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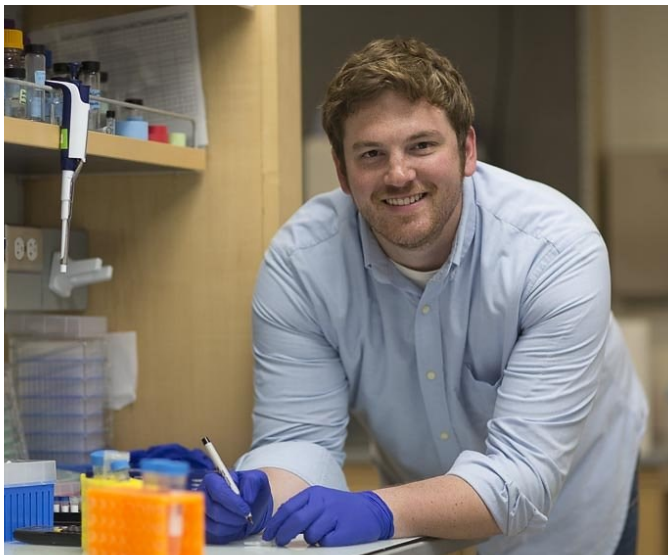
Analytical Seminar

"Activated ion electron transfer dissociation and global profiling of the glycoproteome"

Thursday
May 4, 2017

12:15 p.m.

Seminar Hall
(1315 Chemistry)



Protein glycosylation is a prevalent, chemically complex, and biologically diverse post-translational modification (PTM) associated with cellular proliferation, inter-cellular communication, and metabolic processes – making the characterization of the cellular landscape of protein glycosylation integral to advancing our understanding of cell biology. Glycan microheterogeneity, *i.e.*, different glycans modifying the same amino acid residue, makes glycan identity at a given site crucial to the biological context of the modification. This unique feature of glycosylation makes global analysis of intact glycopeptides imperative for glycoproteome characterization, but current analytical tools are ill-suited for this task.

Tandem mass spectrometry (MS) is an ideal platform to advance glycoproteomic technology, but current dissociation methods are often suitable only for characterization of either peptide or glycan moieties. This mandates multiple analyses of the same precursor ions that limit throughput and challenge data interpretation. We have developed a tandem MS dissociation method called activated ion-electron transfer dissociation (AI-ETD) that addresses several of challenges of intact glycopeptide analysis. Through the use of infrared photo-activation concurrent with ion-ion reactions, AI-ETD can access glycan and peptide information from intact glycopeptides in a single MS/MS scan, providing (1) improved product ion generation for peptide backbone sequencing, (2) higher MS/MS success rates to sequence more glycopeptides per experiment, and (3) valuable fragmentation for glycan composition determination.