The key role of native mass spectrometry in characterising the structure and dynamics of macromolecular complexes

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Elisabetta got her MSc degree in Chemistry from the University of Turin (Italy). She moved to the University of Southern Denmark for her PhD studies in phosphoproteomics under the supervision of Prof. Nørregaard Jensen. As postdoc, she worked at the University of Cambridge in the group of Carol Robinson and at the ETH (Zurich) in the Zenobi's laboratory. Since 2011 she is an independent principal investigator at Institute of Structural Biology (Grenoble) where she studies protein complexes with a specific focus on medically relevant assemblies (e.g., Transthyretin and HIV-1 ribonucleoparticles).

Abstract:

Mass spectrometry (MS) performed under so-called "native conditions" (native MS) can be used to assess the mass of biomolecules that associate noncovalently. One can determine the precise stoichiometry of intact assemblies, the direct interactions between subunits and the relative position (core vs. periphery) of subunits within a complex. By mixing subunits in a stepwise manner, a hierarchy in the assembly pathway can be determined.

I will illustrate the application of native MS to the study of the structure of macromolecular assemblies, including protein complexes involved in host-pathogen interactions. Overall, native MS is useful for gaining important insights into the composition, structure and dynamics of macromolecular complexes.