitor LC and mass spectrometer performance with ease. Our line of proteases and surfactants ensure the most straightforward and robust sample preparation for you every demand.



https://www.promega.com/products/mass-spectrometry/



### **Thermo Fisher Scientific**

Leverage the power of mass spectrometry. Thermo Scientific high resolution mass spectrometry systems take discovery and sample analysis to new heights. We offer easy, high-throughput, quantitative workflows for proteins, drug metabolites, pesticides and many other applications. Whether you are detecting disease biomarkers or performing forensic analysis, our mass spectrometers give you the resolution, accuracy, sensitivity, throughput that you need to advance your science. Browse our complete portfolio below, or let one of our experts help you tailor a selection specific to your application and workflow needs.



https://www.thermofisher.com/us/en/ home/industrial/mass-spectrometry.html

# 2019 Conference Agenda

Activity held in the DeLuca Forum, Discovery Building

# DAY 1 | Sunday, July 21

TIME	ACTIVITY	INSTRUCTOR
5:30-7:00 pm	Registration* Welcome* * Location: Rooftop of the Pyle Center	Josh Coon
Promega	Welcome Reception with Cocktails and Hors d'oeuvres, sponsored by <b>Promega</b>	

### DAY 2 | Monday, July 22

TIME	ACTIVITY	INSTRUCTOR
8:00-8:30 am	Poster Setup and Registration	
	Coffee & Pastries	
8:30-9:45 am	Mass Analyzers	Michael Westphall
9:45-10:45 am	Interactive Mass Analyzer Demos*	Coon Group
	* Location: Atrium outside the Forum	
10:45-11:00 am	Break	
11:00-12:00 pm	Ionization	Evan Williams
12:00-1:00 pm	Lunch Buffet	
1:00-2:00 pm	Tandem MS	Josh Coon
2:00-3:00 pm	Separations	Evgenia Shishkova
3:00-3:15 pm	Break	
3:15-4:30 pm	Workshop, choice of either:	
	A. Negotiations	Charlie Trevor
	B. Intellectual Property*	Michael Falk
	* Location: Orchard Room, meet by regis	tration table
4:30-7:00 pm	Poster Session	

Thermo Fisher SCIENTIFIC

Poster Session with Cocktails and Hors d'oeuvres, sponsored by **Thermo Fisher Scientific** 

<sup>\*</sup> Activity held in a space other than the DeLuca Forum (Noted below)

# **DAY 3** Tuesday, July 23

TIME	ACTIVITY	INSTRUCTOR
8:00-8:30 am	Poster Setup Coffee & Pastries	
8:30-9:45 am	Acquisition Methods - DDA, DIA, and PRM	Jesse Meyer
9:45-10:00 am	Break	
10:00-10:45 am	Quantitative Proteomics	Lingjun Li
10:45-11:00 am	Break	B II I . I . I
11:00-2:00 pm	Spectral Interpretation	Beatrix Ueberheide and Josh Coon
	11:00 am Lecture 11:45 am Box Lunch and Worktime 1:15 pm Review and Discussion	
2:00-2:15 pm	Break	
2:15-4:30 pm	Workshop, choice of either:	
	A. Science Writing	Alicia Williams
	B. Science Illustrations*	Adam Steinberg
	* Location: Orchard Room, meet by registr	ration table
4:30-4:45 pm	Break and Poster Removal	
4:45-6:00 pm	Science Funding	Doug Sheeley

# DAY 4 | Wednesday, July 24

TIME	ACTIVITY	INSTRUCTOR
8:30-9:00 am	Coffee & Pastries	
9:00-10:15 am	PTMs	Judit Villen
10:15-10:30 am	Break	
10:30-11:45 am	Research Lecture	Ulrike Kusebauch
11:45-12:00 pm	Presentation of Poster Awards	
12:00 pm	Adjourn	

# **Instructors**

\* Alphabetized by last name



### **Joshua Coon**

Thomas and Margaret Pyle Chair at the Morgridge Institute for Research Professor, Biomolecular Chemistry and Chemistry University of Wisconsin, Madison

Hailing from a small town in central Michigan, Coon escaped from the cold to earn a Ph.D. at the University of Florida. He went on to conduct his postdoctoral studies with Don Hunt at the University of Virginia. During that time he, along with Hunt and John Syka, co-invented electron transfer dissociation. In 2005 he joined the faculty at Wisconsin to start his own program. Coon's research group aims to advance mass spectrometer technology to make proteome analysis faster and more accessible. Coon's research in these areas has been recognized by several awards including the Biemann Medal from the American Society for Mass Spectrometry and the Ken Standing Award from the University of Manitoba.



### **Michael Falk**

Chief Operating Officer and General Counsel Wisconsin Alumni Research Foundation University of Wisconsin-Madison

Michael Falk heads the intellectual property division of the Wisconsin Alumni Research Foundation, a supporting organization to the University of Wisconsin–Madison with more than \$2.7 billion under management. WARF manages, protects, and licenses intellectual property for the benefit of the university and was recently ranked 7th among the world's top Universities in number of U.S. issued patents. Mr. Falk completed his undergraduate degree at Columbia University and earned a J.D., M.B.A. and an M.S. in bacteriology from the University of Wisconsin–Madison. Previous to working at WARF Mr. Falk was a lawyer with Foley & Lardner.



### **Ulrike Kusebauch**

Senior Research Scientist Institute for Systems Biology

Dr. Kusebauch studied Pharmaceutical Chemistry and obtained her Ph.D. in Biochemistry at the Max Planck Institute of Biochemistry (Germany). For her postdoctoral work, she joined the group of Prof. Ruedi Aebersold where she contributed to the development of targeted proteomics by selected reaction monitoring (SRM). Dr. Kusebauch continued her research at Institute for Systems Biology in the group of Prof. Robert Moritz where she developed complete proteome SRM and SWATH mass spectrometry resources for human and other organisms and applies quantitative technologies to spatial and temporal proteome dynamics. For this work, Dr. Kusebauch received the 2018 HUPO Discovery in Proteomics Sciences Award that recognizes outstanding efforts and achievements of individuals in the field of proteomics.



### Lingjun Li

Charles Melbourne Johnson Distinguished Chair Vilas Distinguished Achievement Professor of Pharmaceutical Sciences and Chemistry University of Wisconsin-Madison Associate Editor, Journal of The American Society for Mass Spectrometry

Professor Li's lab has made seminal contributions in multiple areas of mass spectrometry including new chemical labeling strategies for quantitative proteomics, technologies for glycomics, microscale separations, in vivo microdialysis and imaging MS for the functional discovery of neuropeptides and protein biomarkers in neurodegenerative diseases. Her work has more than appeared in 250 peer-reviewed research papers and she has delivered more than 200 invited lectures. Finally, her work has been recognized with numerous awards, including the ASMS Research Award, NSF CAREER Award, Sloan Fellowship, PittCon Achievement Award, and ASMS Biemann Medal. She was named one of the Top 50 most influential women in the analytical sciences.



### **Jesse Meyer**

NIH Postdoctoral Fellow University of Wisconsin-Madison

Dr. Meyer received his Bachelor of Science degree in Chemistry and Biochemistry from the University of Minnesota–Twin Cities. He was fortunate to engage in undergraduate research with a new assistant professor who taught him about protein structure, mass spectrometry, and metabolomics. Meyer completed his Ph.D. studies at the University of California in San Diego where he developed the first method to detect endogenous SUMOylation sites in human proteins. After graduation, he began a 3-year postdoctoral study of metabolism, aging, and Sirtuins. In the summer of 2018, Dr. Meyer joined the Coon Lab for the further postdoctoral study where his focus is on the prediction of biological responses using multi-omic data and artificial intelligence.



### **Douglas M. Sheeley**

Deputy Director National Institute of Dental and Craniofacial Research National Institutes of Health

Dr. Sheeley joined NIDCR in October 2017, after having served as a senior scientific officer and acting chief of the Biomedical Technology Branch at NIH's National Institute of General Medical Sciences (NIGMS). During his time with NIGMS Dr. Sheeley led programs to develop and expand access to new tools for a wide range of areas including proteomics, carbohydrate research, and modeling of infectious disease dynamics. Prior to NIGMS, Dr. Sheeley worked for 11 years at NIH's National Center for Research Resources, where he served in several leadership positions, including senior scientific officer, acting deputy director of the Division of Biomedical Technology and acting director of the Office of Extramural Activities. As an expert in biomedical mass spectrometry and structural analysis of both proteins and carbohydrates, Dr. Sheeley regularly contributes his knowledge as an advisor and instructor at NIH and beyond, including an annual course for the American Society for Mass Spectrometry since 2001.



### **Evgenia Shishkova**

Assistant Scientist
University of Wisconsin-Madison

Dr. Shishkova received her Ph.D. in Biochemistry from the University of Wisconsin–Madison working with Professor Coon. Her graduate research focused on the interplay between the quality of chromatographic separations and acquisition rates of the mass spectrometer and ways to improve the depth of shotgun proteomic analyses by leveraging this knowledge. She currently works as a research scientist at the National Center for Quantitative Biology of Complex Systems (NCQBCS), where she continues her investigations of quantitative proteomics, high-throughput multi-omic technologies, and functional characterization of biomolecules. In the past, she delivered tutorial lectures on peptide separations at the 1st North American Summer School and on PTM analysis at the 3rd EuPA Proteomics Summer School.



### **H. Adam Steinberg**

Artist/Scientist ArtForScience.com

H. Adam Steinberg visualizes scientific data and teaches scientific communication. Previously for twenty years he was the staff Artist/Scientist at UW-Madison's Department of Biochemistry. Over the last 30 years he has worked on many thousands of research articles, reviews, covers, grants, pitch decks, posters, textbooks, and scientific presentations for researchers, startups, and pharmaceutical companies. Adam enjoys teaching researchers to effectively communicate their science and on how to visualize their data. He also spends considerable time mentoring and teaching students at local K-12 schools.



### **Charlie Trevor**

Pyle Bascom Professor in Business Leadership Chair, Department of Management & Human Resources University of Wisconsin-Madison

Professor Trevor earned his Ph.D. in Industrial and Labor Relations from Cornell University in 1998. He is an expert on negotiations, employee compensation, research methods, statistics, and Human Resource systems. His research focuses on employee turnover, particularly of the employees that companies can least afford to lose, the determinants and consequences of employee compensation, and employee downsizing. Professor Trevor's research on downsizing and turnover rates at 200 companies was awarded the 2009 Scholarly Achievement Award for the best article of the year from the Human Resources Division of the Academy of Management.



### **Beatrix Ueberheide**

Assistant Professor of Biochemistry and Molecular Pharmacology Director Proteomics Laboratory New York University Langone Health

Professor Ueberheide received her Ph.D. in biological mass spectrometry from the University of Virginia with Professor Don Hunt. At Virginia she pioneered new MS technology to characterize histone modifications. Next she joined the lab of Dr. Brian Chait at Rockefeller University for postdoctoral studies. There she developed strategies for high throughout sequencing of bioactive peptides and characterization of patient isolated circulating antibodies from HIV infected individuals. Professor Ueberheide joined the faculty of NYU to build a state-of-the-art Proteomics Laboratory. Her lab is focused on performing large-scale quantitative proteomics, phosphoproteomics, absolute quantitation of proteins and protein complexes, as well as developing tools for higher order structure analysis.



**Judit Villen** 

Associate Professor of Genome Sciences University of Washington

Professor Villen earned her Ph.D. in Chemistry from the University of Barcelona and followed that with postdoctoral studies with Steve Gygi at Harvard Medical School. Her research has pioneered and accelerated technology developments for the robust characterization of thousands of phosphorylation sites and enabled mainstream applications in biomedical research. Her group leverages these technologies to answer fundamental questions in cell biology and disease. Professor Villen's research has been recognized by awards from both the American Society for Mass Spectrometry and the US Human Proteome Organization, among others.



### **Mike Westphall**

Distinguished Instrument Innovator University of Wisconsin-Madison

"Measurement forms the foundation of the scientific method. Scientific theory may be validated through accurate measurement of physical and biological phenomenon; however, it is not possible to measure everything which theory predicts." This limitation has always motivated Dr. Westphall's research and has led to a lifelong career pursuing new techniques and instruments to perform measurements which currently cannot be made. This interest guided the selection of his first job after obtaining a bachelor's degree in Physics, where he developed instruments to measure color. It further influenced his choice of disciplines in graduate school. He received a Ph.D. in astrophysics, not because of an interest in astrophysics, but because of the difficulty in making the desired measurements and lack of instrumentation to do so. His career at the University of Wisconsin has been guided by the same principle; his current research focuses on the development of techniques and instrumentation for measurements in biotechnology.



### **Alicia Williams**

Henry Rutgers Postdoctoral Lecturer Rutgers University

Dr. Williams holds a Ph.D. in English literature from Rutgers University. In addition to teaching graduate student writers across the disciplines, she studies nineteenth-century British fiction and the history of reading. Her work has appeared in Victorian Poetry and NOVEL: A Forum on Fiction—literary equivalents of JASMS and Nature Methods. She was once in-house editor and writing mentor at the Coon lab, for which she now works on a freelance basis.



### **Evan Williams**

Professor of Chemistry and Biophysics University of California at Berkeley

Professor Williams obtained his Ph.D. at Cornell University with mass spectrometry pioneer Fred McLafferty. In 1992, after a postdoctoral fellowship at Stanford University, he joined the faculty at the University of California at Berkeley. His research group develops and applies novel instrumental and computational techniques in mass spectrometry, tandem mass spectrometry, separations, chemical imaging and laser spectroscopy for improved molecular structure elucidation. He also uses these methods to solve problems of fundamental as well as practical interest in chemistry and biophysics. Professor Williams has received numerous honors for his groundbreaking research including the American Chemical Society Frank H. Field and Joe L. Franklin Award for Outstanding Achievement in Mass Spectrometry, the Royal Society of Chemistry Theophilus Redwood Award in Analytical Chemistry, and the American Society for Mass Spectrometry Ron Hites Award, among others.

# 2019 **Poster Guide**

Monday, July 21 | 5:00-6:00 pm

### Poster Session 1

**Odd-Numbered Posters** 

**Poster Session 2** 

**Even-Numbered Posters** Monday, July 21 | 6:00-7:00 pm

\* Poster Abstracts, Alphabetized by last name

POSTER #	POSTER PRESENTATION
1	Enzymatic Labeling of Oligonucleotides for Multiplexed LC-MS/MS Scott Abernathy   University of Cincinnati, Cincinnati, OH, United States
2	Proteome and Phosphoproteome Analysis of Rice Panicle in Response to Heat Stress  Dalal Alonazy   Florida Agricultural and Mechanical University, Tallahassee, FL, United States
3	The Effects of Microbial Volatiles in an Organotypic Lung Model Yasmín Álvarez García   University of Wisconsin-Madison, Madison, WI, United States
4	Bulk lipidomics approach for characterization of Ebola virus protein expressed-cells: investigation of a novel and potential target to break Ebola virus replication cycle Souad Amiar   Purdue University, West Lafayette, IN, United States
5	Cancer Pharmacology Lab, A UW Madison core facility Shannon Andrews   UW-Madison Carbone Cancer Center, Madison, WI, United States
6	A Label-free Quantification Approach to Identify Differentially Expressed Proteins between Wild Type and Transgenic Alzheimer Rat Brains Pritha Bagchi   Emory University, Atlanta, GA, United States
7	O-Acylated Trehalose Probes for Proteomic Profiling of the O-Mycoloylation Post-Translational Modification in Corynebacterineae  Nicholas Banahene   Central Michigan University, Mount Pleasant, MI, United States

POSTER #	POSTER PRESENTATION
8	Exploiting activity-based probes to facilitate the discovery of novel deubiquitinase (DUB) inhibitors  Joao Banha Oliveira   Ubiquigent Ltd., Dundee, Scotland, United Kingdom
9	Changes in membrane protein complexes in the absence of PBRM1  Aida Barreiro Alonso   Institute of Cancer Research, London, England, United Kingdom
10	Using CFRAPS: a cell free antigen processing system to elucidate the generation of immunodominant peptides  Tynan Becker   University of Alaska-Fairbanks, Fairbanks, AK, United States
11	Proteome-wide identification of human protein-metal interactome Christian Beusch   Karolinska Institutet, Solna, Stockholm, Sweden
12	Development of Clickable Photoaffinity Probes to Identify Outer Membrane Proteins in Mycobacteria Kyle Biegas   Central Michigan University, Mt. Pleasant, MI, United States
13	Unbiased Proteomics and Network Propagation Reveals Cancer Drug Targets Mehdi Bouhaddou   University of California-San Francisco, San Francisco, CA, United States
14	Characterizing and Targeting the Hypoxic T Cell Surfaceome to Promote Immune Function in Cancer James Byrnes   University of California-San Francisco, San Francisco, CA, United States
15	Roles of the Sortilin K269E mutation in systemic glucose and lipid homeostasis Nicolas Calo   University of Wisconsin-Madison, Madison, WI, United States
16	Multiscale Approach Provides a New Axis for Single Organelle Peptidomics and Transcriptomics Dan Castro   University of Illinois-Urbana Champaign, Champaign, IL, United States
17	Novel UHPLC-MRM-MS approach allows for absolute quantification of Histone PTMs in as little as 20 minutes  Joseph Cesare   University of Pennsylvania-Philadelphia, Philadelphia, PA, United States

POSTER #	POSTER PRESENTATION
18	Proteomic Characterization of Young and Aged Murine Bones in Response to Mechanical Loading Christopher Chermside-Scabbo   Washington University-St. Louis, St. Louis, MO, United States
19	Generating multi-scale predictive networks of Northern Corn Leaf Blight resistance Natalie Clark   Iowa State University, Ames, IA, United States
20	Microwave-assisted acid hydrolysis for whole bone proteomics and paleoproteomics  Caitlin Colleary   Smithsonian Museum Conservation Institute, Washington DC, United States
21	Developing novel enrichment strategies to facilitate proteomic analysis of NR5A2 in triple negative breast cancer  Valentine Courouble   The Scripps Research Institute, Jupiter, FL, United States
22	Optochemical Control of Biological Processes Taylor Courtney   University of Pennsylvania-Pittsburgh, Pittsburgh, PA, United States
23	Inositol pyrophosphates and the cross-talk between lipids and phosphate sensing  Caitlin Cridland   Virginia Tech, Blacksburg, VA, United States
24	Investigating the role of Ptpn18 in regulating diet induced obesity Emily Cushing   University of Wisconsin-Madison, Madison, WI, United States
25	Quality Control for Biomarker Determination for the Early Diagnosis of Psoriatic Arthritis Li Dai   University of Utah-Salt Lake City, Salt Lake City, UT, United States
26	Investigating the mechanism of arginyltransferase enzyme 1 using mass spectrometry-based approaches Geoffrey Dann   University of Pennsylvania-Philadelphia, Philadelphia, PA, United States
27	Gas Chromatography-Combustion-Isotope Ratio Mass Spectrometry Analysis of the 13C-enrichment of Serum Retinol to Evaluate Efficacy and Effectiveness of Vitamin A Interventions Chris Davis   University of Wisconsin-Madison, Madison, WI, United States

POSTER #	POSTER PRESENTATION
28	"Lean" Mass Spectrometry: Using Kanbans to Uncover the Hidden Recording Capacity of Existing Laboratory Hardware Nicholas Del Grosso   Max Planck Institute of Biochemistry, Munich, Bavaria, Germany
29	Sarcoplasmic Proteome Changes in Response to Aging and Diet Kalina Dimova   Smith College, Northampton, MA, United States
30	Cysteine-selective middle-down proteomics with ultraviolet photodissociation analysis Sean Dunham   University of Texas-Austin, Austin, TX, United States
31	Large Scale EasyPepTM MS Sample Preparation for Phosphopeptide Enrichment Workflows  Amarjeet Flora   Thermo Fisher Scientific, Woodstock, IL, United States
32	Microbial metabolism of gamma-valerolactone Nathaniel Fortney   University of Wisconsin-Madison, Madison, WI, United States
33	From sand to soil: Microbial functional development across a chronosequence of irrigated fields in the desert of southern Peru  Erika Foster   Purdue University, West Lafayette, IN, United States
34	Exploiting activity-based probes to facilitate the discovery of novel deubiquitinase (DUB) inhibitors  Sheelagh Frame   Ubiquigent Ltd, Dundee, Scotland, United Kingdom
35	Novel Rabbit Monoclonal Antibodies for Profiling of Ser/Thr O-GlcNAc modified proteins Matthew Fry   Cell Signaling Technology, Beverly, MA, United States
36	The genomic basis for dysregulation of protein abundance in maize  Joseph Gage   USDA-ARS at Cornell University, Ithaca, NY, United States
37	Investigation of Urinary Metabolites as Potential Biomarkers for Prostate Cancer Detection Sanjeewa Gamagedara   University of Central Oklahoma, Edmond, OK, United States

POSTER #	POSTER PRESENTATION
38	Using the TFAM-FLAG mice to study mtDNA expression in vivo  Rodolfo García-Villegas   Karolinska Institutet, Stockholm, Sweden
39	Cancer Pharmacology Lab, A UW Madison core facility Heather Green   University of Wisconsin-Madison, Madison, WI, United States
40	Natural products and ultrastructural specifications of mycoheterotrophic plant, M.uniflora (ghost plant) Sara Hazinia   Iowa State University, Ames, IA, United States
41	Impact of Charge Sites on Fragmentation of Peptides and Proteins: Carbamylation and Guanidination Amanda Helms   University of Texas-Austin, Austin, TX, United States
42	Proteome-wide mistranslation uncovers proline residues important for protein stability and solubility  Kyle Hess   University of Washington-Seattle, Seattle, WA, United States
43	Proteomic Profiling of the Peritoneal Cavity in Aged Mice: Understanding Host Contributions to Metastatic Success in Ovarian Cancer Nicole Hudson   University of Notre Dame, Notre Dame, IN, United States
44	Chemical Proteomic Strategy Utilizing a Photoreactive Cleavable Chloroalkane Capture Tag for Target Discovery Robin Hurst   Promega Corporation, Madison, WI, United States
45	Proteomic analysis of extracellular matrix dynamics during mouse forelimb development  Kathryn Jacobson   Purdue University, West Lafayette, IN, United States
46	Decomposition of H+(GlyProAla): A Guided Ion Beam and Computational Study Roland Jones   University of Utah-Salt Lake City, Salt Lake City, UT, United States
47	Quantitative Proteomic Analysis of Cdc14 interactors in Candida albicans Using SILAC-based Mass Spectrometry Iliyana Kaneva   MRC London Institute of Medical Sciences, London, England, United Kingdom

POSTER #	POSTER PRESENTATION
48	Elucidating the phosphoproteome of a central regulator of intracellular survival during Listeria monocytogenes infection  Jess Kelliher   University of Wisconsin-Madison, Madison, WI, United States
49	Hyperspectral Raman Light Sheet Microscope for In Vivo Imaging of Leaf Metabolism Roxana Khoshravesh   University of New Mexico-Albuquerque, Albuquerque, NM, United States
50	Characterizing and Targeting the Surface Proteome of Hypoxic Pancreatic Cancer Lisa Kirkemo   University of California-San Francisco, San Francisco, CA, United States
51	The roles of SR-BI and CD36 in maintenance of macrophage cholesterol homeostasis  Darcy Knaack   Medical College of Wisconsin, Milwaukee, WI, United States
52	In Vitro Toxicity Assessment of Emitted Materials Collected during the Manufacture of Water Pipe Plastic Linings Lisa Kobos   Purdue University, West Lafayette, IN, United States
53	Proteome profiling of platelet disorders using mass spectrometry  Iris Kreft   Sanquin Research, Amsterdam, North Holland, The Netherlands
54	Mitochondrial proteome changes in mouse models of mitochondrial disorders  Laura Kremer   Karolinska Institutet, Stockholm, Sweden
55	Phenotype-guided ultrasensitive Proteomics for discovery of conserved injury mechanisms in podocytes and nephrocytes  Lucas Kühne   University of Cologne, Cologne, North Rhine-Westfalia, Germany
56	Influence of nitrogen supply and biorefinery fractionation on the proteome of green biomasses  Rasmus la Cour   University of Copenhagen, PLEN, Frederiksberg C, Capital Region, Denmark
57	Metabolic Perturbations Include Homocysteine Degradation and Polyamine Synthesis in Pathogenesis of Bronchopulmonary Dysplasia Daniel Lee   Indiana University School of Medicine, Indianapolis, IN, United States

POSTER #	POSTER PRESENTATION
58	A specific transmembrane domain-mediated dimerization is required for the receptor-like, plasmodesmata-located protein to regulate cell-to-cell movement in plants  Jung-Youn Lee   University of Delaware, Newark, DE, United States
59	Functional proteomics analysis of epiblast self-organization  Jianhua Li   Max Planck Institute for Molecular Biomedicine, Münster, North Rhine-Westphalia, Germany
60	Identifying redox modifications of the mitotic kinase Aurora A Dan Lim   Massachusetts Institute of Technology, Cambridge, MA, United States
61	Plasma Protein Changes Analysis in Colorectal Adenocarcinoma by Label-Free Quantitative Proteomics lasmim Lopes de Lima   Keizo Asami Immunopathology Lab, Recife, Pernambuco, Brazil
62	Development of a Mass Spectrometry Assay to Analyze the Ovarian Cancer Biomarker CA125 Sergio Madera   University of Notre Dame, Notre Dame, IN, United States
63	Isoform Specific Protein Interaction Mapping of BRD4-mediated Airway Inflammation via Immunoprecipitation Mass Spectrometry Morgan Mann   University of Wisconsin-Madison, Madison, WI, United States
64	Elucidating HAPLN1 Regulation and Processing in Multiple Myeloma Disease Progression Christina Mark   University of Wisconsin-Madison, Madison, WI, United States
65	Systems-level analysis of environmental perturbation in Zymomonas mobilis: Applications for biofuel production Julia Martien   University of Wisconsin-Madison, Madison, WI, United States
66	Dissecting the platelet proteome, reactome and secretome under inflammation: potential biomarkers and therapeutic applications  Patricia Martínez-Botía   University of Oviedo, Oviedo, Principality of Asturias, Spain
67	Proteomic Analysis of the Impact of Circadian Rhythm Disruption on Adipose and Muscle Tissue Mobilization in Periparturient Dairy Cows Conor McCabe   Purdue University, West Lafayette, IN, United States

POSTER #	POSTER PRESENTATION
68	Single Muscle Fiber Proteomics Enabled by High Sensitivity Top-Down Mass Spectrometry Jake Melby   University of Wisconsin-Madison, Madison, WI, United States
69	Cellular Senescence: A Novel Mechanism of Doxorubicin-induced Cardiotoxicity Giselle Melendez   Wake Health, Winston-Salem, NC, United States
70	TRIM28 as a candidate mutant p53 interacting partner in cancer cells  Mariel Mendoza   University of Pennsylvania-Philadelphia, Philadelphia, PA, United States
71	Protocol optimization for proteomic analysis of formalin fixed paraffin embedded clot analogs  Oana Madalina Mereuta   National University of Ireland Galway, Galway, Ireland
72	Shotgun proteome analysis of seminal plasma proteins differentiate boars by reproductive performance Kayla Mills   Purdue University, West Lafayette, IN, United States
73	Identifying disinfection byproducts in groundwater using ultrahigh-resolution mass spectrometry  Reid Milstead   University of Wisconsin-Madison, Madison, WI, United States
74	Top-down Proteomics for Deciphering Hypertrophic Cardiomyopathy in A Patient-Specific Engineered Cardiac Tissue Disease Model Stanford Mitchell   University of Wisconsin-Madison, Madison, WI, United States
75	Characterization of Ribonucleoprotein Assembly Defects in a Cellular Model of Spinal Muscular Atrophy Dmytro Morderer   Mayo Clinic, Jacksonville, FL, United States
76	Label-free quantification of phosphorylation changes in Chlamydomonas reinhardtii upon TORC1 inhibition Umarah Mubeen   Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany
77	Quantitative proteomics approach for identification of dopamine transporter interaction proteins using validated DAT-knockout rats

Carina Müller | University of Vienna, Vienna, Austria

POSTER #	POSTER PRESENTATION
78	Quantitative Proteomics in Xenopus tropicalis brains to study the functions of Autism Spectrum Disorder (ASD) risk genes  Snow Naing   University of California-San Francisco, San Francisco, CA, United States
79	Monitoring the human serum albumin adductome Lorena Ndreu   Stockholm University, Stockholm, Sweden
80	Construction of a signaling network phosphoproteome generated by M6P/IGF2R in a trophoblast cell model Francisco Olea   Universidad Nacional de Colombia, Bogota, Cundinamarca, Colombia
81	Non-HDL and Non-fasting Lipid Contributions to Foam Cell Formation Carleena Ortega   University of British Columbia, Vancouver, British Columbia, Canada
82	Analysis of nutritional components in edible parts of eastern redbud (Cercis canadensis L.)  Nancy Paiva   Southeastern Oklahoma State University, Durant, OK, United States
83	A novel bacterial uridyl-transferase is essential for bacterial cell wall homeostasis and virulence  Dan Pensinger   University of Wisconsin-Madison, Madison, WI, United States
84	Molecular characterization of the in vivo effects of the hemorrhagic metalloproteinase HF3: analysis of the proteome of mice muscle tissue  Eric Pereira   University of Sao Paulo and Butantan Institute, Sao Paulo, Brazil
85	Characterization of the mitochondrial CLPXP complex in Arabidopsis thaliana  Jakob Petereit   ARC Centre of Excellence in Plant Energy Biology, Crawley, Australia
86	Amino acid profiling of soybean roots infected by soybean cyst nematode reveals tight regulation of amino acid metabolism

Arati Poudel | University of Missouri-Columbia, Columbia, MO, United States

POSTER #	POSTER PRESENTATION
87	High-fructose diet alters proteins involved in glucose and cholesterol metabolism in the liver  Ellen Quillen   Wake Forest School of Medicine, Winston-Salem, NC, United States
88	Exploring EMAPII/STAT3 signaling axis in lung development and lung diseases  Dushani Ranasinghe   University of Notre Dame, Notre Dame, IN, United States
89	Novel mass spec compatible surfactant for in-solution protein mass spec sample preparation  Val Ressler   Promega Corporation, Madison, WI, United States
90	Clarifying the role of glucosinolates during abiotic stress in the Brassicaceae  Angela Ricono   University of Minnesota-Minneapolis, Minneapolis, MN, United States
91	Acute Ischemic Stroke Clot Project: Focus on a Proteomic Approach for Novel Biomarker Discovery Rosanna Rossi   National University of Ireland, Galway, Galway, Ireland
92	Functional selections to investigate the effects of amino acid substitutions across the proteome  Bianca Ruiz   University of Washington-Seattle, Seattle, WA, United States
93	Quantitative Mass Spectrometry-based Proteomics to decode rules of Targeted Protein Degradation Scott Rusin   Kymera Therapeutics, Cambridge, MA, United States
94	Analysis of protein dynamics in developing mouse using non-canonical amino acids labeling  Aya Saleh   Purdue University, West Lafayette, IN, United States
95	Improving Accuracy and Repeatability with Single Injection MS/Polyarc Split for Extractables and Leachables Tommy Saunders   Activated Research Company, Eden Prairie, MN, United States
96	Development of a Mass Spectrometry Assay to Analyze the Ovarian Cancer Biomarker CA125  Naviya Schuster-Little   University of Notre Dame, Notre Dame, IN, United States

POSTER #	POSTER PRESENTATION
97	Characterisation of function and regulation of chromatin remodelling complex subunit ARID1A and its role in oncogenesis Liudmila Shcherbakova   The Institute of Cancer Research, London, England, United Kingdom
98	Developing methods for the scalable monitoring and maturation of induced pluripotent stem cell-derived cardiomyocytes (iPSC-CMs) through 'omics' and systems biology  Aaron Simmons   University of Wisconsin-Madison, Madison, WI, United States
99	A proteomic insight into liver dysfunction and metabolism during obesity  Ben Stocks   University of Copenhagen, Copenhagen, Denmark
100	Examining the role of zinc on the proteome, growth and morphology of Klebsiella pneumoniae  Arjun Sukumaran   University of Guelph, Guelph, Ontario, Canada
101	Overexpression and Metabolic Regulation of Z. mobilis MEP Pathway Enzymes Mehmet Tatli   University of Wisconsin-Madison, Madison, WI, United States
102	A novel selective reaction monitoring mass spectrometry (SRM-MS) assay to monitor HIV protease activation in intact viruses  John Tilton   Case Western Reserve University, Cleveland, OH, United States
103	Use of Mass Spectrometry for Cancer Therapeutics Bhairavi (Vivi) Tolani   University of California-San Francisco, San Francisco, CA, United States
104	Ssu72-L84F Disrupts RNAPII Termination and Outlines Modules of CPF Jose Victorino   Indiana University School of Medicine, Indianapolis, IN, United States
105	PABPs regulate plant immunity through association with R-motifs Jinlong Wang   Duke University, Durham, NC, United States
106	Analytical Strategy for Bacterial Metabolites Identification by MS Technologies Yu Wang   Rutgers University, Edison, NJ, United States

POSTER #	POSTER PRESENTATION
107	Identification of Proteomic Biomarkers in Response to Soy-Based Diets Pamela Westmark   University of Wisconsin-Madison, Madison, WI, United States
108	Understanding epigenome and proteome remodeling caused by novel germline histone H3.3 mutations during neurodevelopment  Khadija Wilson   University of Pennsylvania-Philadelphia, Philadelphia, PA, United States
109	Using plasma induced modification of biomolecules to assess changes in exposed protein surface with inhibitor bound kinases  Nate Wlodarchak   University of Wisconsin-Madison, Madison, WI, United States
110	Establishing and applying mass spectrometric tools to measure levels and 13C-labeling kinetics of metabolites in Camelina sativa leaves and seeds  Yuan Xu   Michigan State University, East Lansing, MI, United States
111	Size and Mass Heterogeneity of the NISTmAb: From Reference Values to Reference Cell Line Katharina Yandrofski   National Institute of Standards and Technology, Rockville, MD, United States
112	Multimodal Chemical Imaging Approach Based on Optical and Mass Spectrometries to Simultaneously Generate High-Resolution Element- and Molecule-Specific Chemical Images  Montwaun Young   Rensselaer Polytechnic Institute, Troy, NY, United States
113	High-Throughput MALDI-TOF Stem Cell Quality Assurance Stephen Zambrzycki   Georgia Institute of Technology, Atlanta, GA, United States
114	Filter aided, single tip based (FAST) method for high throughput, ultrasensitive proteomics analysis Zhenbin Zhang   University of Notre Dame, Notre Dame, IN, United States
115	A proteomic approach to study the mitochondrial outer membrane proteome  Katharina Zittlau   University of Tübingen, Tübingen, Baden-Württemberg, Germany

# National Center for Quantitative Biology of Complex Systems



https://www.ncqbcs.com/

National Center for Quantitative Biology of Complex Systems (NCQBCS) was founded in 2016 through a grant from the National Institute of General Medical Sciences and is located on the campus of the University of Wisconsin-Madison. The development, application, and dissemination of mass spectrometry technology for proteomic analysis is our core mission.

At NCQBCS we are developing next-generation protein measurement technologies for a wide variety of biomedical applications. Our technologies are focused on making whole proteome analysis faster and broadly accessible. In addition to our technology development mission, we apply these technologies to various biomedical problems through collaboration. For those seeking to learn basic proteomic methodology or advanced training in our techniques, we offer hands-on learning experiences.



#### **Innovate**

New technologies that will permit faster, more thorough, proteome analysis.



### **Collaborate**

Work with us to apply NCQBCS technologies to your research.



#### Learn

Visit the NCQBCS for hands-on proteomics training and workshops.



### **Dear Fellow Mass Spectrometrists,**

Thank you for attending the **2nd Annual North American Mass Spectrometry Summer School** at the University of Wisconsin-Madison.

We would like to thank everyone who has worked diligently to organize this program and our instructors, many who have traveled far to participate. We are also grateful for all of our students for making this possible. Finally, we could not put on this program without the support of our sponsors - NSF, NIH, Promega, Thermo Fisher, and the Morgridge Institute for Research.

We look forward to hosting this summer school again in 2019. We hope you will recommend the program to a colleague.

Best wishes,

Josh Coon Evgenia Shishkova Laura Van Toll



# 2nd ANNUAL NORTH AMERICAN MASS SPECTROMETRY SUMMER SCHOOL

JULY 21-24, 2019 | MADISON, WISCONSIN 

The Discovery Building







