SHIMADZU

Excellence in Science

Taking MALDI-TOF MS Beyond the Standard

AXIMA Confidence

AXIMA Confidence™ - Sensitivity and Flexibility

The AXIMA Confidence is designed with the general analytical and life science laboratory in mind. Incorporating a variable repetition rate 50Hz N$_2$ laser, the system provides rapid, high quality MALDI mass spectra and an array of software tools for data processing and reporting.

Linear mode allows the interrogation of high molecular weight samples, whilst reflectron mode, incorporating the patented curved field reflectron (CFR), provides the high resolution and mass accuracy necessary for successful proteomics and life science experiments.

Positive and negative ion modes are included as standard allowing greater flexibility and extending the compound categories that may be analyzed. The system also incorporates a patented beam blanker to optionally remove unwanted low mass ions and prevent detector saturation.

Excellent sensitivity is achieved using near-normal (on-axis) laser irradiation and advanced ion optics for enhanced ion transmission. Pulsed extraction of ions from the MALDI source, in combination with the unique reflectron design, improves resolution and enhanced calibration algorithms with easy-to-use software facilitate the generation of more accurate data.

MS/MS may be easily performed using a seamless approach – ions of interest can be isolated using a precursor ion selection device, incorporated as standard, and data-rich fragment ion spectra quickly and simply acquired. The curved field reflectron design augments the low mass fragment region providing useful additional information.

Unparalleled flexibility is achieved by a variety of sample target formats including standard microtitre plate-format 96 or 384 well targets. FlexiMass™ microscope slide-format targets (plain or 48 well targets) and a wide variety of adaptors for unconventional sample layouts are also available. The standard sample target formats are fully compatible with common laboratory robots.
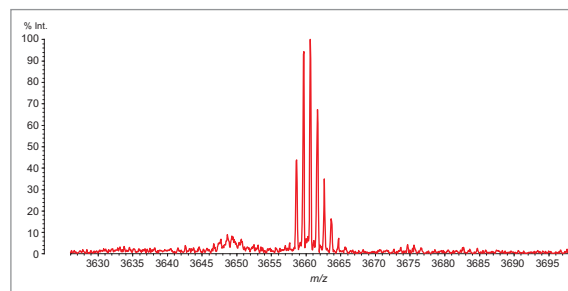
ACTH fragment 7-38 showing >15,000 resolution FWHM
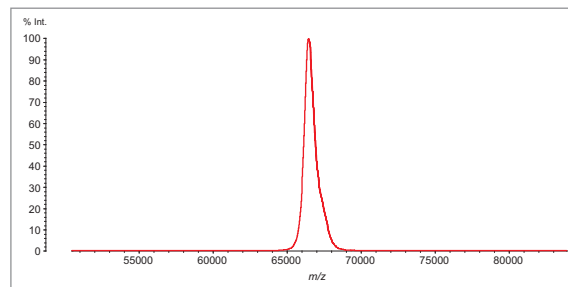
Bovine serum albumin in linear mode

AXIMA Confidence™ - Software Solutions

Intuitive software incorporating data-dependent workflows for achieving maximum results with minimum user input, making the system ideal for novice and expert users alike.

The AXIMA Confidence is controlled by the Launchpad™ suite of software, common to all AXIMA mass spectrometers, permitting manual or fully automated operation facilitating the seamless analysis of as few or as many samples as required. Intelligent optimization of acquisition conditions may be employed allowing auto-tuning for specific samples.

Ideally suited for life science and analytical environments alike, the system offers software packages specifically created for:

- Proteomics experiments
  - LC-MALDI
    - Polymer analysis
      - Biomarker discovery
        - Oligonucleotide/primer analysis

Application-centric data processing software packages are available to provide solutions to many commonly asked questions.

Intellimarque™ for automated protein identification

Designed with the flexibility to adapt to user workflows: from a handful of samples to high-throughput fully automated data generation, data-dependent peptide mass fingerprinting (PMF) and MS/MS for protein identification are integrated into easy-to-use intuitive software. The flexibility of the software means it can also be applied to other applications requiring automated acquisitions other than just protein identification.

- Peptide mass fingerprints are acquired and subjected to an optional integrated Mascot® database search.
- User-definable limits for acceptance of PMF-based protein identification.
- Data-dependent MS/MS: using the results of the PMF search, MS/MS may be performed on ions that were matched to the top ranked protein hit (confirmation MS/MS), in addition to those that were not (investigation MS/MS).
- Batch searching of these MS/MS spectra is then performed automatically to provide additional and higher confidence protein identifications.
- Data may be reprocessed and resubmitted for database searching at a later time to provide additional information.

Synthetic polymers

Polymers and copolymers can be characterized using our unique polymer software, Polymer Analysis™, providing useful structural information and statistics in a text report format.

Oligonucleotides

Oligo Analysis™ offers fully automated QC analysis of large numbers of oligonucleotides or peptides, complete with a report indicating the presence or absence of the target compound, an estimate of the purity and occurrence of known contaminants, adducts or truncated/expanded analogues.
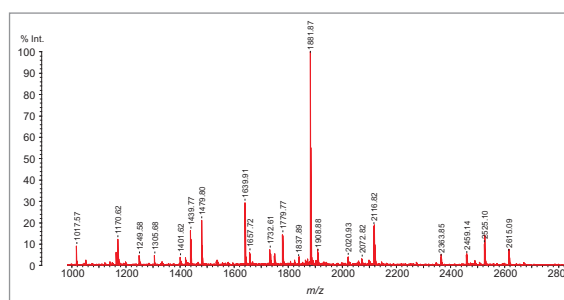
Biomarker discovery

This exciting area encompassing clinical sample screening and profiling is comprehensively addressed using automated acquisition methods and refined data processing.

Data can be easily exported to third party software packages to allow comparative experiments using a number of standard data formats including ASCII, mzXML and mzData.

System support

All AXIMA systems can be fully supported throughout their lifetime using sophisticated web-based service diagnostics and realtime remote monitoring. Highly trained specialist local service support engineers are available to install and maintain AXIMA mass spectrometers. A wide range of service contracts is available, catering for all budgets and requirements, including IQ/OQ environments.

Full training courses are offered by MALDI experts at our regional corporate training centers or at the customer site and may be tailored for specific requirements and applications.

Bovine serum albumin peptide mass fingerprint

AXIMA Confidence

ISO 9001 — UKAS MANAGEMENT SYSTEMS 001

ISO 13485 — UKAS MANAGEMENT SYSTEMS 001

Kratos Analytical Ltd.
Wharfside, Trafford Wharf Road, Manchester M17 1GP, UK
Phone: +44 161 888 4400 Fax. +44 161 888 4402
URL http://www.shimadzu.com/an/

SHIMADZU

Shimadzu Corporation
www.shimadzu.com/an/