

Hydrogen scrambling in non-covalent complexes of peptides.

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Mass spectrometry analysis combined with hydrogen-deuterium exchange (HDX-MS) is arising as a tool for quick analysis of native protein conformation. However, during collision-induced dissociation (CID) the spatial distribution of deuterium is not always conserved. It is therefore important to find out how hydrogen scrambling occurs--this study concentrates on the possibility of scrambling between amino acid residues spatially close together, but not connected by covalent bonds.

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