Waters

MICROMASS[®] MALDI micro MX[™] MASS SPECTROMETER

Looking for a simple route to high quality MALDI data?

- Need sequence for higher confidence and specificity in protein identification?
- Need to identify biomolecules and bacteria with higher sensitivity and confidence?
- Want a rugged research tool capable of analyzing a variety of sample types?
- Limited by your available laboratory bench space?

Best in class MALDI-TOF technology

The Waters[®] Micromass[®] MALDI micro MX[™] Time-of-Flight Mass Spectrometer is a high performance benchtop research tool, which now delivers the power of advanced MALDI analysis into the hands of even the most inexperienced user. The MALDI micro MX incorporates innovative Parallel Post-Source Decay (PSD MX[™]) and novel MassPREP[™] Target plate technology, to provide superior MS and PSD MX analyses with unparalleled sensitivity and efficiency for compound identification and confirmation.

Flexibility, productivity, and confidence

The MALDI micro MX mass spectrometer is the simplest route to high quality MALDI MS and PSD data. This compact, highly sensitive system is simple to set up, easy to operate, reliable and provides scientists with accurate molecular weight measurements of proteins, peptides, polysaccharides, nucleic acids, synthetic polymers and small molecules. In addition, confident assignment of high quality peptide sequence information can be obtained in the revolutionary new PSD MX mode.

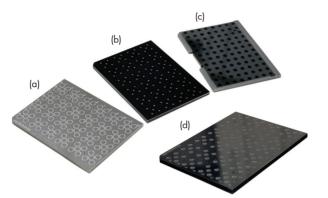
The MALDI micro MX is powered by the market-leading Mass-Informatics[™] platform, MassLynx[™] 4.0 and its Application Managers, that are tailored to maximize productivity and confidence in proteomics and bacterial studies.



Waters[®] Micromass[®] MALDI micro MX[™] Time-of-Flight Mass Spectrometer puts the simplicity, sensitivity and speed of Parallel PSD on the laboratory bench.

Why MALDI micro MX?

Matrix Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF-MS) is a common research tool for the successful analysis of biomolecules. The MALDI micro MX mass spectrometer incorporates a wide range of innovative technologies that enable you to analyze more sample types with more confidence, sensitivity and speed than ever before.



The target plate family includes (a) 96- and 384-spot stainless steel targets, (b) the MassPREP[™] PROtarget[™] (c) the DIOS-target[™] and (d) the MicrobeLynx[™] target plate.

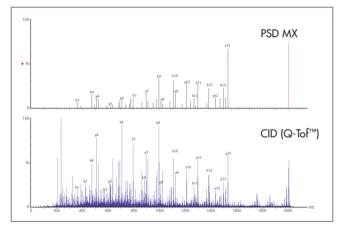
Accurate, sensitive MS analysis

A wide range of operating modes and specifically designed target plate technologies enable a broad range of biomolecules to be analyzed with high mass accuracy and sensitivity.

- MALDI Reflectron Mode-e.g. peptides
- MALDI Linear Mode—e.g. intact proteins, bacterial identification, bacterial speciation
- MALDI Negative Ion—e.g. oligosaccharides, nucleotide analysis
- DIOS (Desorption Ionization on Silicon) e.g. Small Molecules

Parallel Post Source Decay (PSD MX)

PSD MX is a novel technique for the simultaneous acquisition of sequence data from a mixture of precursors, e.g. from a protein digest or an HPLC-separated digest mixture. This novel technique brings many unique benefits to the researcher:



Sequence analysis of the peptide DDQNPHSSNICNISCDK [M+H]⁺ 2003.79 Da from Alpha Lactalbumin with PSD MX on a MALDI micro MX (top) and MS/MS on a Q-Tof Ultima[™] MALDI (bottom) generates comprehensive fragment ion information.

- Faster analyses—PSD MX significantly reduces the time needed to analyze each sample because no precursor ion selection (for example, with an ion gate) is required.
- Ease of use—A single experiment is required for each sample regardless of sample complexity and is easily defined via a wizard-driven setup.
- Enhanced Data Quality—The use of an ion gate can produce artefacts and can lead to a loss of sensitivity and resolution. Parallel acquisition results in lower sample consumption. PSD MX data processing generates clean, uncomplicated PSD spectra.
- Improved results—Collection of PSD MX spectra on all precursors provides greater confidence for database search results.

A compact, powerful technology platform

Featuring innovative industrial design and proprietary enabling technology, the MALDI micro MX mass spectrometer encapsulates best-in-class PSD performance within an easy-to-use, robust instrument.

The new Waters Micromass MALDI micro MX Mass Spectrometer offers:

- New Multiplexed Post-Source-Decay—PSD MX enables faster, more sensitive structural analyses with enhanced data quality and significantly reduced sample consumption.
- **Sensitivity**—Subfemtomolar sensitivity is possible through high instrument sampling efficiency and proprietary MALDI target plate technology.
- Resolution—The system acquires high-resolution spectra in reflectron mode (10,000 FWHM) and linear mode (1,000 FWHM).
- Mass Measurement Accuracy—Routine high mass measurement (10 ppm RMS) accuracy with on-plate near point lock mass correction provides high quality data.
- **Negative ion capability**—MALDI applications can be extended to include genotyping, oligonucleotide and polysaccharide analysis.
- Linear mode—The linear configuration uses a Post Acceleration Detector (PAD), to enable large molecules to be effectively analyzed (e.g. for intact protein analysis).
- MALDI target plate range—The MassPREP PROtarget Plate for on-target peptide sample cleanup and up to 10x sensitivity; DIOStarget for analysis of small molecules; and standard 96- or 384-spot format steel target plates.
- Linear Detector Post-Acceleration Detector Reflectron Laser Attenuator Lenses Mirror Camera Reflectron Detector Reflectron Detector Reflectron Detector

The MALDI micro MX mass spectrometer incorporates the widest ever range of features and functionality as part of a standard Waters MALDI-TOF-MS configuration.

- High magnification camera-Clear sample viewing is enhanced from your acquisition PC.
- Fully automated acquisition and processing—Features include wizard-driven setup, automated instrument calibration and the real-time data acquisition algorithm.
- High productivity for application-focused research—Dedicated software Application Managers—ProteinLynx[™] Global SERVER and MicrobeLynx[™]—feature advanced scoring routines for protein identification, bacterial identification and speciation.
- Achieve greater confidence in your results—New, high quality reference standards and purified matrices calibrate and troubleshoot chromatography and mass spectrometry systems.

Proteomics

The MALDI micro MX is a key component of the Waters Protein Identification System. This is a high performance solution for protein identification and characterization, designed to streamline the process of analyzing samples from gel and HPLC-separated samples by simplifying sample preparation, mass spectral data acquisition and processing. This system increases the confidence of protein identification through sophisticated software and the class-leading PSD MX technology.

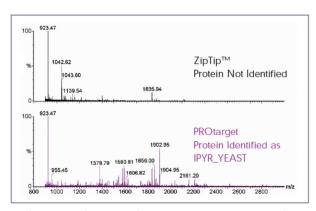
Protein Identification

Low abundance proteins are often the most biologically interesting components but are often the most challenging to analyze in proteomics samples. The Waters Protein Identification System enables the detection and identification of these proteins by combining unique capabilities:

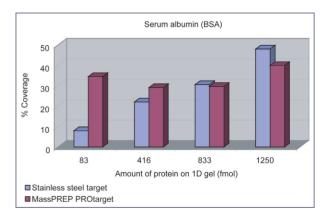
- High sensitivity—In situ sample cleanup and concentration: MassPREP target plate technologies increase sequence coverage, enhance detection limits up to 10x and enable analysis of previously unidentifiable samples.
- High coverage—Highly purified MassPREP matrices allow even more low mw peptides to be detected.
- High confidence—Rapid, reliable protein identifications are obtained from processed PMF and PSD MX data using advanced scoring routines in ProteinLynx Global SERVER.



Waters Protein Identification System incorporates the Waters Micromass MALDI micro MX Mass Spectrometer, the MassPREP Station, MassPREP Target family, MassPREP digest standards and purified matrices, and MassLynx 4.0 Software and ProteinLynx Global SERVER.



In this example, an endogenous yeast protein is identified from a silver-stained 2D-gel spot. Sample cleanup and concentration with the MassPREP PROtarget Plate considerably aids the identification of proteins from samples not previously amenable to analysis.

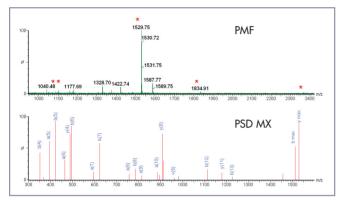


Sequence coverage from peptide mass fingerprinting can be significantly increased for low abundance samples with the MassPREP PROtarget Plate. These data show % sequence coverage vs. the amount of BSA protein loaded on the 1D gel.

New PSD MX technology for rapid protein identification

The new proprietary PSD MX technology provides a unique route to obtaining structural information and allows unambiguous protein identification and amino acid sequence information to be determined.

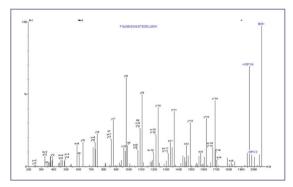
• **Rapid analysis**—PSD MX enables the simultaneous analysis of a mixture of peptides with PSD, leading to a significant reduction in overall time taken.



Analysis of 50 fmol (on target) of Hemoglobin alpha I chain. Peptide mass fingerprinting identified 5 peptides and led to a tentative identification with low confidence (top). Sequence analysis of the sample by PSD MX led to an unambiguous identification with high confidence.

PSD MX data shown above is for the peptide at m/z 1529*.

- High data quality—PSD MX acquisition and data processing enables improved specificity and sensitivity for sequencing peptides and locating modifications.
- More identifications—PSD MX requires only one experiment per sample, as multiple PSD spectra are acquired in parallel. This results in reduced sample consumption, higher sensitivity, and more protein identifications.

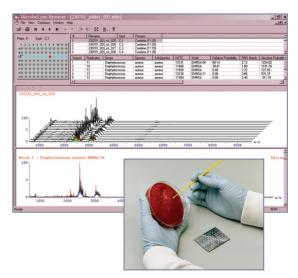


The PSD MX (sequence) spectrum of the monophosphopeptide (FQpSEEQQQTEDELQDK) [MH+]=2061.8 from Beta casein, reveals detailed sequence information and the location of the phosphate group.

Waters Bacterial Identification System

Waters Bacterial "Mass-Fingerprinting" System enables rapid speciation and typing of micro-organisms in pharmaceutical R&D, food science, environmental health, clinical research and homeland security. MALDI-TOF-MS is employed to analyze the unique population of macromolecules expressed on the surface of a bacterium. The resulting mass spectra provide a unique physicochemical fingerprint for the strain tested.

Mass-Fingerprinting can confidently identify unknowns by interrogating a database of quality controlled reference mass spectra (e.g. MMU) with the Waters MicrobeLynx Application Manager.



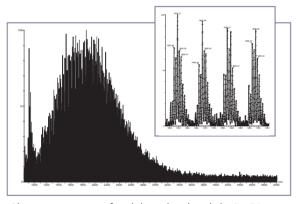
The MMU 2004 database of bacterial spectra for MicrobeLynx contains fingerprints from more than 3,400 NCTC reference strains representing over 150 genera.

Flexibility for your laboratory

This MALDI micro MX is a high performance platform capable of successfully analyzing a wide variety of sample types.

GPC/MALDI for polymer analysis

- Acquire extremely accurate molecular weight, structural and compositional data for synthetic polymers.
- Rapidly characterize repeat unit, end group and molecular weight distributions of a wide range of synthetic polymers.
- Analyze materials that are difficult to characterize by traditional methods (e.g. copolymers).



Characterization of polylactide glycolide (PLG), a highly polydisperse polymer, using Waters GPC/MALDI MS System.

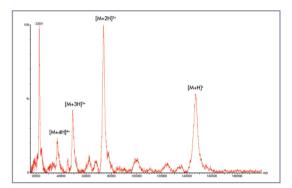
DIOS MS for discovery drug profiling

This novel, matrix-free technique represents a breakthrough for the rapid screening of small molecules. It eliminates matrix-related ions and crystallization effects commonly observed with MALDI MS at lower mass ranges.

- Allows for detection of low picogram levels of small molecules.
- Frees up time since minimal sample preparation is required.
- Provides qualitative and quantitative analysis with an internal standard.

High molecular weight analysis

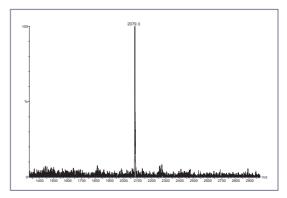
Detection and analysis of high molecular weight compounds in linear mode of operation are increased with the use of a software-retractable Post Acceleration Detector (PAD).



Immunoglobin detected in linear mode with PAD enabled.

Negative ion analysis

The negative ion mode of operation on the MALDI micro MX enables the accurate, sensitive analysis of compounds not readily amenable to ionization in positive ion mode.



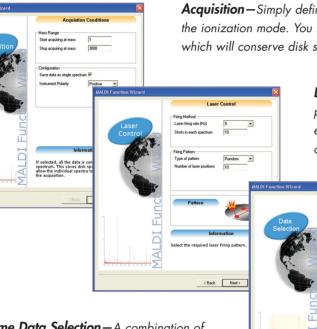
[M-H] ion of a silylated oligosaccharide A2G2S1F.

Easy to optimize

The MALDI micro MX is fully controlled with Waters MassLynx 4.0 Software, incorporating advanced features for instrument operation, experimental setup and data management. New, automated set-up procedures designed to simplify calibration and tuning, enhance the MassLynx instrument control for MALDI. With the introduction of this new MS system, MALDI is now universally accessible to users with a wide range of backgrounds and experience in mass spectrometry.

Intuitive to set up

In just a few quick steps, the MALDI micro MX experimental set-up wizard guides the user through basic acquisition conditions, laser control and real time data selection parameters. Self-explanatory descriptions of fields and intelligent presentation of relevant parameters assist in simplifying the method setup. The user is assisted by a mouse-over help function, which provides further information.



Real Time Data Selection—A combination of automated laser energy tuning and an intelligent data selection algorithm ensure the data you acquire are on scale and of the highest quality.

Acquisition—Simply define the mass spectral range you are interested in and select the ionization mode. You have the option to save all your data as a single spectrum, which will conserve disk space and significantly reduce processing time.

Laser Control—Data can be acquired using user-defined patterns or by choosing from a selection of eight pre-set examples. Enter the repetition rate of the laser and method or pattern of firing.



Sales Offices:

34 Maple St. Milford, MA 01757 U.S.A. T: 508 478 2000 F: 508 872 1990 www.waters.com

Sample Preparation Products for MALDI MS

Waters offers a dedicated range of sample preparation products for MALDI mass spectrometry, designed to simplify procedures and improve results:



- Robotic sample preparation systems, specialized
 reagents, kits and cleanup technologies together with
 Waters novel line of MassPREP target plates for both large and small molecule applications.
- A range of specifically designed NanoEase[™], Trapping and Capillary columns for LC and 2D LC separation biological components.
- Innovative, high quality reference standards and purified matrices to calibrate and troubleshoot chromatographic and mass spectrometry systems, simplifying system validation and ensuring reproducibility of results.

Worldwide services and support

Waters Connections[®] Programs provide the solutions you need to maintain uptime across your Waters systems.

- Analytical Instrumentation and Software Services include Total Assurance Plans and Warranties that extend and enhance the original warranty you receive when you buy a Waters product. These plans minimize the level of insurance investment and deliver the value you need to avoid costly and time-consuming system downtime.
- Connections Compliance Services provide you with timely and cost-efficient solutions for your regulatory compliance challenges. You can use Waters Compliance Services to verify proper equipment operation for CGMP/GLP compliance, significantly reducing operating costs.
- Connections University is the center of our Educational Services, providing extensive LC and MS training and education at your site, at our corporate headquarters or at our local offices around the world.
- Representatives of Waters Global Customer Assurance Organization, trained and certified in all Waters products and current in HPLC and MS applications, are available in person, on the phone, via FAX or at www.waters.com to answer questions and provide you with service, support and information.





For Complete Confidence

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