Rosetta Briegel Barton Lecture

CHEMISTRY AND BIOCHEMISTRY DEPARTMENT, THE UNIVERSITY OF OKLAHOMA NORMAN, OK 73019-3051 (405) 325-4811

We Are Pleased to Announce A Seminar
Presented By

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Friday, March 24, 2023
4:15 pm
NWC 1313

Measuring proteoform signatures in human disease: Leveling up proteomics to bridge the gap from genotype to phenotype

Since the completion of the Human Genome Project, much has been made of the need to bridge the gap from genes and traits. As a key nexus for the many interacting '-omes' (genome, transcriptome, proteome, metabolome, exposome, interactome, etc.), the proteome should offer a tight link between genotype and phenotype. Why then is proteomics challenged in this connection after 20 years of intense development? The proteoform concept offers a potential solution by considering protein composition with complete molecular specificity. Proteoforms, or all of the precise molecular forms of a protein, capture all sources of variability in protein composition (i.e., SNPs, isoforms, post-translational modifications, etc.), and thus provide crucial insights into biological function of a protein by integrating primary sequence and post-translational modifications (e.g., enabling discovery of allele- or isoform-specific PTM patterns). This level of characterization is not possible at the peptide level, the unit of measurement of traditional 'bottom-up' proteomics, or the epitope level, the target of antibody-based techniques. Our group's studies of disease-related genes have demonstrated the importance of proteoform measurement in clinically relevant protein targets such as KRAS (Adams et al., JBC, 2023), ApoA-1 (Wilkins et al., JAHA, 2021), and immunoproteoforms (Melani et al., Science, 2022). Now, "single molecule" mass spectrometry is poised to convert genes to proteoform signatures at a far faster rate. The latest technologies for scalable and systematic mapping of proteoforms to promote human health will be described in this seminar.

Refreshments will be served.