

LCMS-IT-TOF™

A revolutionary quadrupole ion trap – time of flight instrument

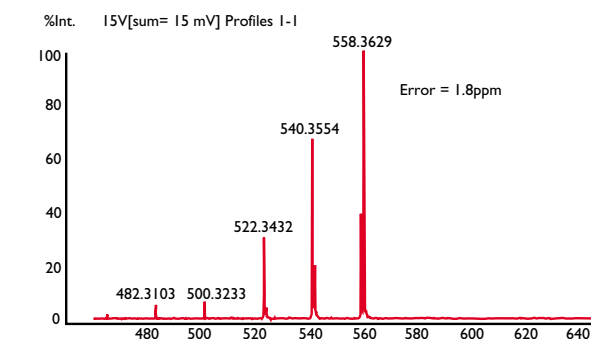
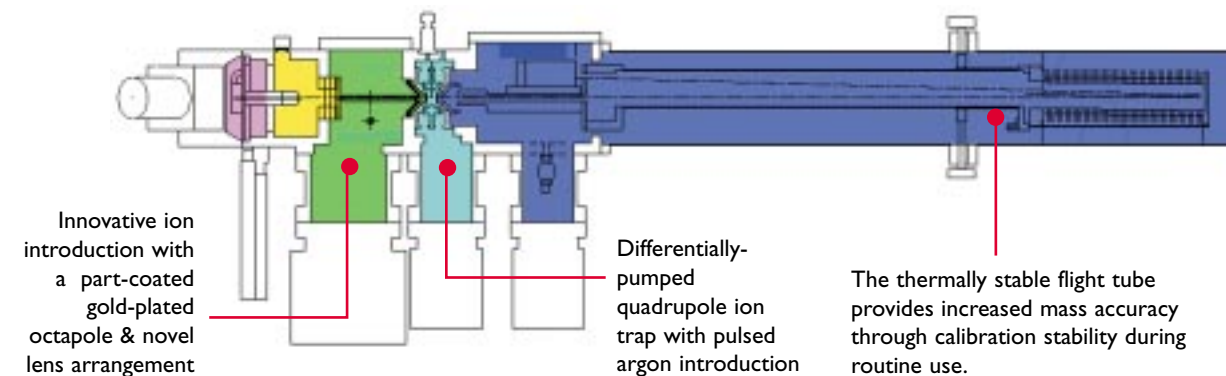
This new hybrid LC TRAP TOF™ mass spectrometer delivers high sensitivity, high mass accuracy and resolution in all MS modes.

Key points

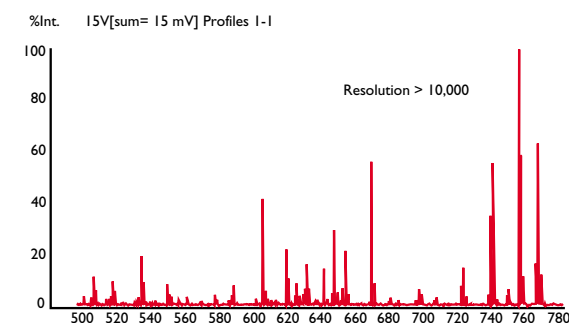
- Mass accuracy remains constant in all modes and is independent of the ion processing prior to the ion trap
- Unique design not only maximises trapping efficiency, but also provides extremely high extraction efficiency, leading to increased sensitivity in comparison to linear trapping devices.
- Advanced electronics allow the use of an axial TOF analyser without any loss of resolution. This overcomes the disadvantages of orthogonal TOF configurations, such as limited mass window and lowered sensitivity.
- Using a 2-stage gridless reflectron, ions released from the ion trap follow a 1.8 metre flight path, which provides resolution in excess of 10,000 in all MS modes.

Key features of ion transmission and detection

- Ions generated at atmospheric pressure using electrospray ionisation were transferred to a 3-D quadrupole ion trap (QIT) using Rf ion guides. The trapping efficiency of the trap was maximised using a novel ion introduction method consisting of a quadrupole array ion guide, octapole and a unique lens arrangement.
- After the ions were trapped they were then collisionally cooled following the introduction of argon and extracted out of the ion trap following CID by simultaneously stopping the Rf and applying fast rising pulses to the endcap electrodes.
- Precursor and product ions were ejected from the trap into a time of flight mass analyser specifically designed to maximise reproducible mass accuracy measurements.
- When the ions exited the trap, they entered a floating flight tube kept at the same potential as the pulse of the second endcap electrode (field-free region).



Mass accuracy for erythromycin at 1.8 ppm in MS₃ mode.



Mass resolution greater than 10,000 for Angiotensin 11 in MS₃ mode.

- This novel LC-QIT-TOF mass spectrometer configuration provides a platform for the structural elucidation of pharmaceutical compounds or metabolites and de novo sequencing of peptides.
- The high resolution afforded by the ion trap provides high specificity in precursor-ion selection, leading to simplified interpretation of spectra as the numbers of unassignable peaks is greatly reduced.
- The high mass accuracy of the time of flight mass analyzer provides the exact mass assignment necessary for confident elucidation of the structures of unknown compounds, which remains constant in all MS modes.