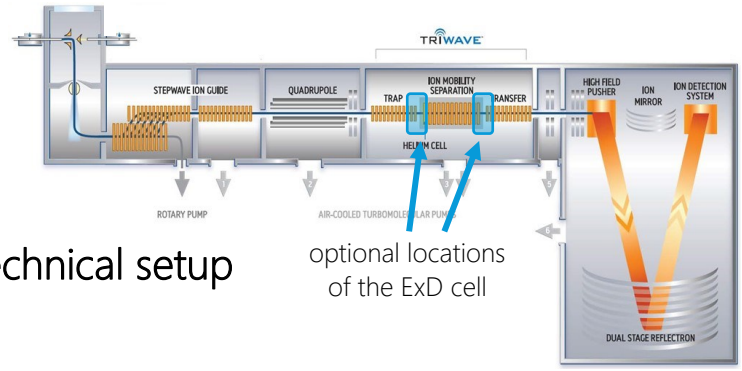
MSVision

eMSion

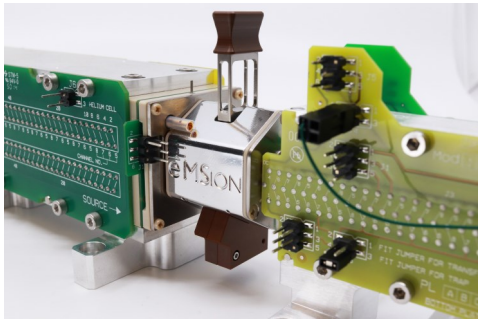
ECD for the Masses

ECD Upgrade for Synapt HDMS Systems for High Mass and Top-down Mass Spectrometry



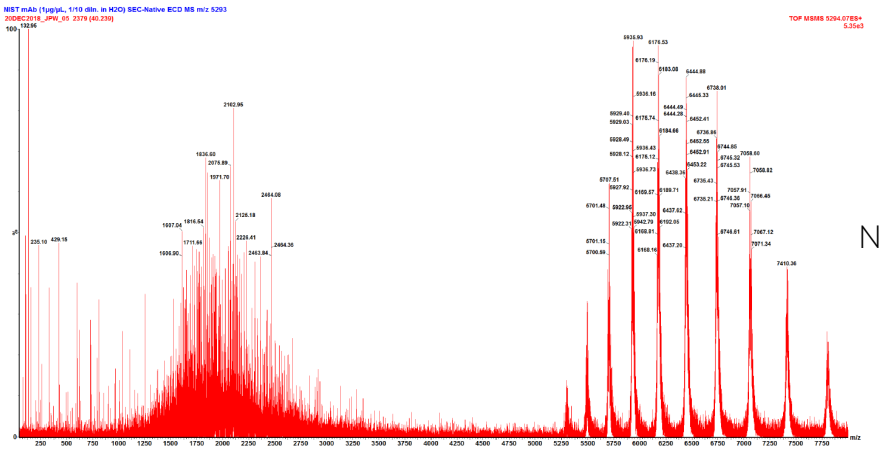
Technical setup

optional locations of the ExD cell



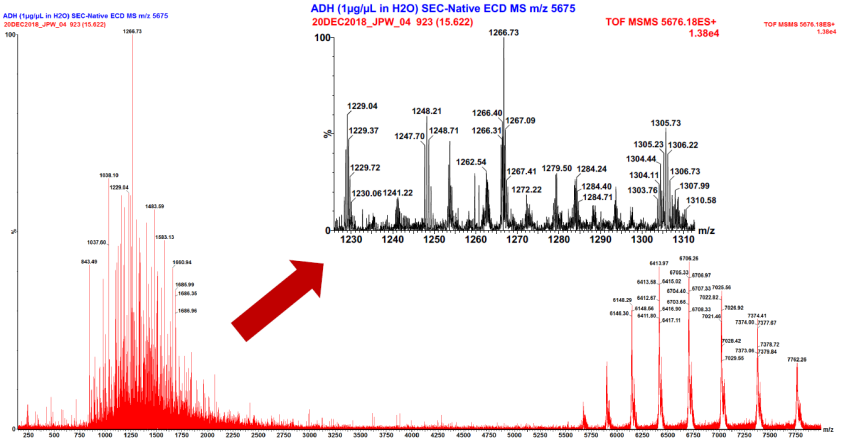
Picture of the pre-IMS-ExD cell

The ECD cell can located between the trap collision cell and the ion mobility cell as well as between IM and transfer section of the TriWave. The trap collision can be used to open up the structure of globular proteins, thus promoting subsequent ECD fragmentation. Additionally, IMS separation can be used to separate fragment ion charge states to reduce charge state overlap and simplify spectra.



ECD-Fragmentation of NIST monoclonal antibody

Fragmentation of ADH tetramer complex under native conditions. Rich ECD fragmentation allowing for detailed sequence characterization



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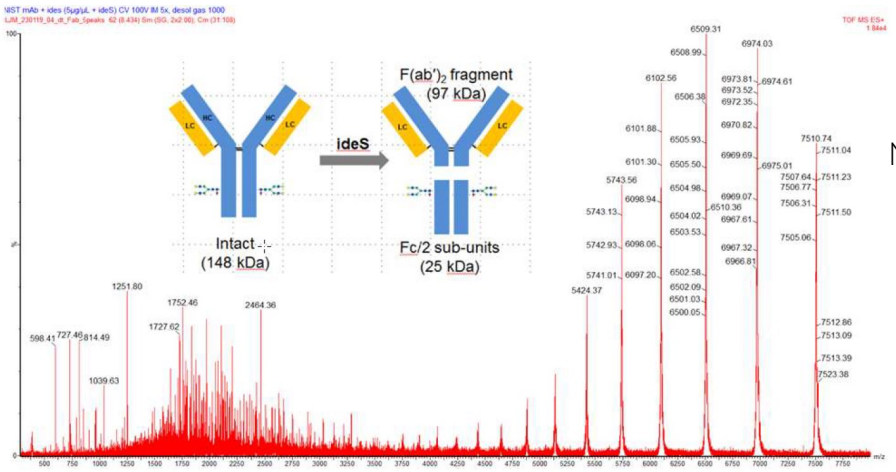
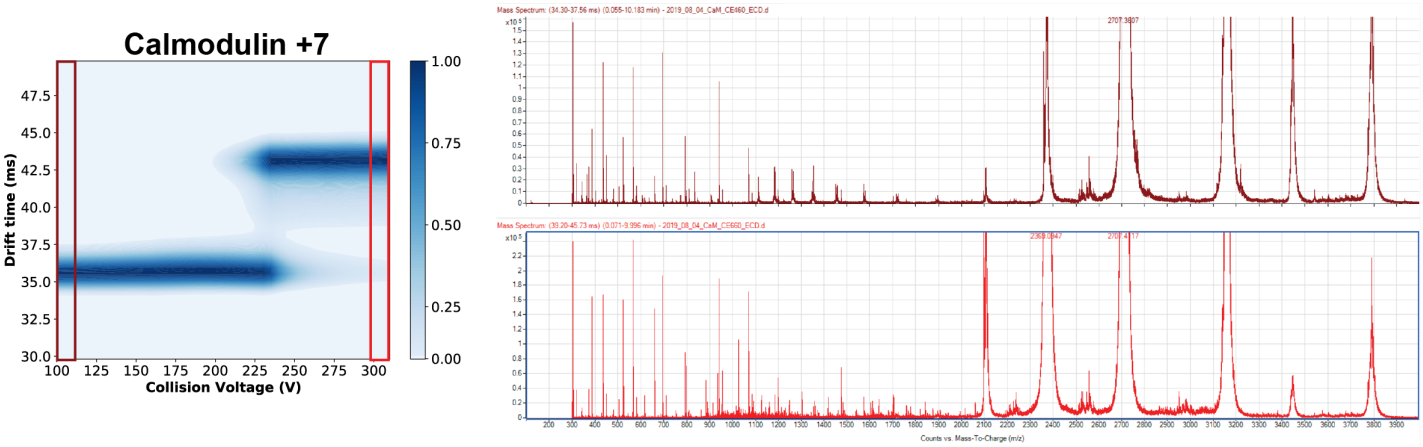


Native IMS-ECD spectrum of IdeS digested NIST mAb resulting in 97kDa F(ab´)$_2$ fragment

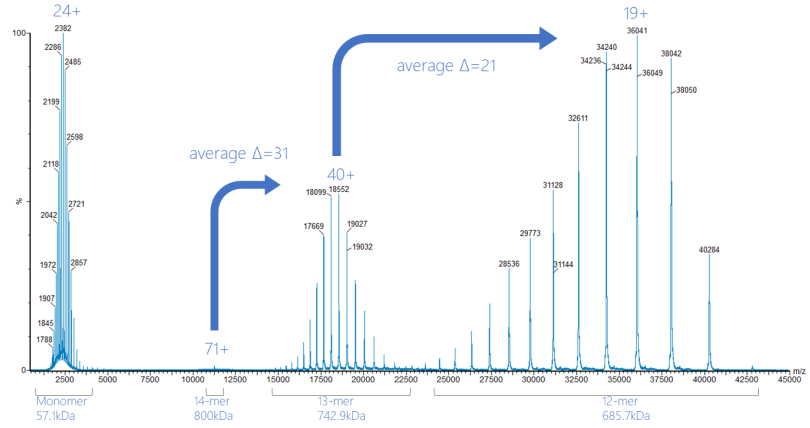
Activated Ion ECD

A recent paper by V.V. Gadkari *et al.* („Enhanced Collision Induced Unfolding and Electron Capture Dissociation of Native-like Protein Ions", Anal. Chem. 2020, 92, 15489−15496) exploits the possibilities to open up and unfold globular protein structures and non-covalent complexes by collision-induced unfolding. The different structures can be separated by IMS and subsequently fragmented by ECD as in this example of the analysis of two different structures of the 16 kDa 2-domain protein Calmodulin:



Data courtesy of Carolina Rojas and Brandon Ruotolo, University of Michigan

Non-covalent complex analysis



Top-down analysis of the 801 kDa GroEL complex on MS Vision Native Synapt.

MS Visions dedicated high mass modifications for Waters Synapt systems allow you to go even further: where conventional systems can isolate up to 4.000 Da, the MS Vision Native Synapt can go up to 32.000 Da for precursor isolation. This allows you to run experiments with analytes in the Megadalton range.

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