Creative Proteomics

Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS)

Proteins play a pivotal role in various biological processes, including signal transduction, enzymatic catalysis, and cellular structural support. Gaining insights into protein structure and function is crucial for advancing drug discovery and the development of innovative therapies. Hydrogen-deuterium exchange mass spectrometry (HDX-MS) emerges as a robust technique, enabling researchers to delve into the structure and dynamics of proteins in solution.

At Creative Proteomics, we take pride in our exceptional proficiency in HDX-MS services, leveraging over a decade of experience in the mass spectrometric analysis of protein interactions and complexes. Our cutting-edge technology ensures reliable results, delivered within a predetermined time frame, setting us apart as a leading service provider in the field.

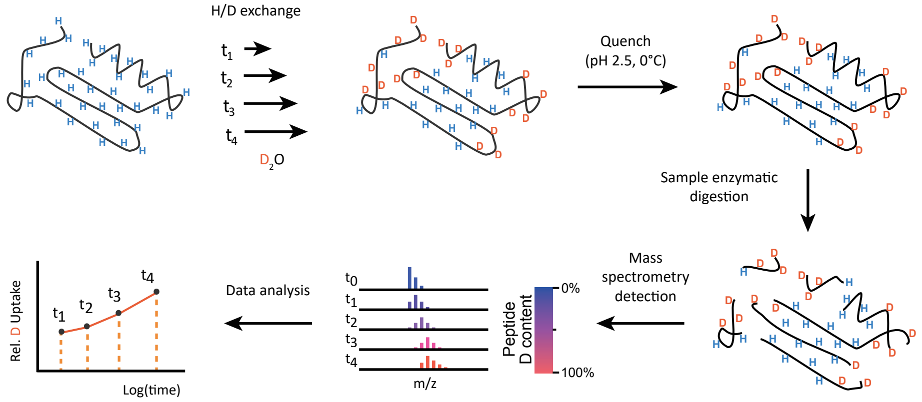

Fig 1. Workflow of HDX-MS

Advantages of HDX-MS

1) Solution-phase measurement: allowing analysis of proteins in their native, bioactive solution environment
2) Label-free analysis: simplifying the sample preparation and shortening experimental time consumption
3) High Sensitivity: performing assays with low sample consumption (microgram level)
4) Versatility: working well under diverse scenarios, targeting peptides to large proteins

What Can HDX-MS Offer?

- Protein conformation and dynamics
- Epitope mapping
- Binding site identification for protein-related interactions
- Binding dynamics between proteins and drugs
- Effects of protein mutations or other treatments on protein conformation and dynamics

Notable Benefits with Creative Proteomics HDX-MS Service

- **Advanced Technology and Expertise**

The state-of-the-art HDX-MS system is equipped with the latest UPLC technology and an advanced Q Exactive™ Hybrid Quadrupole-Orbitrap™ Mass Spectrometer.

nanoACQUITY UPLC System

Q Exactive™ Plus Hybrid Quadrupole-Orbitrap™
Mass Spectrometer

- **Precise Control and High Sensitivity**

The UPLC-HDX-MS system provides precise temperature control at 0±1˚C, which minimizes the hydrogen-deuterium atom back-crossing reaction and ensures accurate results.

Automated pre-treatment and injection analysis with precise control of the hydrogen-deuterium atom exchange reaction time ensure reproducible results with high sensitivity and accuracy.

- **Timely, Interactive Results Management**

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