

Project Title

The study of proteins function using mass spectrometry and proteomics



Researcher

Prof. John R. Yates

Country	USA
Field	Biotechnology
Scientific Affiliation	The Scripps Research Institute

Abstract

The field of proteomics arose from two critical inventions: tandem mass spectrometry peptide sequencing and large-scale database searching. This convergence resulted in the development of shotgun proteomics, a new paradigm revolutionizing molecular and cellular biology research that is employed throughout the world for the study of proteins. These methods enabled large-scale studies to identify the components of protein complexes in microorganisms and mammalian cells, and almost every organelle in prokaryotic and eukaryotic cells has been characterized using shotgun methods. The comprehensive analysis of cells and tissues is now performed to understand differences between normal and disease states. These methods have had substantial impact in the study of cancer, malaria, cystic fibrosis and many other diseases to create a greater understanding of disease and disease mechanisms. Additionally, these technologies created or accelerated development of other fields, including chemical biology, metaproteomics, paleoproteomics, and disease biomarker discovery for early and accurate diagnosis.

Biography

Prof. Yates is the Ernest W. Hahn Professor at The Scripps Research Institute. His research includes 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 developed proteomic techniques to analyze protein complexes, posttranslational modifications, organelles & quantitative analysis of protein expression for the discovery of new biology. He received the ASMS research award, the Edman Award in Protein Chemistry, the ASMS Biemann Medal, HUPO Distinguished Achievement Award in Proteomics, Herbert Sober Award from ASBMB, Christian Anfinsen Award from The Protein Society, the 2015 ACS's Analytical Chemistry award, 2015 Ralph N. Adams Award in Bioanalytical Chemistry & the 2018 Thomson Medal from IMSF.

