



4th EuPA MEETING
6th ProCura MEETING

2010
PROTEOMICS
ODYSSEY
TOWARDS NEXT DECADES

EuPA Educational WORKSHOP II

“Phospho- and ADP-ribo-Protein Sequencing”

1 p.m. 24 October 2010, Estoril Congress Center, Portugal

Chairs:- David Goodlett, Nick Morrice and Garry Corthals.

In this workshop we will describe methods that have been successfully used to enrich and detect phosphorylated and ADP-ribosylated peptides. Assigning the sites of these post-translational modifications from MSMS spectra can be very challenging and in this workshop we will describe methods and the bioinformatic tools that make this job easier. Primarily we will concentrate on the assignment of protein phosphorylation and ADP-ribosylation sites from the tandem MS spectra acquired on both electrospray and MALDI-TOF-TOF mass spectrometers. We will also show the differences in fragmentation patterns observed when using different fragmentation pathways such as CID and ETD in ion traps as well as CID in the HCD cell of an orbitrap or Q-TOF instrument.

Teacher's biography



David Goodlett

Professor at the University of Washington, currently Director of Mass Spectrometry Center, School of Pharmacy, UW. He was recently elected as Member-at-Large chair of the Digital Communications Committee of American Society for Mass Spectrometry (ASMS). His Bioanalytical Laboratory has developed separation science and MS methods to solve biological problems of interest. In general, they seek to use MS to extract the maximum amount of information with a minimum of fractionation prior to MS analysis, which the group refer to as Indolent Driven Science. Among others, his group has implemented a simple version of Dynamic Range Expansion Applied to MS (DREAMS) developed by the R.D. Smith lab on this instrument. Goodlett's group is

currently pursuing data-independent analysis of complex mixtures using a protocol they refer to as Precursor Acquisition Independent From Ion Count (PACIFIC; see Panchaud Anal Chem 2009) that is related to a type of data produced by a novel tandem MS (see Wang RCMS 2007). Most recently they implemented an ion funnel on our Thermo LTQ-FT instrument (see Kelly et al. Mass Spectrom Rev 2009).

The Goodlett 'lab is part of the University of Washington's Proteomics Resource**** (UWPR) consortium developed to aid proteomics research on campus.



Nicholas Morrice

Head of Proteomics, MRC Protein Phosphorylation Unit, College of Life Sciences, University of Dundee, Dundee DD1 5EH. He worked with Prof Dick Wettenhall (1987-1994) at the University of Melbourne honing his protein sequencing and protein purification skills, before returning to the UK in 1994 to join the MRC Protein Phosphorylation Unit, in Dundee with Sir Philip Cohen. Morrice was Principle Investigator and Head of Proteomics within the same Unit until 2010. Currently he is Principle Investigator and Head of Proteomics at the Beatson Institute for Cancer Research in Glasgow. His work has focussed on developing methods for the identification of protein phosphorylation sites by both mass spectrometry and Edman sequencing. More recently his work has focussed on the use of quantitative phosphoproteomics to identify novel substrates of protein kinases and developing mass spectrometry methods to study protein ubiquitination.