

HYDROGEN-DEUTERIUM EXCHANGE MASS SPECTROMETRY SOLUTION

Proteins are complex biomolecules that are important for a wide range of biological processes, such as signal transduction, enzymatic catalysis, and supporting the structure of cells. Understanding the structure and function of proteins is essential for drug discovery and the development of new therapies. Hydrogen deuterium exchange mass spectrometry (HDX-MS) is a powerful tool that allows researchers to study the structure and dynamics of proteins in solution.

What Can Hydrogen-Deuterium Exchange Mass Spectrometry Offer?

Study of protein-ligand interactions: HDX-MS can provide information on the binding site and conformational changes of a protein upon ligand binding. This information is essential for drug discovery, as it can guide the design of new drugs that target specific proteins.

Study of protein conformational changes: HDX-MS can provide information on the stability and flexibility of a protein under different conditions, such as changes in pH, temperature, or binding to other proteins. This information is useful for understanding the mechanisms of protein function and can guide the design of new therapeutic interventions.

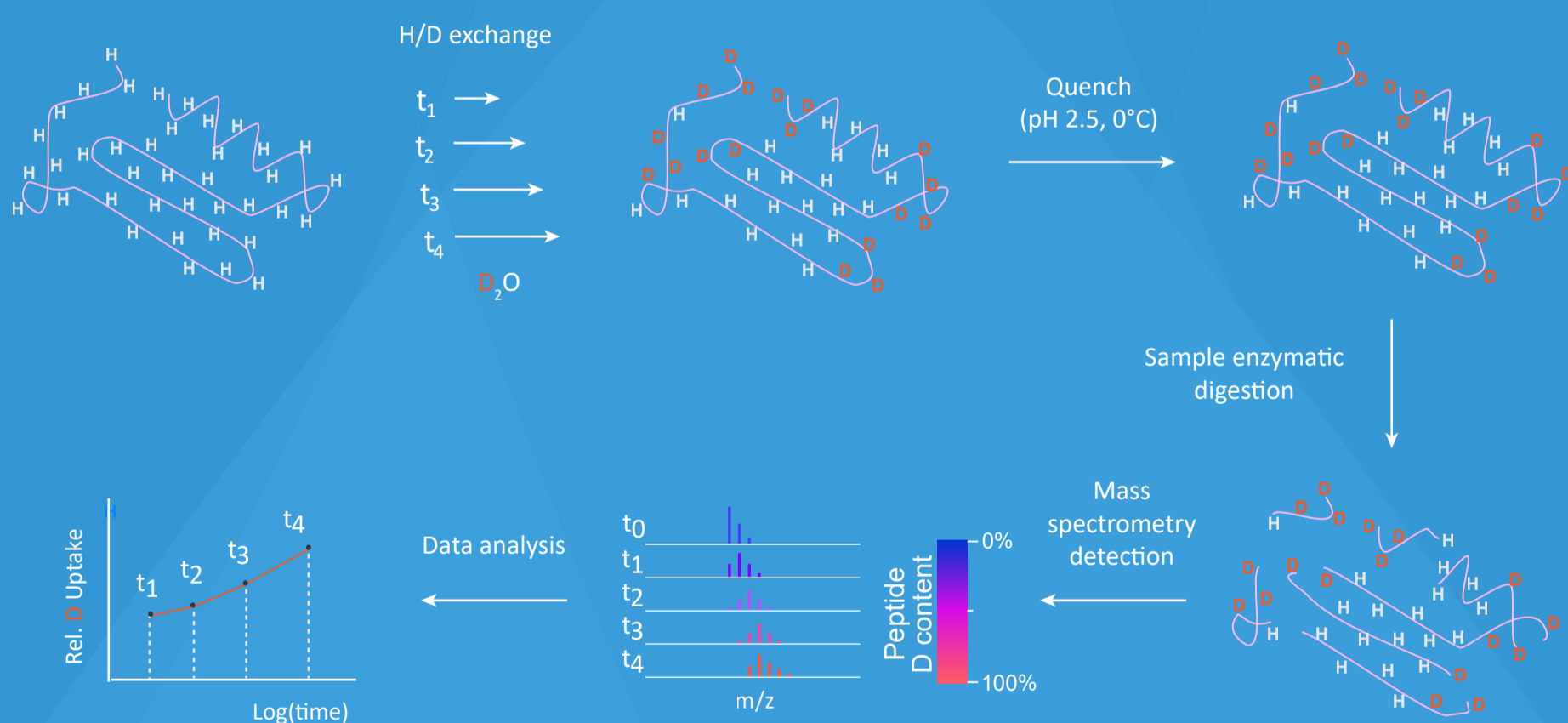
Study of protein-protein interactions and the structure and dynamics of protein complexes: determine protein-ligand binding sites and structural changes in proteins by comparing the H-D exchange rates of N-H bonds of amino acids at the same positions under different conditions.

Workflow of Hydrogen-Deuterium Exchange Mass Spectrometry

HDX-MS involves three main steps: (1) labeling the protein with deuterium, (2) quenching the HDX reaction, and (3) mass spectrometry analysis. In the labeling step, a protein sample is exposed to a deuterated solution for a specific period of time, typically ranging from a few seconds to several hours. The deuterium atoms in the solution exchange with the hydrogen atoms in the protein backbone, and the rate of exchange depends on the accessibility of the hydrogen atoms.

In the quenching step, the exchange reaction is stopped by lowering the pH and temperature of the solution.

In the mass spectrometry analysis step, the enzymatic peptides are ionized and fragmented, and the mass spectra are used to determine the degree of deuterium labeling at each amide in the protein backbone. By comparing the rate of protein labeling by deuterium under different conditions, researchers can obtain information on the structural changes and dynamics of the protein.



Why Choose Creative Proteomics?

Advanced Technology and Expertise

State-of-the-art HDX-MS system is equipped with the latest UPLC technology and advanced Orbitrap Exploris 240 Mass Spectrometer.

Precise Control and High Sensitivity

Temperature control at $0 \pm 1^\circ C$ and accurate control of the hydrogen deuterium reaction time by an automated process ensure reproducible results with high sensitivity and accuracy.

Timely, Interactive Results Management

Provide extensive and timely data analysis and results management with our advanced software tools, including MassLynx, DynamX HDX data analysis, IDENTIFYE, and ProteinLynx Global SERVER.

Customized Services and Rapid Turnaround Time

Customized HDX-MS services to meet the specific needs of our clients, including method optimization based on sample type, size, and service.