



## Structural MS of proteasome complexes: a test-case study

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Structural Mass Spectrometry (MS) approaches are now important tools for integrative structural biology. They give access to a wide range of information, from protein primary to quaternary structure, dynamics and interactions. Top-Down MS [1-2] provides a thorough description of proteoforms present in the sample. Native MS [3] and Mass Photometry [4] of entire complexes inform about their stoichiometry as well as ligand binding. Cross-linking MS [5] can identify new binding partners and provides distance restraints that can be further used for molecular modeling. Finally, Hydrogen-Deuterium eXchange MS (HDX-MS) investigates solvent accessibility, providing information on dynamics and highlighting binding interfaces or long-range allosteric changes [6].

This talk will take advantage of the wide diversity of proteasome complexes to illustrate how these innovative techniques can be applied, complementarily to shotgun proteomics and high-resolution structural methods, to gather precious and orthogonal structural information.

### References:

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