Hydrogen Exchange-Mass Spectrometry (HX-MS) for Analysis of Higher-Order Structure of Protein Therapeutics from Discovery to Production

Over the past three decades, hydrogen exchange-mass spectrometry (HX-MS) has advanced from an esoteric research tool to a highly repeatable analytical method sensitive to subtle changes in the higher-order structure of proteins. The method is now widely employed in drug discovery and vaccine development for the mapping of conformational epitopes. More recent work suggests that HX-MS data might also support in development and with regulatory considerations. This talk will begin with a brief overview of what is measured in HX-MS and how results are interpreted. Some examples of our recent work will illustrate some of the potential applications:

1. Broad characterization of the epitopic surface of ricin toxin
2. Mapping effects of preservatives and other excipients on mAb aggregation hotspots
3. Mapping sites of mAb reversible self-association
4. Rapid prediction of deamidation rates under long-term storage conditions
5. Development of an analytical framework to explore structural similarity of proteins

Wednesday, January 10, 2018
10:30 AM – 11:30 AM
Young Hall 2033

(Food and refreshments at 10:00 AM)

This Agilent Hydrogen Exchange-Mass Spectrometry Seminar will explore HX-MS of proteins as it relates to fundamentals, methods, and applications.

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