Chemical modifications combined with mass spectrometry have been extensively used for identification and quantification of compounds of interest. Applications range from sample derivatization to the use of bioconjugation and chemical probes of protein structure. The Webb Lab uses solution and gaseous chemistries to facilitate the identification of compounds and their three-dimensional structures. We have used derivatization in the gas phase, a highly pure environment that accelerates reactions by orders of magnitude, with anion to cation charge inversion reactions coupled with ion mobility/mass spectrometry, to separate sugar isomers. Our group also uses chemical crosslinking, conducted in native-like solutions, to gain insight on the structures and conformational heterogeneity of dynamic protein systems. Finally, we use a combination of solution and gas-phase approaches with model folded and unfolded proteins to quantify the changes in structure upon ionization and analysis in the gas phase by mass spectrometry. We expect that these experiments will help us characterize to what extent so-called “native” mass spectrometry approaches, which in principle are high throughput and require minute amounts of sample, can be used to accurately solve structures of proteins and protein complexes.

DATE: THURSDAY, NOVEMBER 3rd, 2022
TIME: 12:05 PM – 1435 Learning Studio, North Tower

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