ANALYTICAL SEMINAR

Professor Ying Ge

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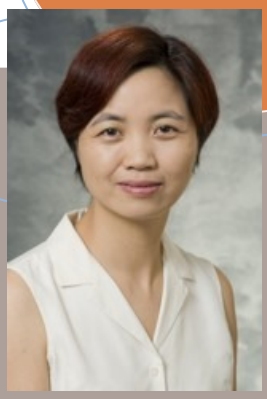

Thursday, Sept. 29, 2016

12:15 PM in 1315 Chem

Novel Strategies in Top-down Proteomics

Proteomics is essential for deciphering how molecules interact as a system and for understanding the functions of cellular systems in human disease; however, the human proteome is extremely complex due to a plethora of post-translational modifications (PTMs) and sequence variations. The emerging top-down mass spectrometry (MS)-based proteomics, which is based on analysis of intact proteins, is arguably the most powerful method to comprehensively characterize proteoforms that arise from genetic variations, alternative splicing, and PTMs. We have shown that top-down MS has unique advantages for unraveling the molecular complexity, quantifying multiple modified protein forms, complete mapping of modifications with full sequence coverage, and discovering unexpected modifications. However, the top-down approach still faces significant challenges in terms of protein solubility, protein separation, the detection of low-abundance proteins, and the under-developed data analysis tools. Recently we are employing a multi-pronged approach to address these challenges in a comprehensive manner by developing new MS-compatible surfactants for protein solubilization, novel materials and new strategies for multi-dimensional chromatography separation of proteins, novel nanomaterials for enrichment of low-abundance proteins, and a new comprehensive software package for top-down proteomics. In this talk I will present our recent technology developments in top-down mass spectrometry-based proteomics and its application to cardiac systems biology.

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