University of Louisville
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Literature Seminar

When: December 1, 2022
Time: **2:30 p.m**.
Location: CBLL-16

Topic: LC-MS^3 Methods for TMT Phosphoproteomic Analysis

Abstract:

Phosphoproteins are the products of protein post-translational modification. They play a significant role in cellular signaling and modulate enzyme activities within cells. The combination of liquid chromatograph-mass spectrometry (LC-MS) and tandem mass tag (TMT) has been used to identify and quantify phosphoproteins in biological samples. This seminar will review the LC-MS^3 methods developed to improve TMT phosphoproteomics analysis. The improvements are achieved by optimizing the instrumentation parameters of high-resolution mass spectrometers or coupling additional devices to the instrument. Mathew and coworkers developed an LC-MS^3 method in which the MS^3 spectra were used in conjunction with MS^2 spectra to improve the identification and quantification of phosphorylated protein.[1] Devin and coworkers developed an LC-MS^3 method using high-field waveform ion mobility mass spectrometry (FIAMS)[2]. Xiaoyue and coworkers optimized instrumentation parameters for a multistage activation and neutral loss-triggered LC-MS^3 strategy, demonstrating their method improved in phosphopeptide identification than traditional LC-MS^3 methods[3].

References:

1. Matthew J. Berberich, Joao A. Paulo *et al*, "Utilizing MS3 Spectra beyond Quantification Yields Increased Coverage of the Phosphoproteome in Isobaric Tag Experiments", *Journal of Proteome Research* **2018** 17 (4), 1741-1747.

2. Devin K. Schweppe, Scott F. Rusin, *et al* "Optimized Workflow for Multiplexed Phosphorylation Analysis of TMT-Labeled Peptides Using High-Field Asymmetric Waveform Ion Mobility Spectrometry", *Journal of Proteome Research* **2020** 19 (1), 554-560.

3. Xiaoyue Jiang, Ryan Bomgarden, *et al* "Sensitive and Accurate Quantitation of Phosphopeptides Using TMT Isobaric Labeling Technique", *Journal of Proteome Research* **2017** *16* (11), 4244-4252.