# Crosslinking and Hydrogen/Deuterium Exchange Mass Spectrometry infrastructure service in the ISB platform

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Crosslinking Mass Spectrometry (XL-MS) is a method that uses sidechain reactive chemical crosslinkers to covalently link amino acid residues in a distance-dependent manner and offers comprehensive data on protein structure. The data generated by XL-MS can be employed to examine large protein complexes or to provide distance restraints that assist in the modeling of protein structure. Recent advancements have led to the increased use of crosslinking for system-level studies, such as the identification of protein-protein interaction networks within complex systems Figure 1.

Hydrogen/Deuterium Exchange Mass Spectrometry (HDX-MS) is a powerful technique for investigating higher-order protein structures, including protein conformation, dynamics, and interactions. This method relies on the natural exchange of backbone amide hydrogen with deuterium, resulting in a detectable mass increase by MS Figure 2. The use of this technology is expanding rapidly in both academic and biopharmaceutical settings, where HDX-MS is commonly used for evaluating batch consistency, protein stability, and epitope mapping.

We provide HDX-MS and cross-linking analysis as a service through the SciLifeLab, Integrated Structural Biology platform (ISB), and BioMS infrastructure at subsidized cost on an equal opportunity basis. Examples from published user projects covering; protein dynamics(1), protein-small ligand interaction(2), epitope mapping(3), protein-RNA interaction(4), protein complex analysis(5), and protein-protein interactions (6) will be presented.

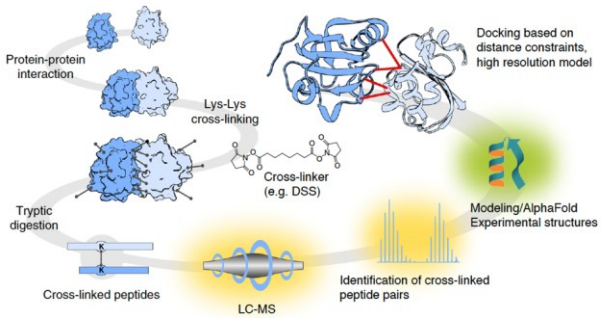


Figure 1. Bottom-up, chemical crosslinking MS with structural modeling.

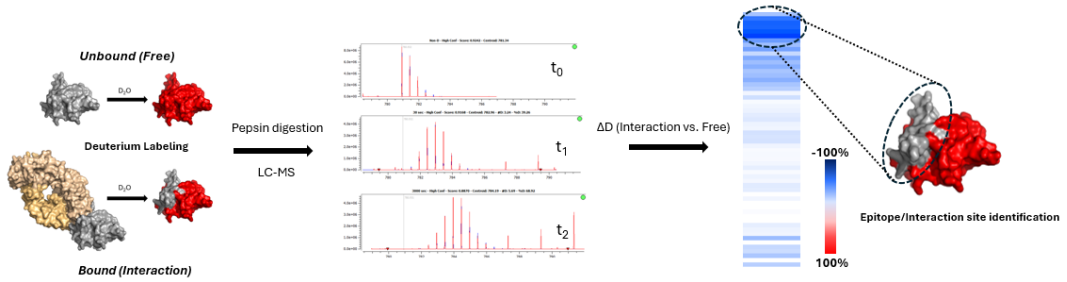


Figure 2. Bottom-up, continuous uptake, proteolytic fragmentation HDX-MS experiment.

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