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Native ion mobility-mass spectrometry: from flexible proteins to ion channels.

Frank SOBOTT
Biomolecular & Analytical Mass Spectrometry and Center for Proteomics, University of Antwerp, BELGIUM

After a brief introduction into the field of native mass spectrometry and ion mobility analysis of protein complexes, we discuss how native IM-MS can give powerful insights into the stoichiometry, subunit composition, size and shape of biomolecular particles. A novel approach, top-down ETD of native proteins, is used to map exposed surfaces of proteins and complexes. In combination with ion mobility, we can achieve conformation-sensitive fragmentation and score structural models in conjunction with steered molecular dynamics calculations.

We will show recent data on protein conformational studies and protein complexes which are involved in the regulation of gene expression. The example of SMC proteins, which are crucial for the structural maintenance of chromosomes, illustrates the ability of ion mobility approaches to link information on complex assembly with the topology of the functional unit in heterogeneous systems, in conjunction with EM and AFM data.

Recently, we have also been studying ion channels in detergent micelles and nanodiscs, and have been able to show the gradual opening of the Mechanosensitive Channel of Large Conductance (MscL) in response to the binding of a charged drug molecule inside the channel which mimics the pressure on the bulk membrane.