



“A single protein complex, multiple forms - Towards uncovering the inherent complexity of protein complexes”

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Abstract

The way we perceive protein complexes is changing in the last years with the realization that what were once thought to be single entities may actually represent variable assemblies with distinct functions and regulation. This increased complexity is enabled through a variety of protein diversification mechanisms that exist at every step of the protein biosynthesis pathway, such as alternative splicing and post translational modifications. Since the resulting protein variants are highly related but chemically different, it is not surprising that they generate compositionally distinct protein assemblies. These different forms of a single protein assembly may comprise functional variances that enable response and adaption to varying cellular conditions.

Yet, despite the biological importance of this layer of complexity, relatively little is known about the compositional heterogeneity of protein complexes, mostly due to technical barriers of studying such closely related species. In my talk I will describe our recent advancement in native mass spectrometry capabilities that enable to investigate the multilevel diversity of protein assemblies.