

Analytical Seminar

Thursday at 12:15 pm
November 12, 2015

Room 1315
Chemistry Bldg.



Dr. Michael Shortreed

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“Proteomics from Bottom to Top”

Changes, adaptations and responses of complex systems such as cells or organisms are governed and actuated at the genomic, epigenetic, transcriptional, translational, post-translational and metabolomics levels. Proteoforms, the distinct molecular forms of a protein, defined as its base amino acid sequence plus any posttranslational modifications (PTMs), are the key actors in each of these six different levels. Variations in sequence and simple PTM changes can substantially alter the structure and function of proteoforms, therefore perturbing the pathways and the processes in which they are involved. Comprehensive characterization of sample proteoforms, which include detecting sequence variations and posttranslational modifications, is thus essential to understanding how a biological system functions. Our group is interested in developing new analytical tools for the accurate and comprehensive analysis of proteoforms in complex samples. We have developed new software tools to connect the expression of mRNA molecules with their companion proteins and to reveal the translation of nucleotide variants into amino acid polymorphisms. We have developed new software tools to reveal the protein products of novel and previously unknown mRNA splicing variants. We have developed new software tools that reveal an incredibly variety of different post-translational modifications with high statistical confidence. We have also developed a new strategy to reveal the intact proteoforms in complex samples. In this seminar, I'll describe our most recent efforts in these areas and describe how this work has led to unprecedented levels of clarity and accuracy in characterization of the proteome of complex systems.