SPEAKERS

Lissa Anderson, PHD

Benjamin Garcia, PhD

Tom Muir, PhD

Ping Ma, PhD

DECIPHERING BIOLOGICAL CODES:

LEVERAGING THE POWER OF CHEMICAL BIOLOGY, BIOLOGICAL PHYSICS, BIG DATA, AI, AND NATIONAL FACILITIES
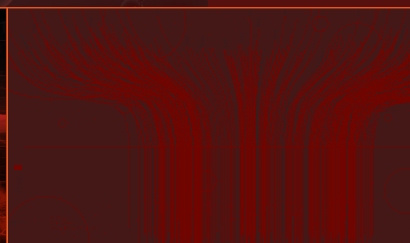
DATE
September 9

TIME
11 am - 1 pm

LOCATION
Register

National Science Foundation
WHERE DISCOVERIES BEGIN

DECIPHERING BIOLOGICAL CODES:

Leveraging the Power of Chemical Biology, Biological Physics, Big Data, AI, and National Facilities

ABSTRACT

Nearly all cells comprising an individual contain the same DNA blueprint, yet humans are a complex amalgamation of ~200 different cell types of various functions. Distinctions lie in which genes are ultimately "switched ON" and translated into proteins that function in the cell — their "proteome." Epigenetic mechanisms affect biological processes by regulating the ways in which genes are expressed, altering phenotype. By understanding these mechanisms, scientists will be able to better understand key relationships between genotype and phenotype.

Histone proteins play a pivotal role in epigenetic regulation. While there are only five families of histone proteins, their structures and functions are expanded in innumerable ways, including combinations of gene sequence variants and post-translational modifications (PTMs). Understanding these structure-function relationships requires a platform capable of unequivocally distinguishing between nearly identical protein sequences while concurrently identifying and site-localizing all PTMs. Mass spectrometry (MS) has proven essential for identification and quantitation of proteins and their PTMs. Complementing these analytical advances, great strides have also been made in the development of chemical biology approaches that allow precise installation of PTMs into chromatin for downstream biochemical studies. Together, these approaches show great promise in cracking 'histone code' regulation mechanisms.

Analytical and computational technologies, such as statistical and machine learning methods can also provide insight into biological phenomena. These methods, which rely on new mathematical theory and emerging computing paradigm, help sort through large data sets — the "data deluge" — at rapid pace and promise to revolutionize many fields on their own and through the creation of novel biotechnologies. Combined, these novel methods could help identify key genetic signatures and mechanisms associated with a disease, leading to the innovation of new treatments.

LISSA ANDERSON, PHD

RESEARCH FACULTY
AND DIRECTOR
OF BIOLOGICAL
APPLICATIONS

NATIONAL HIGH
MAGNETIC FIELD
LABORATORY
(MAGLAB)

ABOUT DR. LISSA ANDERSON

Dr. Lissa Anderson is Research Faculty and the Director of Biological Applications for the Ion Cyclotron Resonance User Facility of the National High Magnetic Field Laboratory (MagLab) located at Florida State University. The facility is charged with developing and exploiting the unique capabilities of high-field Fourier-transform ion cyclotron resonance mass spectrometry (FT-ICR MS) and leads the word in instrument and technique development as well as well as novel applications of FT-ICR MS. The facility's four FT-ICR mass spectrometers feature high magnetic fields – including the world-record 21 tesla ICR magnet – and are freely available to users for sample analysis requiring ultrahigh resolution and mass measurement accuracy.

Born and raised in Virginia, Dr. Anderson attended the College of William and Mary as an undergraduate and obtained her PhD in Chemistry at the University of Virginia in 2014. While at UVA, she studied under Professor Donald Hunt and Dr. Jeffrey Shabanowitz, pioneers in the development of mass spectrometry instrumentation and methods that set the standard for ultrasensitive detection and characterization of proteins and their post-translational modifications. In 2015, she moved to Tallahassee, FL to become a postdoctoral associate of the MagLab's ICR Program and was promoted to Research Faculty the following year. Dr. Anderson's research is organized under several interrelated topics of top-down proteomics (i.e., intact proteoform analysis). These include development and application of new technologies to perform ion-ion chemistry inside the mass spectrometer to improve proteoform detection sensitivity and primary structure determination. As part of a team of collaborators from UVA, the MagLab, and Thermo Fisher Scientific, these technologies were installed on the 14.5 and 21 tesla FT-ICR systems at the MagLab, and later commercialized. She has also been privileged to work with dozens of users and collaborators, in the US and abroad, to develop optimized strategies to characterize proteoforms involved in phenotypes of interest. Dr. Anderson is committed to communicating research to a diverse array of audience and is a staunch advocate for the FAIR (Findable, Accessible, Interoperable, and Reusable) principles of data stewardship. When she's not in the lab, she assists in coordinating efforts to converge on broadly applicable data standards and in adapting tools that ease the burden of generating FAIR data in service to MagLab users.

TOM MUIR, PHD

VAN ZANDT WILLIAMS JR. CLASS OF 1965

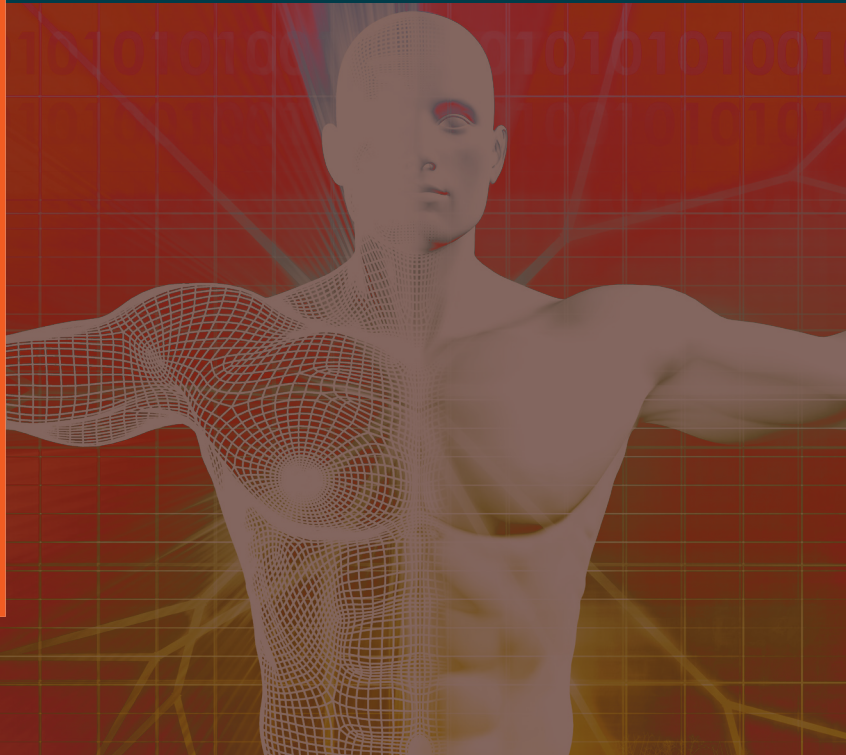**CHAIR, DEPARTMENT OF CHEMISTRY**

PRINCETON UNIVERSITY

ABOUT ABOUT DR. TOM MUIR

Tom W. Muir received his B.Sc. in chemistry from the University of Edinburgh in 1989 and his Ph.D. in chemistry from the same institute in 1993 under the direction of Professor Robert Ramage. After postdoc studies with Stephen B.H. Kent at The Scripps Research Institute, he joined the faculty of The Rockefeller University in 1996, where he was, until 2011, the Richard E. Salomon Family Professor and Director of the Pels Center of Chemistry, Biochemistry and Structural Biology. In 2011, Dr. Muir joined the faculty of Princeton University as the Van Zandt Williams Jr. Class of '65 Professor of Chemistry. He currently serves as Chair of the Chemistry Department. He has published over 250 scientific articles in the area of chemical biology and is best known for developing methods for the preparation of proteins containing unnatural amino acids, posttranslational modifications and spectroscopic probes. These approaches are now widely employed in academia and industry. His current interests lie in the area of epigenetics, where he tries to illuminate how chemical changes to chromatin drive different cellular phenotypes.

ABOUT DR. BENJAMIN GARCIA

Benjamin A. Garcia obtained his BS in Chemistry at UC Davis in 2000, where he worked as an undergraduate researcher in Prof. Carlito Lebrilla's laboratory. He then received his PhD in Chemistry in 2005 at the University of Virginia under Prof. Donald Hunt and then was an NIH NRSA Postdoctoral Fellow at the University of Illinois under Prof. Neil Kelleher from 2005-2008. From there he was appointed as an Assistant Professor in the Molecular Biology Department at Princeton University from 2008-2012, until his recruitment as the Presidential Associate Professor of Biochemistry and Biophysics at the University of Pennsylvania Perelman School of Medicine in 2012, promoted to full Professor in 2016, and named the John McCrea Dickson M.D. Presidential Professor in 2017.

Dr. Garcia moved in the summer of 2021 to the Washington University School of Medicine in St. Louis to become the Chair of the Department of Biochemistry and Molecular Biophysics. The Garcia lab has been developing and applying novel proteomic approaches and bioinformatics for interrogating protein modifications, especially those involved in epigenetic mechanisms such as histones during human disease, publishing over 350 publications.

Dr. Garcia is on the editorial boards for the Molecular Omics, the Journal of Proteome Research, Mass Spectrometry Reviews, and the Molecular and Cellular Proteomics journals. He also serves on the Board of Directors for the U.S. Human Proteome Organization (HUPO) and the HUPO Governing Council and Executive Committee. He has also been recognized with many honors and awards for his mass spectrometry research including the American Society for Mass Spectrometry (ASMS) Research Award, a National Science Foundation CAREER award, an NIH Director's New Innovator Award, the Presidential Early Career Award for Scientists and Engineers, an Alfred P. Sloan Fellowship, the PITTCON Achievement Award, the American Chemical Society Arthur F. Findeis, The Protein Society Young Investigator Award, the ASMS Biemann Medal, the HUPO Discovery in Proteomic Sciences Award and was named a Fellow of the Royal Society of Chemistry.

PING MA, PHD

DISTINGUISHED RESEARCH PROFESSOR, STATISTICS

UNIVERSITY OF GEORGIA

ABOUT DR. PING MA

Ping Ma is a Professor of Statistics at the University of Georgia. He was recently appointed as a Distinguished Research Professor and co-directs the big data analytics lab. Prior to joining the faculty of the University of Georgia, he was an Associate Professor in the Department of Statistics and the Institute of Genome Biology at University of Illinois at Urbana-Champaign.

Dr. Ma has made many fundamental contributions to modernize statistics theory and methods in big data analytics. More significantly, Dr. Ma's research has had profound impact on the area of biological sciences. Dr. Ma's work in sorting through the vast volume of biological information now available to scientists to identify key genetic signatures associated with a disease could unlock the mechanisms of the disease, leading to the innovation of new treatments.

Dr. Ma obtained his PhD in statistics from Purdue University and completed his postdoctoral fellowship in the Department of Statistics and the Bauer Center for Genomics Research at Harvard University. He was Beckman Fellow at the Center for Advanced Study at the University of Illinois at Urbana-Champaign, Faculty Fellow at the National Center for Supercomputing Applications, and a recipient of the National Science Foundation CAREER Award. He also serves on multiple editorial boards, including the Statistical Applications in Genetics and Molecular Biology, and is a Fellow of the American Statistical Association.

ABOUT THE
LECTURE SERIES

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