



Hydrogen Deuterium Exchange (HDX) coupled to Mass Spectrometry (MS) analyses of protein structure/function

Understanding molecular details of proteins is critical for successful drug discovery, protein engineering or formulation development. However, traditional techniques often struggle to capture the dynamic nature of proteins in solution. Let us help you overcome this challenge using HDX-MS!

BACKGROUND

The concept of protein structure-function correlation has stimulated and guided applied research over the past decades. However, a detailed structural characterization of many systems is challenged by their intrinsic conformational dynamics that complicate analyses using standard techniques like x-ray crystallography, NMR or cryo-EM. HDX-MS (Hydrogen-Deuterium-eXchange – Mass Spectrometry) offers a complementary approach by directly addressing the conformational dynamics of proteins and providing straight-forward access to the characterization of multiple functionally relevant states.

TECHNOLOGY

HDX-MS enables the quantification of deuterium exchange at the amide position of the protein backbone. Since exchange at this position depends on solvent accessibility and secondary structure stability, the analysis of exchange kinetics of individual parts of the protein enables an assignment of their involvement in structural and functional perturbations of the system of interest. By using protease digestion after deuterium incorporation, a resolution of around 4-12 amino acids can typically be achieved for the functional interpretation.

OFFER

We offer a flexible approach to a range of scientific questions including, but not limited to:

- identification of ligand (drug) binding sites
- analysis of allosteric changes induced by drugs/ligands
- protein-protein interaction interfaces
- effects of post-translational modifications (heterogeneity, dynamics)
- analysis of conformational dynamics / assigning unstructured regions
- effects of solvent, pH, buffer composition on protein dynamics
- identification of allosteric effects in mutational analyses of proteins
- epitope mapping

Ready to elucidate the hidden potential of your protein? Contact us to discuss specifically tailored approaches to your scientific question - from project planning, to measurement, to analysis and final reports. We will show you how HDX-MS can be beneficial for your research and

acib-EXPERTS:

Dr. Andreas Winkler
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DEVELOPMENT STATUS:

Technology Readiness Level 2-7
(Problem set dependent from technology concept formulated to complete established analytical workflow)

IPR:

Can be generated and transferred to industrial partners / investors

PARTNER(S):

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KEYWORDS:

Epitope mapping
Protein-protein interactions
Mutational analysis
Post-translational modifications
Structural analysis

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development analyses, but also for routine measurements aiding e.g. the assessment of batch-to-batch reproducibility or ensemble heterogeneity in protein formulations.