Native Synapt

PROVEN TECHNOLOGY TAILORED FOR HIGH MASS ANALYSIS

Seeing the big picture made easy

Challenging the mass spectrometer

Overcoming the limitations of standard MS instrumentation in the analysis of large protein structures has been the focus of our efforts over the past decade. By working together closely with leading academic groups, we learnt how to get the best out of the mass spectrometer. The result is an instrument which allows researchers to unleash the full capability of the Synapt in the analysis of intact proteins and complexes.

Antibody analysis

purity, molecular weight

Ag-Ab interaction studies

stoichiometry, affinity

Ab PTM analysis

glycosylation, ADC's

Protein complexes

protein-protein interactions

Virus capsids

composition analysis

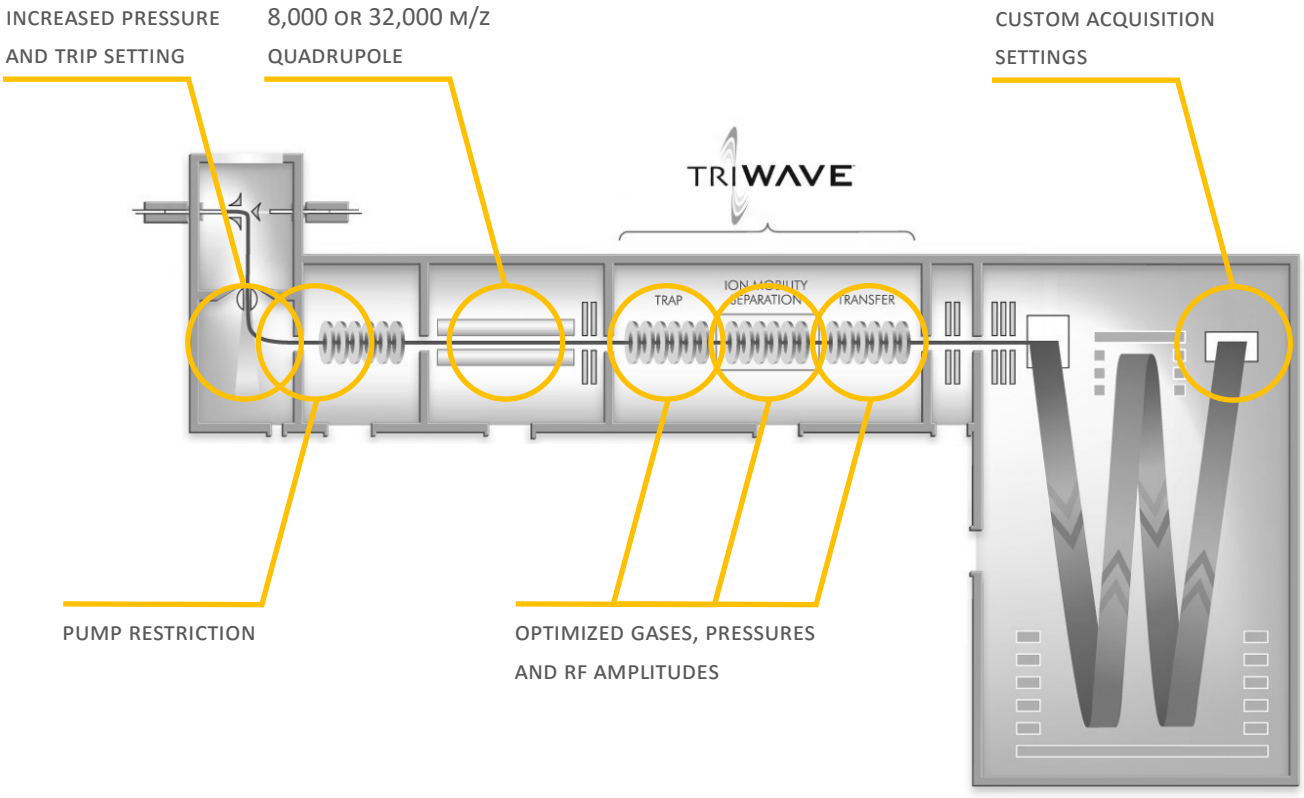
MSVision

Dedicated to Mass Spectrometry

Native Synapt

Turning the Synapt into a Native MS platform

The interest in MS of large biomolecules and biomolecular complexes has increased in recent years. Mass spectrometric study of intact proteins and their function in non-covalently bound complexes is providing more information about complicated biological systems. It is well known that intact large protein complexes can be transferred into the gas phase using nano-electrospray ionisation under native conditions, but subsequent MS or MS/MS analysis is prohibited by mass-scale, ion transmission or ion thermalisation limitations on standard instrumentation. These limitations have now been overcome, and all analytical tools available on the Synapt can be fully exploited in the study and analysis of large proteins and their complexes.



Making it work better

By careful consideration of the conditions that exist in the consecutive sections of the instrument, the performance of the Synapt for large ions can be improved considerably by changing the characteristics of the ion optical elements.

No compromise

All functionality of the original instrument is available on the Native Synapt. Simply choose between modes and analyze your samples. Soft conditions for preservation of complexes, high energy dissociation, Ion Mobility - it's all possible.

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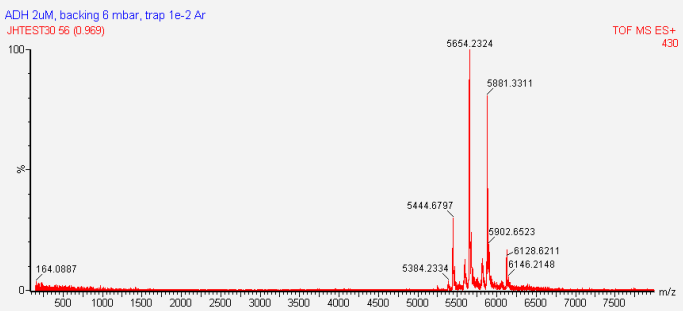
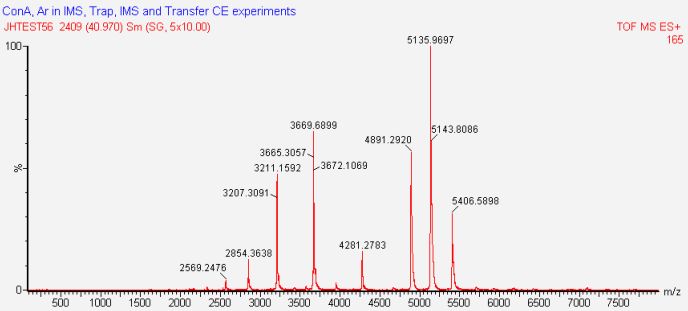


SENSITIVITY SINGLE SCAN DATA FOR 2µM ADH



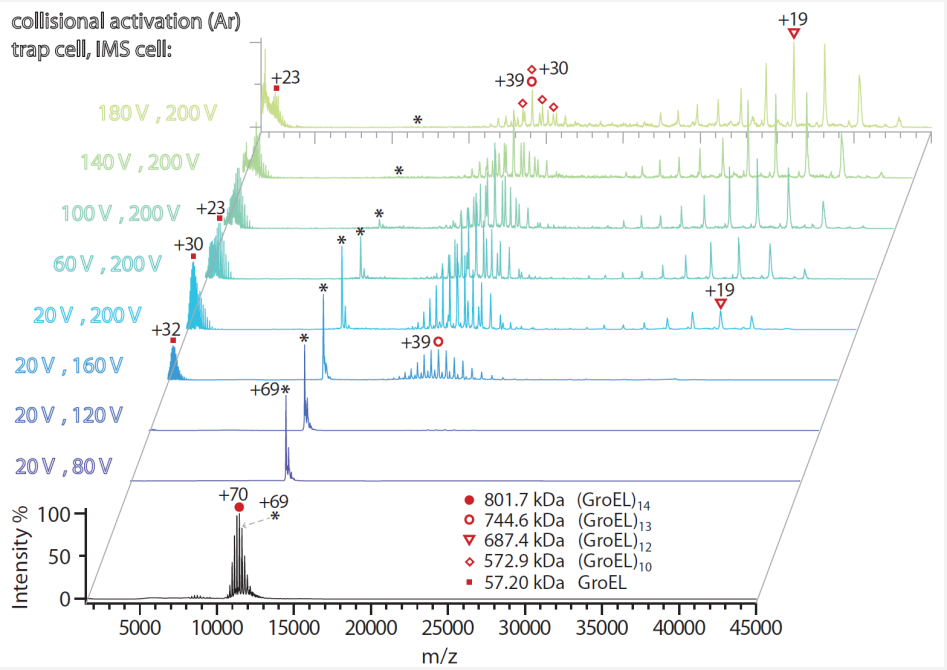
LOW ENERGY ACTIVATION OF CONCANAVALIN-A

Refolded E. Coli GroEL in 200 mM ammonium acetate pH6.7

ToF MS spectrum (black) of the GroEL tetradecamer and MS/MS spectra (blue to green) recorded after isolation and collisional activation of its +69 charge state. Acceleration voltages for collisional activation as indicated on the left side of each spectrum.

Argon, 4.0E-2 mbar in IMS cell, trap cell 1.2E-2, transfer cell <1E-3

Data courtesy of Dr. Friedel Drepper, University of Freiburg



Upgrade or full instrument

Whether you want to have your own Synapt upgraded or need a complete instrument, MS Vision has the solution. We offer full support by our highly skilled engineers so you can concentrate on running your samples.

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