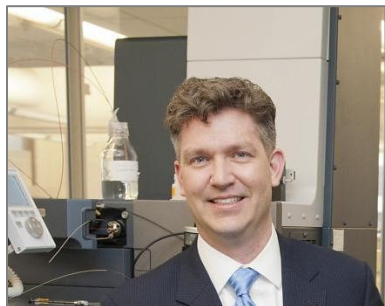


PICTURE:



TITLE

Hydrogen exchange mass spectrometry to probe the conformation of proteins both in solution and in membranes

ABSTRACT

An established use for mass spectrometry is the analysis of protein conformation and dynamics. One classic approach is to label protein molecules in solution under physiological conditions as the incorporation of the labeling agent is a function of the folded conformation. Hydrogen exchange (HX) methods label the backbone amide hydrogens of proteins with deuterium and the location and magnitude of the labeling can then be determined with mass spectrometry (MS). HX MS studies are particularly well suited for analysis of proteins that will not crystallize, proteins not amenable to NMR, or proteins available in only small quantities. This presentation will explore the recent popularity of HX MS, current methodology, and applications of HX MS, both for systems in solution and for the analysis of membrane proteins. The use of HX MS in understanding protein degradation machinery, mapping the structural effects of post-translational modifications, and membrane protein analyses will be described.

SHORT BIOGRAPHY

John R. Engen is a Professor of Bioanalytical Chemistry at Northeastern University. Professor Engen holds two B.S. degrees (molecular biology and biochemistry) from Union College and a Ph.D. in Chemistry from the University of Nebraska (working with David L. Smith). He completed postdoctoral work at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany and at the Los Alamos National Laboratory. He is a Fellow of the European Molecular Biology Organization (EMBO), received the 2009 Arthur F. Findeis Award from the American Chemical Society, and served on the Board of Directors for the American Society for Mass Spectrometry (ASMS) from 2009-2011. In 2012-2013, he was a Visiting Professor of Biochemistry in the laboratory of Prof. F. Ulrich Hartl at the Max Planck Institute of Biochemistry in Martinsried, Germany

Professor Engen is a recognized expert in the area of understanding proteins and protein conformation with mass spectrometry. He uses hydrogen-deuterium exchange to probe conformation and dynamics during various activation states. Proteins that are not amenable to mainstream structural techniques such as X-ray diffraction and NMR can be probed with such methods. Such experiments, among other things, can reveal the effects and locations of binding, be diagnostic for proper protein folding, and be used to determine conformational changes during protein function.

Professor Engen has published over 125 papers on the topic of hydrogen exchange and given hundreds of invited lectures worldwide to academia and industry. He teaches a yearly ASMS short course on protein structural analysis by mass spectrometry. Current research projects in his laboratory include (1) investigations of protein conformation to understand regulation and aberrant signaling in various disease states including cancer, (2) analysis of protein folding and stability, (3) studies of protein conformation at biological membranes, and (4) optimization and methods development in hydrogen exchange mass spectrometry.

More information available at <http://www.hxms.neu.edu>