

AWARD FOR A DISTINGUISHED CONTRIBUTION IN MASS SPECTROMETRY

Award Lecture: 4:45 pm, Monday, Exhibit Hall C

2009 Recipients: Simon J. Gaskell and Vicki H. Wysocki



In a series of publications beginning in 1992 a group led by **Simon J. Gaskell** and another led by **Vicki H. Wysocki** contributed in parallel to the development of the “Mobile Proton Model.” This model unified diverse observations of real-world collision-induced peptide fragmentation so widely used for peptide sequencing and protein inference. Based on fundamental thermodynamic considerations and many observations, this has become the accepted model for understanding peptide fragmentation spectra. The model provides both very specific predictions concerning fragmentation and enables spectra to be interpreted and simulated. It now serves as a foundation both for increased sophistication in database search algorithms, as well as the basis on which many other researchers in the area of peptide mass spectrometry to build more advanced models of fragmentation.



Professor Gaskell is Director of the Michael Barber Centre for Mass Spectrometry and Vice President (Research), University of Manchester.

Vicki Wysocki is Professor with the Department of Chemistry, the Department of Biochemistry and Molecular Biophysics and the BIOS Institute for Collaborative Research at the University of Arizona.

THE BIEMANN MEDAL

Award Lecture: 4:45 pm, Tuesday, Exhibit Hall C

2009 Recipient: Neil L. Kelleher



Top-down proteomics is now a household word among ASMS members, and this is largely due to Neil L. Kelleher, who started top-down analysis and has vigorously promoted this technology starting as a graduate student and continuing today. Unlike the bottom-up approach that starts with protein fragments, top-down proteomics preserves information concerning protein isoforms and the interplay between posttranslational modifications by isolating and fragmenting whole proteins in the gas phase. The analytical software he has developed, ProSight PTM, provides the charge- and isotope-deconvolution needed for top-down proteomics data and is used by over 450 laboratories worldwide. Dr. Kelleher has applied top-down analysis to a number of important biological systems, such as the protein component of human chromatin and determination of the post-translational dynamics of histone H4 through the cell cycle. His laboratory is a major driving force in the extension of tandem mass spectrometry to high mass ions, generating over 130 papers in peer-reviewed journals and already leading to a number of major awards.

Neil Kelleher is Professor of Chemistry at the University of Illinois (Urbana-Champaign).

RON HITES AWARD FOR AN OUTSTANDING RESEARCH PUBLICATION IN JASMS

Award Presentation: 4:45 pm, Wednesday, Exhibit Hall C

The Ron Hites Award recognizes a high quality presentation of outstanding original research. Selection is based on a paper’s innovative aspects, technical quality, likely stimulation of future research, likely impact on future applications, and quality of presentation. The Award is named in honor of Professor Ronald A. Hites of Indiana University, who led the creation of *JASMS* in 1988 while president of ASMS.



The inaugural award is presented to **Dr. Alison E. Ashcroft** for the article *Monitoring Copopulated Conformational States during Protein Folding Events Using Electrospray Ionization-Ion Mobility Spectrometry-Mass Spectrometry*, David P. Smith, Kevin Giles, Robert H. Bateman, Sheena E. Radford, Alison E. Ashcroft, *JASMS* **2007**, *18*, 2180-2190. Dr Ashcroft is Manager of the Mass Spectrometry Facility in the Astbury Centre for Structural Molecular Biology, Leeds University.

