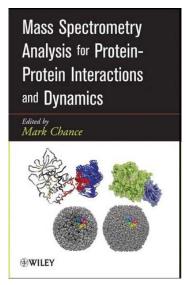
Protein Structural Analysis by Mass Spectrometry: Hydrogen Exchange and Covalent Labeling

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Obtain information about protein conformation and structure by selectively labeling proteins in solution, then using mass spectrometry to locate the label



Course textbook

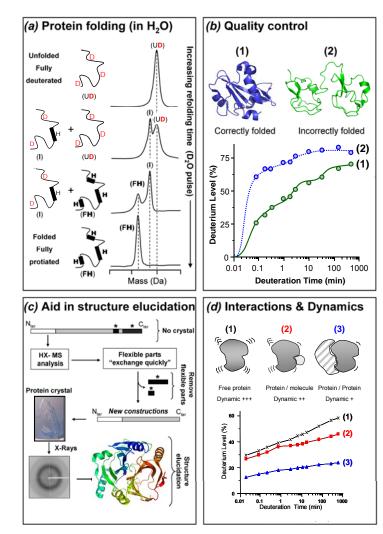
Day 1: Protein structure refresher, as applied to MS

Methods of hydrogen exchange mass spectrometry

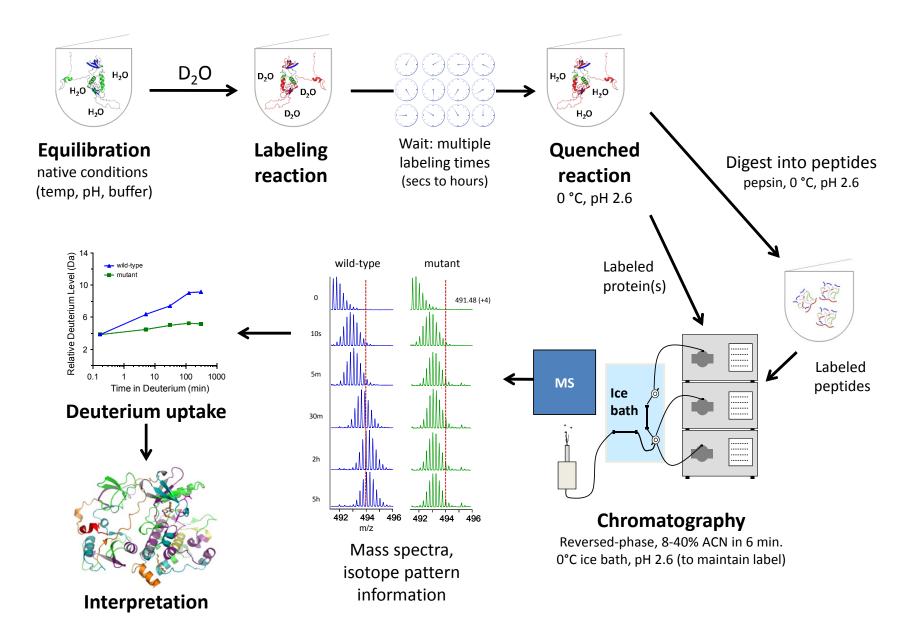
Day 2: Methods of covalent labeling and crosslinking

What can be learned from Hydrogen Exchange (HX) Mass Spectrometry (MS)?

- Protein folding pathways
- Proper folding of proteins
- Structural information
 - those that cannot be crystallized
 - those too big for NMR
 - those that are hard to prepare/purify
- Protein dynamics
 - where structures are mobile
 - where structures change
 - complexes, epitope mapping
 - conformational changes during function, binding, activation, etc.



Continuous Labeling HX MS Experiment



What can be learned from Footprinting MS?

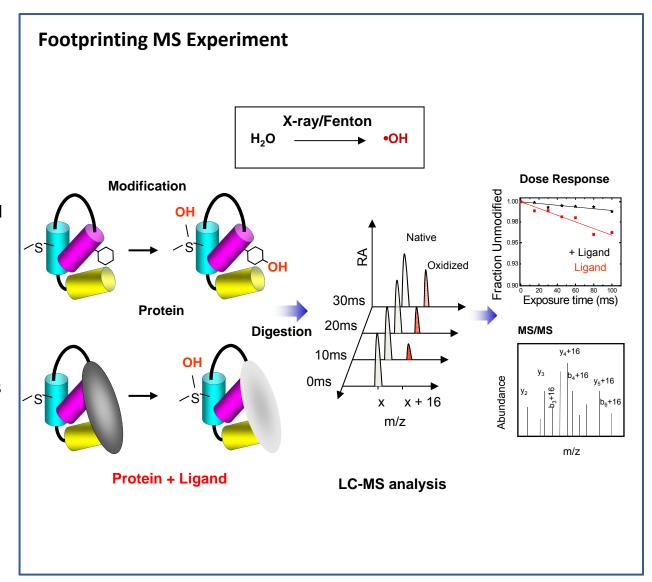
Protein folding

Structural information

- macromolecular assemblies that can not be crystallized or too big for NMR
- membrane proteins
- proteins in various physiological conditions
- interactions of bulk, bound, ordered water

Protein Dynamics

- changes in protein structure
 - > binding interfaces, complexes
 - conformational changes during activation, ligand binding, function, etc.
- water dynamics within the transmembrane region
- structure of mobile protein regions



What can be learned from Cross-linking MS?

Structural information

- protein subunits
- conformational changes of proteins
- big protein assemblies that can not be crystallized or too big for NMR

Protein interactions

- interactive analysis
- analysis of transient interactions
 - > in vitro cross-linking
 - > in vivo cross-linking

Bioconjugation

- immunotoxin construction
- immunogenic preparation
- protein-protein conjugation
- Solid-Phase Immobilization
- DNA/RNA Cross-linking to proteins

