The Chemistry Department is pleased to present

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"Hybrid mass spectrometry approaches targeting cellular signaling"

ANALYTICAL MELOCHE SEMINAR

Around for more than a century mass spectrometry is blooming more than ever, and applied in nearly all aspects of the natural and life sciences. In the last two decades mass spectrometry has become routine for the high-throughput analysis of peptides and their post-translational modifications. In this talk I will highlight some of these hybrid mass spectrometry approaches targeting cellular signaling.

In the first part of the talk I will briefly discuss some of our most recent advances in acquiring comprehensive phosphoproteomes, in a robust and reproducible manner, targeting ideally minute amounts of starting materials, comparing also the performance of different enrichment protocols.

Secondly I will discuss how alternative enzyme and fragmentation techniques help us to further cover the proteome, and especially peptides being modified by (multiple) PTMs. In particular, the hybrid fragmentation technique EThcD, provide much better ion score and unambiguous assignments of localization sites. We also used it to enhance our understanding of the immunopeptidome, whereby I will specially focus on presented HLA peptides bearing post-translational modifications, such as phosphorylation, Arg-methylation, OGlcNAcylation and those formed by proteasome induced splicing.

In a final topic I will focus on the application of native MS and top-down proteomics for monitoring two of the most important PTMs in cells; phosphorylation and O-GlcNAcylation. The interplay between these two modifications has been shown to play a critical role in cancer and neurodegenerative diseases. Native MS was used to monitor the reaction kinetics of O-GlcNAcylation and phosphorylation on the collapse mediator response protein, CRMP2. The data highlights the criticality of the phosphosite location in determining CRMP2 O-GlcNAcylation rate. Indeed, phosphorylation on the P-3 residue with respect to the O-GlcNAcylation site dramatically decreases the O-GlcNAcylation rate compared with its unphosphorylated counterpart. The data reveal the power of Native MS in not only monitoring O-GlcNAcylation and phosphorylation, but also the dynamic interplay that exists between these two modifications.

Tuesday
April 18

1:00 pm
1315
Chemistry