Analytical Seminar

Presented by

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"The Utilization of NeuCode SILAC to Improve Data-dependent Peptide Identification and Enable Multi-plexed Data-dependent Peptide Quantification by Tandem Mass Spectrometry"

SILAC (stable isotope labeling of amino acids in cell culture) is a proteomic technique in which the metabolic incorporation of stable isotopes is used to differentially label biological samples for the sake of quantitative comparison. Our group recently introduced NeuCode SILAC, a quantification strategy which exploits the subtle mass differences inherent in stable isotopes due to discrepancies in nuclear binding energy. The use of NeuCode SILAC labeling generates closely spaced peptide precursor isotopologue partners (<40 mDa) that often permit the determination of peptide sequence and/or relative peptide abundance without further complicating tandem MS (MS/MS) spectra. We have developed software which uses this NeuCode technology to increase the speed and accuracy with which we can achieve peptide identification and to perform large-scale multi-plexed analyses without survey scan acquisition. We present a machine-learning algorithm, *yzID*, that facilitates peptide identification by rapid annotation of C-terminal fragment ions using NeuCode-specific spectral features (e.g., the isotopic doublet) from MS/MS scans. We also present software that utilizes these signature isotopic NeuCode clusters to perform multiplexed peptide quantification within MS/MS spectra resulting from the co-isolation and co-fragmentation of multiple precursors (SWATH methodology).

Thursday, March 6 at 12:15 p.m. in 1315 Chemistry