

## FROM PROTEIN CHEMICAL MODIFICATION TO CROSS- LINKING AND BEYOND

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Even the first protein structural models were built using X-ray crystallography sixty years ago; there are still many protein sequences with unknown 3-D structure. The tremendous progress in mass spectrometry in last decades opened the space for studying protein folding, protein/ligand interactions and protein dynamics in solution. The potential of ion mobility, chemical cross-linking and hydrogen/deuterium exchange for structural biology will be discussed.

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CFEL  
SEMINAR ROOMS I-III

