**Wednesday February 18th, 2015 – 10h30**  
EPFL, Lausanne  
Conference Room SV 1717A

**Yibo WU**  
Laboratory of Pr. Rudolf Aebersold, Institute fur Molekulare Systembiology, ETH Zurich

**Mass Spectrometry-based Proteomics - Options, Potential, limits and future directions**

**Hosts:** Kristina Schoonjans and Johan Auwerx (EPFL)

**Abstract:**  
The proteome is more than a mere translation of a given genome. Proteomics has emerged as a tool to characterize the proteome in various cell types under different conditions. Currently, the majority of proteomics strategies rely on mass spectrometric techniques, and differ in instrument used and their performance, reliance on internal standards, and bioinformatics analysis. These strategies effectively support the identification of proteins and their variants, i.e. post-translational modifications (PTMs), and the quantification of them in various cell types, organs and species. The pros and cons of each strategy necessitate the consideration of selecting the optimal method based on the specific research interest. Proteome in different systems have been reported to be nominally correlated with the corresponding genome, demonstrating the value of integrated multilayered omics approach to test biological hypothesis or model processes[1, 2]. Current techniques have generated unprecedentedly sensitive, accurate and reproducible proteomics data, and will increase the impact of proteomics in biomedical research.
