

### **James E. Bruce**

James E. Bruce, Ph.D. is a Professor in the Department of Genome Sciences at the University of Washington. His lab develops and applies advanced mass spectrometry instrumentation and novel chemical cross-linking technology to study protein and protein-protein interaction topologies in cells and biological systems, protein posttranslational modifications relevant to metabolism and cell signaling, and proteins interactions involved in host-pathogen interactions.

### **Ileana Cristea**

Ileana Cristea, Ph.D. is an Assistant Professor at Princeton University. Her research is at the interface between mass spectrometry and virology. Her goal is to build a systems biology view of molecular processes underlying viral infection using emerging mass spectrometry complemented by molecular biology tools. Her lab has developed methods for characterizing and quantifying protein interactions of stable or transient nature, which were successful at capturing dynamic virus-host interactions during infection. Her lab integrates these modern proteomics methods with genomics, microscopy, bioinformatics, and virology. These multidisciplinary approaches allowed her group to bridge developments in mass spectrometry to critical findings in biology, and identify mechanisms utilized by viruses to manipulate host cell processes at different stages of the virus life cycle. She is an Editorial Board member of *Molecular & Cellular Proteomics* and *Journal of Neuroimmune Pharmacology*, has served on the ASMS Education and Program Review Committees, and is currently serving on the US HUPO Education Committee. She is a head instructor of the summer Proteomics Course at Cold Spring Harbor.

### **John R. Engen**

John R. Engen Ph.D. is a Professor of Bioanalytical Chemistry at Northeastern University in Boston. He also holds the position of Faculty Fellow in the Barnett Institute of Chemical and Biological Analysis. He is a Fellow of the European Molecular Biology Organization (EMBO), was recently recognized with the 2009 Arthur F. Fideis Award from the American Chemical Society, and has served on the Board of Directors for the American Society for Mass Spectrometry (ASMS). Professor Engen has become a recognized expert in the area of understanding proteins and protein conformation with mass spectrometry (MS). He uses hydrogen-deuterium exchange (HX) to probe conformation and dynamics during various activation states. Proteins that are not amenable to mainstream structural techniques such as X-ray crystallography and NMR can be probed with such methods. Such experiments, among other things, can reveal the effects and locations of protein:ligand binding, be diagnostic for proper protein folding, and be used to determine conformational changes during protein function.

### **David Fenyo**

David Fenyo is an Associate Professor in the Department of Biochemistry and the Center for Health Informatics and Bioinformatics at New York University Langone Medical Center. He has 25 years of experience with all aspects of proteomic and mass spectrometric data analysis in both academia and industry. During these years, he has laid a statistical foundation for testing the significance of protein identification results, developed search engines that identify proteins by matching mass spectrometric and sequence data, and built commercial software packages for fully automatic high-throughput identification and quantitation of proteins. He has 88 scientific publications in these areas.

### **Donita L. Garland\***

Donita Garland, Ph.D. is an Investigator at Massachusetts Eye and Ear Infirmary, Boston, MA. She is a US HUPO Board Member and serves on the Membership Committee. Her research has utilized proteomic technology to understand underlying mechanisms of age-related ocular pathology. To understand mechanisms involved in early stage age related macular degeneration, her research is presently focused on understanding the mechanisms involved in the formation of sub retinal basal deposits in the retina of animal models of inherited macular degenerations. This involves application of proteomic technology to the study of the deposits, the extracellular matrix of the retina and the pigmented epithelia and the post-translational modifications of the proteins involved in the pathology.

### **Scott A. Gerber**

Scott A. Gerber, Ph.D. is an Assistant Professor of Genetics at Dartmouth Medical School and an Investigator in the Dartmouth Institute for Quantitative Biomedical Sciences and at the Norris Cotton Cancer Center. The long-term goal of Dr. Gerber's research program is to understand the molecular mechanisms by which oncogenic kinases contribute to the development and maintenance of cancer. Currently, the lab is focused on the mitotic oncogenes Aurora kinase A and polo-like kinase 1, and their suitability as drug targets for cancer chemotherapy.

### **William Hancock**

William Hancock, Ph.D. is a Professor in the Department of Chemistry and Analytical Biology at Northeastern University and Faculty Fellow, Bradstreet Chair in Bioanalytical Chemistry at the Barnett Institute. He is Editor-in-Chief of the *Journal of Proteome Research* (ACS) and serves on the international HUPO Council and Executive Committee. The mission of Dr. Hancock's research program is the study of Glycoproteomics and glycans associated with cancer and infectious disease. His studies involve the analysis of candidate biomarkers from both patient tissue and blood samples as well as panels of lectins (sugar binding proteins) to isolate and detect changes in glycan composition in disease. Current active area include breast and renal cancer and study of the AIDS virus. The second area of research is the study of biotechnology protein drugs which is an area which requires that latest in mass spectrometry technology especially with the emergence of biogeneric drugs. We are currently analyzing growth hormone, interferon and antibody drugs and developing new analytical approaches for study variants caused by changes in disulfides, glycosylation as well as degradative reactions such as oxidation, deamidation and aggregation.

### **Stanley Hefta\***

Stanley Hefta, Ph.D. is a Professor and BioSystems Division Director at the Virginia Bioinformatics Institute of Virginia Tech. His research division combines computational and experimental sciences to study human, plant and microbial biosystems, with an emphasis on infectious diseases and modeling of the immune response to infections. This work utilizes all of the technologies typically associated with genomics and proteomics, as well as advanced mathematical models. Prior to joining VT, he was a Director of functional genomics at the Bristol-Myers Squibb Company, and before that an Associate Professor of Immunology at the City of Hope Medical Center.

### **Andrew N. Hoofnagle**

Andrew N. Hoofnagle, M.D., Ph.D., is an assistant professor of laboratory medicine and director of clinical mass spectrometry at the University of Washington in Seattle. He has pioneered the use of peptide immunoaffinity enrichment-liquid chromatography-tandem mass spectrometry in the measurement of low abundance proteins in clinical samples. He has also used targeted proteomics to better understand lipoprotein metabolism in people at increased risk for cardiovascular disease. Other projects in his laboratory investigate the importance of local complement activation in the development of atherosclerotic lesions as well as the role vitamin D may have in cardiovascular disease. Dr. Hoofnagle serves as associate editor for the journal *Clinical Chemistry*.

### **Lan Huang**

Lan Huang, Ph.D. is an Associate Professor of Physiology & Biophysics at the University of California, Irvine. Her research interests are centered at developing and employing integrated mass spectrometry-based proteomic strategies for comprehensive analysis of macromolecular protein complexes, and understanding how "protein machines" function in the ubiquitin-proteasome system. In particular, her lab has developed novel approaches combining affinity purification, chemical cross-linking, quantitative mass spectrometry and bioinformatics to effectively study protein interaction networks and structural topologies of protein complexes. She is currently an editorial board member of *Molecular & Cellular Proteomics*.

**Lingjun Li**

Lingjun Li, Ph.D. is a Professor of Pharmacy and Chemistry at the University of Wisconsin-Madison. Her lab focuses on the development of mass spectrometry (MS)-based tools such as new chemical labeling strategies coupled with microscale separations and imaging MS for functional discovery of neuropeptides and biomarker discovery in neurodegenerative diseases. She has published over 100 papers, and received numerous awards including ASMS Research Award, NSF CAREER Award, Sloan Fellowship, and 2011 PittCon Achievement Award. Dr. Li served as a panelist/reviewer for 19 federal grant review panels. She has served on the ASMS Education Committee and ASMS Conference Program Review Committee.

**Andrew J. Link**

Andrew J. Link, PhD is an Associate Professor of Pathology, Microbiology, and Immunology at Vanderbilt University. His lab couples protein affinity purification approaches with proteomics technologies to identify novel protein interactions and posttranslational modification in protein translation. More recently, his group has begun a program using system biology to understand the human immune response to vaccines. His lab's approaches include protein profiling by multidimensional LC/MS/MS, label-free and isotope quantification approaches, and novel computational algorithms and visualization strategies for peptide identification and proteomic data analysis. He has been a principal instructor at the CSHL Proteomics course for the past 10 years.

**Joseph A. Loo\***

Joseph A. Loo, Ph.D. is Professor of Biological Chemistry (School of Medicine), and Chemistry and Biochemistry at the University of California, Los Angeles. His group uses mass spectrometry and proteomics strategies, including top-down MS, ion mobility, and label-free quantification, to characterize proteins and protein complexes, and profile proteins involved in human diseases. Dr. Loo is an Associate Editor for the *Journal of the American Society for Mass Spectrometry*. He has served US HUPO as a member of the Board of Directors (2009-2011), Education Committee (2009-2010), and Organizing Committees of the 2011 (Raleigh) and 2012 (San Francisco) annual conferences.

**David M. Lubman**

David M. Lubman, Ph.D. is the Maude T. Lane Professor of Surgical Immunology and Professor of Pathology and Chemistry at the University of Michigan Medical Center. He is also an associate member of the UM Comprehensive Cancer Center and of the Bioinformatics Program and is an associate member of the NCI Early Detection Research Network. His lab develops proteomics technologies including mass spectrometry for clinical based problems involving cancer biology, protein serum markers for cancer, glycoproteomics of disease states and cancer stem cell research. The work includes research in pancreatic, colon, melanoma, hepatocellular and ovarian cancers. He is currently a co-leader on the UM GI SPORE grant.

**Michael MacCoss**

Michael MacCoss, Ph.D., is Associate Professor in the Department of Genome Sciences at the University of Washington. The focus of his research is in the development of stable isotope and mass spectrometry based approaches to improve our understanding of biology on a molecular, cellular, and whole organism level. Presently, individuals in the laboratory are working on technology for 1) automating biochemical sample preparation methods for the analysis of protein mixtures; 2) developing in vivo stable isotope methods for studying protein metabolism; 3) increasing the dynamic range of liquid chromatography-mass spectrometry for the analysis of peptides; and 4) developing computational tools for the automated conversion of mass spectrometry data into biologically meaningful results. These technologies are presently being demonstrated in the model organisms *C. elegans* and *S. cerevisiae*. Although our current research interests are presently in model systems, our long-term goal is have technologies robust enough to handle the automated high-throughput characterization of human clinical samples.

**Sanford P. Markey\***

Sanford P. Markey, Ph.D. is Chief of the Laboratory of Neurotoxicology in the intramural research program at the National Institute of Mental Health in Bethesda, MD. His lab investigates synaptic proteomics as related to normal neurotransmission and the effects of drugs used to treat psychiatric diseases on synaptic architecture. His group is targeting proteins implicated by familial genomic studies in psychiatry. Current research activity is the development of automated methods for protein capture from laser capture microdissection suitable for the analysis of subcellular organelles.

**David C. Muddiman\***

David C. Muddiman is currently a Professor of Chemistry and Founder and Director of the W.M. Keck FT-ICR Mass Spectrometry Laboratory at North Carolina State University in Raleigh, NC. David received his B.S. in chemistry from Gannon University (Erie, PA) in 1990 and his Ph.D. in Analytical Chemistry from the University of Pittsburgh in 1995 under the auspices of David M. Hercules. He then was a Department of Energy Postdoctoral Fellow at Pacific Northwest National Laboratory in the Environmental Molecular Sciences Laboratory working with Richard D. Smith from 1995-1997. David has served on over 35 NIH study sections since 1999 and reviews for over 30 scientific journals and is on the editorial advisory board of 6 journals including *Molecular & Cellular Proteomics*. He also serves on the advisory board of the several NSF and NIH funded facilities. His group has presented over 350 invited lectures and presentations at meetings, has published over 180 peer-reviewed papers, and has received three US patents. He was appointed Chair of the 2011 US HUPO Meeting. He is the recipient of the 2010 Biemann Medal, American Society for Mass Spectrometry, 2009 NCSU Alumni Outstanding Research Award, the 2004 ACS Arthur F. Findeis Award and the 1999 American Society for Mass Spectrometry Research Award, and the Safford Award, University of Pittsburgh, for Excellence in Teaching.

**Fred E. Regnier\***

Fred E. Regnier, Ph.D. is J. H. Law Distinguished Professor, Analytical Chemistry at Purdue University. The current objective of his laboratory is to develop integrated analytical systems for the analysis and characterization of complex protein mixtures using multidimensional separation systems (1,2) and mass spectrometry. The current initiative is to develop an automated, "one-pass" system that would identify proteins from cellular extracts that are in regulatory flux. A wide variety of stimuli are being examined ranging from cancer to specific diseases. Both conventional and chip based separation systems are being developed for this purpose. Professor Regnier is a founding Board Member of US HUPO and has served on the organizing committee of several US HUPO conferences.

**Jennifer E. Van Eyk**

Dr. Van Eyk, Ph.D. is a Professor of Medicine, Biological Chemistry and Biomedical Engineering at Johns Hopkins University, Baltimore and Director of both the Hopkins NHLBI Proteomics Innovation Group and the JHU Bayview Proteomics Center that has the mandate to facilitate application of proteomics in medicine. Her research laboratory studies the underlying molecular mechanism of cardiovascular disease using a large number of proteomic methodologies allowing development of better therapeutic intervention and robust biomarkers for the diagnosis, prognosis and risk stratification of heart disease. Dr. Van Eyk has co-edited two books with M. Dunn entitled "Proteomics and Genomic Analysis of Cardiovascular Disease" and "Clinical Proteomics: from diagnosis to therapy".

**Hui Zhang**

Hui Zhang, Ph.D. is an Associate Professor of Pathology at Johns Hopkins University. Her research focus is on developing high-throughput technologies to characterize dynamic protein expressions/modifications and using these proteomics technologies to understand human diseases. Dr. Zhang participates in several research programs and is an investigator in the Early Detection Research Network (EDRN), Clinical Proteomic Tumor Analysis Consortium (CPTAC), NIHBI Proteomics Center, and Programs of Excellence in Glycosciences (PEG).

Before joining Johns Hopkins, Dr. Zhang earned her Ph.D. with Dr. Roland Kallen from University of Pennsylvania. Then she joined New England Biolabs and Cell Signaling Technology to study protein activation by developing modification-specific antibodies and profiling protein modifications. Later, she developed glycoproteomic technologies when she worked with Dr. Ruedi Aebersold at the Institute for Systems Biology.