INVITED LECTURE H1

Functional and structural proteomics using mass spectrometry

Ole N. Jensen

Department of Biochemistry and Molecular Biology, University Southern Denmark

Dynamic cellular processes rely on accurate regulation and modulation of protein activities and protein interactions. We are using mass spectrometry techniques to study cell signalling events that are mediated by phosphorylation and chromatin regulatory mechanisms governed by acetylation/methylation/phosphorylation. I will give an overview of current approaches to study protein phosphorylation, histone modifications and other post-translational modifications. In addition, I will present recent protein structural data obtained by hydrogen-exchange mass spectrometry in studies of phosphorylation-mediated structural flexibility of protein kinases.

References:
1. ThingholmTE *et al. J Proteome Res*. 2008 Aug;7(8):3304-13.
2. Rand KD *et al*. *J Biol Chem*. 2008 May 9;283(19):13378-87.
3. Trelle MB *et al. Expert Rev Proteomics*. 2007 Aug; 4(4):491-503.