

AXIMA-QIT™

**MALDI-Quadrupole Ion Trap-TOF
Mass Spectrometer**

A unique mass analyzer
combining the simplicity of
MALDI, the power of MSⁿ and
accuracy and resolution of TOF
for the next generation of
proteomics challenges



Solving the next generation of proteomics challenges

Every 5 years a new technology is launched on to the market which has a profound influence on the way we solve problems. The AXIMA-QIT™ – the most revolutionary new development since the commercialization of MALDI mass spectrometers – designed to meet the new challenges of proteomics.

The AXIMA-QIT™ is designed for the structural characterization of biomolecules, not just mass measurement. The AXIMA-QIT™ is a unique hybrid instrument employing:

Matrix assisted laser desorption ionization (MALDI)

- Virtually limitless time for sequential sample queries
- Minimal sample preparation, method development and optimization
- Single spectrum analysis of complex mixtures

Quadrupole ion trap (QIT)

- True MSⁿ for structural studies
- Variable energy CID control
- High resolution precursor ion selection

Reflectron time of flight (TOF) mass analyzer

- High mass resolution across MS and MSⁿ analyses
- Constant mass accuracy across MS and MSⁿ analyses

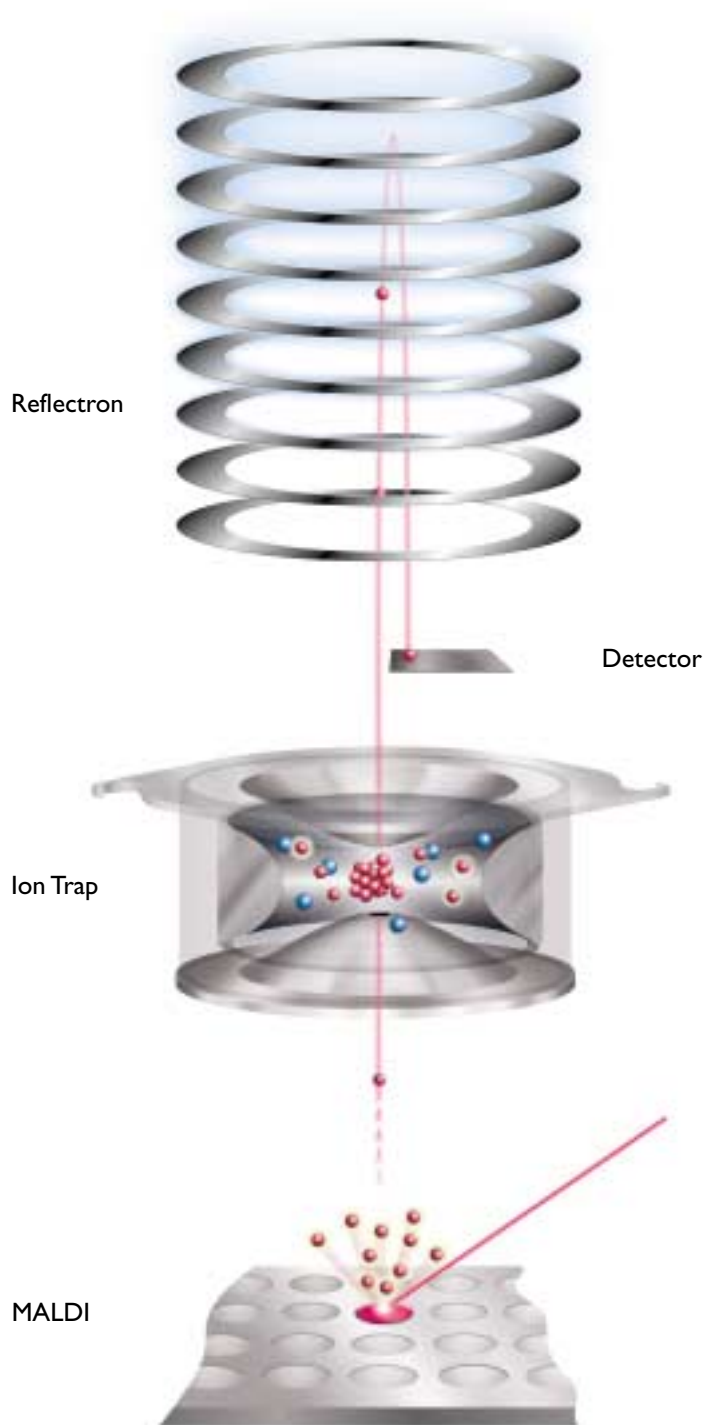
In addition, this unique MALDI QIT TOF combination provides a number of novel features:

- Time-of-flight resolution and accuracy independent of laser energy applied
- Extremely low acceleration voltage (<100 V) providing excellent tolerance to non-conductive non-flat materials, without compromising sensitivity
- Near-perpendicular laser irradiation for high efficiency ion generation and ion transfer to the quadrupole ion trap
- Wide mass range of ions trapped



A unique hybrid combination

The AXIMA-QIT™ is equally able to undertake analysis of complex mixtures, MSⁿ fragmentation for Post-Translational Modification characterisation and high mass MS/MS analysis for protein identification.



The ergonomic design of the AXIMA™ product range makes installation and service easy; the height and wheels allow unhindered mobility through conventional doors while easy internal access and remote modem diagnostics ensure rapid service response.

The powerful and established LAUNCHPAD™ software supports the unique functionality of the AXIMA-QIT™ with the addition of INTELLIMARQUE™ automated data dependent MS/MS analysis.

Offering unparalleled performance

The AXIMA-QIT™ is designed to take full advantage of the best aspects of mass spectrometry. It offers unparalleled performance to help solve the next generation of problems in proteomics where protein identification and understanding of the structural significance of target proteins in biological function or drug discovery will require elucidation of 100% of protein sequences.

- **High Mass Accuracy**

High mass accuracy can be achieved regardless of the MS mode applied, making database searching and target characterisation more effective.

Figure 1 displays superior mass accuracy measured by internal calibration for a selection of ions obtained by MS/MS/MS of Angiotensin II.

- **True MSⁿ capabilities**

The unique characteristics of the instrument allow controlled, flexible and complete fragmentation which remains searchable for target identification and characterisation.

The spectra opposite (fig. 2) for Angiotensin II demonstrate sequential precursor ion selection generating fragment information down to MS⁴ and enabling observation of the immonium ion mass range.

- **High resolution ion selection**

Ion selection resolution of >1000 allows discrete analysis of unit Dalton regions of a precursor ion spectrum.

Selection of a single isotope for an MS/MS study gives the capability to exclude potential contaminant peaks and enhance the analysis of fragmentation patterns in the MS/MS spectra of Angiotensin II (see fig. 3).

- **Wide mass range of ion trapping**

- **A single calibration across all modes of analysis – MS and MSⁿ**

- **High mass MS/MS analysis – a powerful tool for protein ID by database searching**

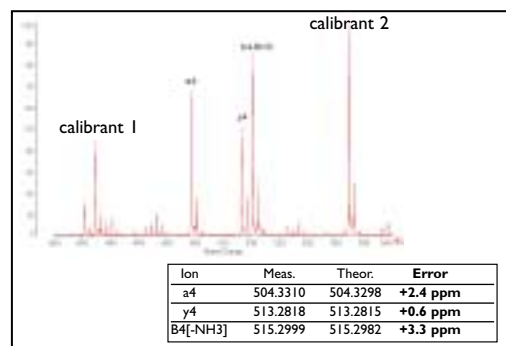


Fig. 1

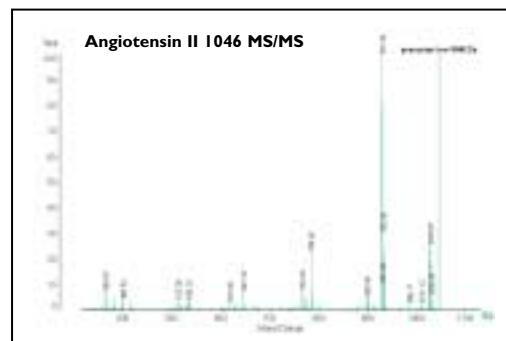


Fig. 2a

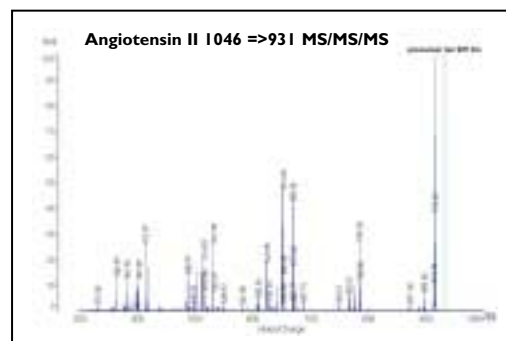


Fig. 2b

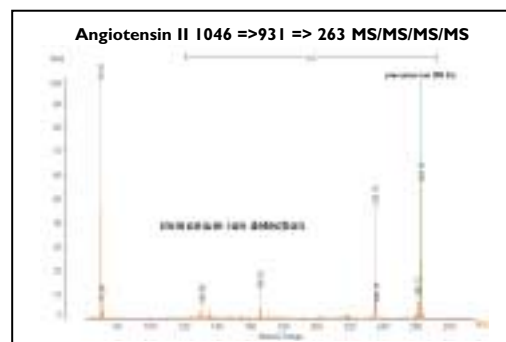


Fig. 2c

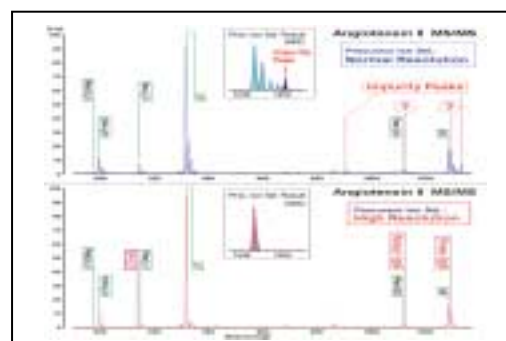


Fig. 3

With data depth and quality

Analysis of a tryptic digest by MS/MS and MS/MS/MS

From the MS spectrum (fig.4a) an ion at 3404.7 Da was selected and subjected to MS/MS (fig. 4b). From this a further ion at 1192.7 was selected to perform MS/MS/MS and provide a new level of structural information.

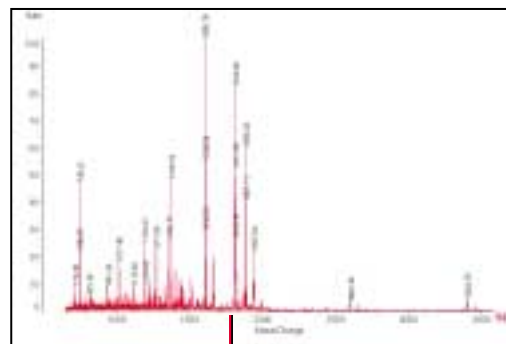


Fig. 4a

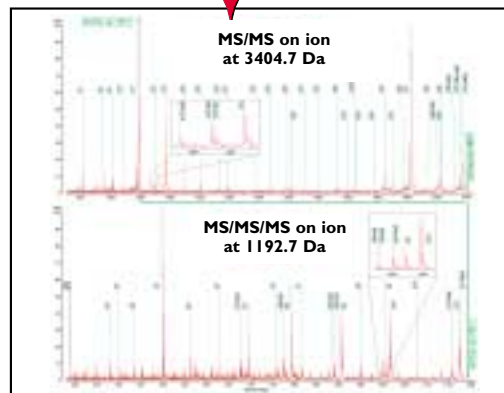


Fig. 4b

MS analysis and MS/MS identification of ICAT™ pairs

Fraction-collected ion-exchange separated ICAT-labelled peptides (*Halobacterium sp.*) were spotted onto a target plate. Spots were analysed for ICAT labelled pairs (one example shown). Once identified by MS (fig. 5a), mono-isotopic ion pairs were subjected to MS/MS (fig. 5b) to confirm pairing and determine identity.

The ability to perform such analysis on a single MS platform defines the capabilities of the AXIMA-QIT™ to utilise techniques such as ICAT and determine post-translational modifications (PTMs) in proteomics studies.

This sample was a kind gift of Drs. Baliga, Ng and Goodlett of the Institute for Systems Biology, Seattle.

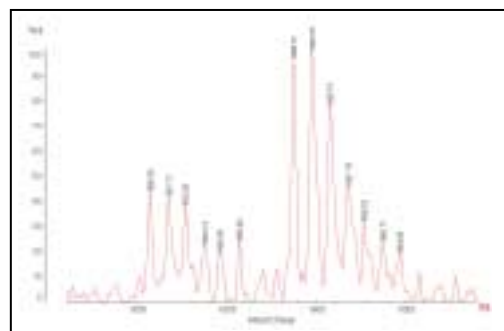


Fig. 5a

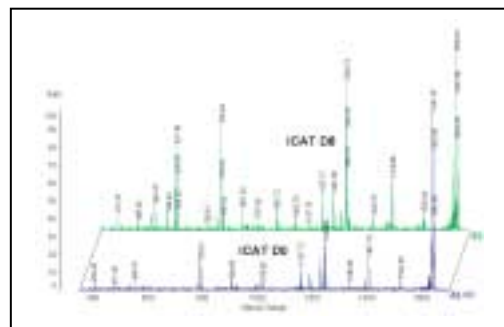
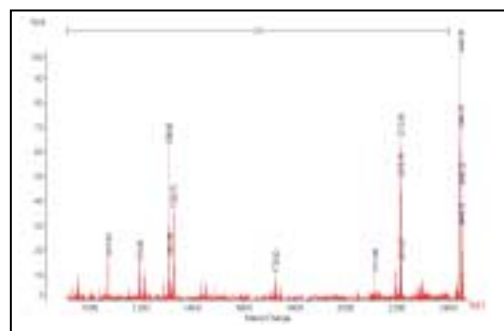


Fig. 5b

High sensitivity MS/MS analysis

1 femtomole of ACTH (18-39) was subjected to MS and MS/MS analysis. A clearly identifiable series of ions (fig. 6) was obtained to allow further identification and characterization.





The AXIMA™ range of instruments is designed and manufactured under Kratos Analytical's Quality Management System and certified for CE approval.

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bringing analysis to life



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