Challenges & Opportunities in Biopharmaceutical Higher Order Structure & Conformation Stability Analysis:

A Focus on HDX Applications

Live Webcast: Tuesday, March 27, 2012 at 7:30 a.m. PDT, 10:30 a.m. EDT, 14:30 GMT

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EVENT OVERVIEW

Regulators are encouraging the biopharmaceutical industry to improve biophysical characterization of protein therapeutics when performing drug safety evaluations. This is especially important for higher order structure integrity, conformation stability, and epitope mapping, all crucial steps for therapeutic antibody characterization. However, previously there was no widely available, high-resolution analytical method to characterize protein therapeutics in solutions. Hydrogen/deuterium-exchange mass spectrometry (HDX-MS) has become increasingly popular with academia and industry investigating protein dynamics, as well as protein-ligand and protein-protein interactions. Recent development of automation and data-extraction software enables the application of HDX-MS to protein characterization in the biopharmaceutical industry. Several companies have used or are considering using HDX-MS data for their regulatory agency filings. This webinar will detail the fundamentals of HDX-MS and its application to biopharmaceutical development.

Who Should Attend:

- Scientists who perform or will be performing protein conformational analysis using HDX
- Scientists who have been unable to obtain crystal structure data because of sample stability issues
- Early-stage protein therapeutic R&D scientists
- MS analysts who work with proteins
- IP professionals working with biopharmaceuticals
- Assay developers for small molecule and biotherapeutic groups
- Group leaders interested in familiarizing themselves with widely available technologies

Key Learning Objectives:

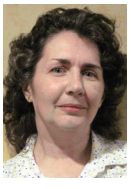
- Fundamentals of HDX-MS
- Application of HDX-MS for higher order structure characterization
- Application of HDX-MS for epitope mapping
- Challenges and utility of a commercial HDX automation solution
- Value of and uses for data from HDX studies
- Comparison with other protein characterization methods
- Approach for applying HDX data to traditional assays and for enhancement of computational docking

Presenters

Yoshitomo Hamuro
Senior Director of Technology Development
ExSAR Corporation

Eric Monroe
Post-doctoral Fellow
Department of Chemistry
University of Arizona

Moderator:



Amy Ritter
Scientific Editor
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For questions, contact Jamie Carpenter at jcarpenter@advanstar.com