AXIMA

The AXIMA Series of

MALDI-TOF Mass Spectrometers

AXIMA-CFR™*plus* NEW!

AXIMA-CFR[™]

AXIMA-LNR[™]





Taking MALDI-TOF MS beyond the standard

Proteomics is increasingly used to bridge the gap between genetics and disease. The difference in protein expression between normal and diseased states enables researchers to identify potentially important biomarkers and targets for drug screening.

Mass spectrometry offers both high sensitivity and the ability to search protein and EST databases to identify proteins and is key to the characterisation of large protein populations in subcellular, tissue and whole organism biochemistry. MALDI mass spectrometers will provide the next explosion in biological information.

Shimadzu Biotech offers an integrated approach to drug discovery and proteomics, developing exciting new technologies and taking mass spectrometry further.



The innovative AXIMA[™] series

Drawing on the innovative technology developed by Kratos Analytical, the AXIMA series of MALDI-TOF mass spectrometers offers powerful performance for a diverse range of high throughput biochemical applications:

AXIMA-LNR[™] - High performance mass detection

Intended for users requiring mass detection but not structural information and ideally suited for high throughput QA / QC applications in areas such as:

- Oligonucleotide QA / QC
- Protein detection
- Micro-satellite DNA characterisation
- Polymer analysis

AXIMA-CFR[™] - Purpose built for frontline proteomics

- High performance linear / reflectron MALDI-TOF
- Ultra-fast Seamless PSD[™]
- Automated functionality for unattended PMF and data-dependent PSD experiments

AXIMA-CFR[™]*plus* - The highest MALDI-TOF performance available

All the strengths of the AXIMA-CFR^{M*} with:

- Superior mass accuracy and resolution ultrafast reflectron detector & 2 GHz transient recorder
- Autoloader and biochip-ready new stage design
- CID-enhanced PSD fragmentation
- Beam blanking for low mass / matrix ion cut-off

*Field upgrades for the components of AXIMA-CFR^{**} *plus* are available for AXIMA-CFR^{**} owners

AXIMA-CFR[™] and the new AXIMA-CFR[™]*plus* – Powerful performance in high throughput protein identification

The AXIMA-CFR[™] MALDI-TOF mass spectrometer demonstrates performance levels only seen previously on large, workstation-like systems. The ergonomic AXIMA has a small footprint and is easily manoeuvrable making best use of precious laboratory space.

The AXIMA-CFR[™] provides both the high mass accuracy and the high resolution required for effective protein identification by peptide mass fingerprinting (PMF).

The unique curved field reflectron on the AXIMA-CFR[™] enables the acquisition of Seamless PSD[™] data in as little as 60 seconds. The data from this convenient and economical process is used for further identification or confirmation and can be acquired for masses up to 4000 Da. It can be readily combined with chemical modifications to enhance ion series for sequence elucidation. This capability makes PSD a useful and automatable method which is clumsy to perform on other MALDI-TOF instruments.

In frontline proteomics, the INTELLIMARQUE[™] function offers a powerful new tool for automated and data-dependent protein identification. Using this, the investigator can set up an unattended PMF and data-dependent PSD experiment to generate the most information from MALDI-TOF with the minimum effort. PMF data is automatically submitted for a MASCOT[®] database search and the results flag the selection of a pre-determined number of precursor ions for Seamless PSD analysis. The outcome of the PSD analysis is then re-submitted to MASCOT for further identification or confirmation. When the experiment is completed for all the selected wells the results are available in an easy to use tree format showing summary data, MASCOT reports and individual spectra.

The AXIMA[™] is controlled by the powerful LAUNCHPAD[™] software. This friendly user interface allows even the novice user to quickly gain quality data while offering open access areas for expert users and for more challenging research applications.



Fig. 1: Sample introduction



Fig. 2: Set up screen for an automated experiment



Fig. 3: The results viewer page showing one specific spectrum

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Fig. 4: The MASCOT[®] search result: a high-confidence PMF ID for Cytochrome P450

A choice of sample preparation accessories – for workflow and flexibility

Two alternative options are offered to enhance the workflow and automation of the AXIMA MALDI-TOF

For 1D/2D gel-based proteomics, the Xcise "3 in 1" automated gel processor combines all of the functions from gel imaging through to deposition onto a MALDI target plate in a single integrated benchtop instrument.

The combination of Xcise and AXIMA-CFR[™] with their respective automation components releases significant manpower resources while delivering the frontline capabilities required in a proteomics research facility.

Xcise is a unique and integrated solution to the processing of gel-based proteomics and offers the following key features:

- Gel imaging, spot detection & spot excision
- Protein digestion, peptide extraction and target plate spotting
- Seamless transfer of sample tracking data to MALDI-TOF software

The Xcise was developed in collaboration with Proteome Systems Ltd as an integral part of their proteomics discovery programme. It is designed to minimise the risk of both internal and external contamination and is supported by certified, dedicated consumables kits.

The combination of an AXIMA MALDI-TOF mass spectrometer and Tecan Genesis RSP 100 represent a powerful package of complementary technologies designed to sit at the centre of all modern analytical laboratories.

The Tecan Genesis RSP 100 is used not only for preparation of samples on an AXIMA-CFR[®] MALDI target, but also for a wide range of automated applications, many of which ultimately lead to mass spectrometric analysis.

The primary features of the Genesis RSP 100 that make it the liquid handling robot of choice are:

- an adaptable worktable for user-defined layout & user-friendly Gemini software
- a range of pipetting including sample / matrix deposition on a MALDI target
- sensitive detection and tracking of both conductive and nonconductive liquids

A variety of options are available to increase the versatility of the Genesis RSP 100 and the productivity of the AXIMA-CFR[™] user: a robotic arm for moving microplates; barcode reading for sample tracking; shaker incubators for chemical and enzymatic reactions; vacuum modules for filtration & SPE units for sample clean up.



Fig. 5: Xcise "3 in 1" automated gel processor

AXIMA[™] is ready for future developments in proteomics and protein analysis

With the development of the new flexible sample-stage design on the AXIMA-CFR^{**}*plus* (available as an upgrade on the AXIMA-CFR^{**} & AXIMA-LNR^{**}) the instrument will accept a variety of different miniaturised sample preparation devices and biochips. This further enables robotic autoloading of sample targets into the AXIMA under instrument software control.



Fig. 6: Tecan Genesis RSP 100

Critical requirements for reliable protein identification from peptide mass fingerprinting are high resolution and mass accuracy. In proteomics, rapid and easy monoisotopic resolution is required across a wide mass range for automated experiments.

The analysis of Insulin B in figure 7 with the AXIMA-CFR[®]*plus* shows resolution of greater than 20,000 and is maintained even at low concentrations (10 fmol/ul) as shown in figure 8. In one example of a tryptic digest (Cytochrome P450, figure 9a) resolution is maintained across the mass range. An example is shown (figure 9b) for a very low intensity tryptic fragment (15% relative intensity) with a resolution of 19,800 from the same Cytochrome P450 analysis.

The study of a mixture of 4 insulin species (in figure 10) demonstrates the extremely high mass accuracy of the AXIMA-CFR[™]*plus* for which the average of all peaks is well below 5 ppm. The importance of mass accuracy is demonstrated by the confidence of the identification from the mass list submitted to MASCOT from figure 9a and shown in figure 4.

PSD is a valuable tool for further protein identification and confirmation. However, in most MALDI mass spectrometers this is a clumsy, slow technique that cannot be automated. The requirement to "stitch" together several spectra



across the mass range for one precursor limits the sensitivity of the technique due to the laser ablation required.

Using the patented curved field reflectron employed in the AXIMA-CFR^{**} and AXIMA-CFR^{**} *plus* it is possible to acquire Seamless PSD^{**} in less than one minute and in a single acquisition minimising use of your precious samples. An example of this (figure 11) shows the high signal-to-noise ratio and the option to enhance low mass fragmentation with the additional CID function on the AXIMA-CFR^{**}*plus* (blue trace).

Seamless PSD[™] makes the automation of peptide identification using PMF and data-dependent PSD a reality. This powerful INTELLIMARQUE[™] function allows for fully unattended protein ID experiments to be run that take full advantage of the instrument's high performance features.





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



Mascot* is a registered trademark of Matrix Science Ltd., London, UK. AXIMA^{**}, AXIMA LNR^{**}, AXIMA CFR^{**}, LAUNCHPAD^{**}, INTELLIMARQUE^{**} and Seamless PSD^{**} are trademarks of Kratos Analytical Ltd., Manchester, UK.



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