

Mass spectrometry goes viral – an introduction to structural MS

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Over the last twenty years, mass spectrometry (MS) with its ability to analyze small sample amounts with high speed and sensitivity has more and more entered the structural biology with the goal to investigate the structure and dynamics of proteins as close to their native environment as possible. The use of non-perturbing labels in hydrogen-deuterium exchange MS allows for the analysis of interactions between proteins as well as their dynamic responses to the environment. Cross-linking MS on the other hand can analyze interactions in protein complexes and identify interactions in cells. Native MS allows transferring multi-protein complexes into the gas phase and has broken boundaries to overcome size limitations, so that now even the analysis of intact virions is possible. In this presentation I will introduce the principles structural MS methods and give an overview of how they bridge the gap to other biophysical techniques, and provide valuable constraints for integrative structural modeling of protein assemblies that are inaccessible by single technique approaches.