SBS Seminar Announcement

From Yeast to Brain: Disruption in Protein Analysis Technologies

Professor John R. Yates

Department of Chemical Physiology and Department of Molecular and Cellular Neurobiology,
The Scripps Research Institute

Abstract

A component to understanding biological processes involves identifying the proteins expressed in cells as well as their modifications and the dynamics of processes. The technology to sequence proteins underwent significant disruption with the sequencing of genomes. Mass spectrometry has benefited from large-scale genome sequencing of organisms resulting in new methods for rapid and large-scale quantitative analysis of protein data from experiments. We've been developing mass spectrometry based methods for large-scale analysis of proteins in cells and recent developments will be discussed. We have also been using these methods to the study of brain function and disease. Application of these methods to the study depression models in rats will be described.

Biography

John R. Yates is the Ernest W. Hahn Professor in the Department of Chemical Physiology and Molecular and Cellular Neurobiology at The Scripps Research Institute. His research interests include development of integrated methods for tandem mass spectrometry analysis of protein mixtures, bioinformatics using mass spectrometry data, and biological studies involving proteomics. He is the lead inventor of the SEQUEST software for correlating tandem mass spectrometry data to sequences in the database and developer of the shotgun proteomics technique for the analysis of protein mixtures. His laboratory has developed the use of proteomic techniques to analyze protein complexes, posttranslational modifications, organelles and quantitative analysis of protein expression for the discovery of new biology. Many proteomic approaches developed by Yates have become a national and international resource to many investigators in the scientific community. He has received the American Society for Mass Spectrometry research award, the Pehr Edman Award in Protein Chemistry, the American Society for Mass Spectrometry Biemann Medal, the HUPO Distinguished Achievement Award in Proteomics, Herbert Sober Award from the ASBMB, and the Christian Anfinsen Award from The Protein Society, the 2015 ACS's Analytical Chemistry award and 2015 The Ralph N. Adams Award in Bioanalytical Chemistry. He was ranked by Citation Impact, Science Watch as one of the Top 100 Chemists for the decade, 2000-2010. He was #1 on a List of Most Influential in Analytical Chemistry compiled by *The Analytical Scientist* 10/30/2013 and is on the List Of Most Highly Influential Biomedical Researchers, 1996-2011, *European J. Clinical Investigation* 2013, 43, 1339-1365. He has published over **750** scientific articles with **~60,000** citations, and an H index **122**.

Tuesday, 02 December 2014 2.00pm to 3.00pm SBS Classroom 2 (SBS-01n-22)
Host: A/Prof Newman Sze