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# Waters Maldi MX



The Waters<sup>®</sup> Micromass<sup>®</sup> MALDI micro MX<sup>TM</sup> is a new matrix-assisted laser desorption/ionization time-of-flight mass spectrometer (MALDI-TOF MS). The MALDI micro offers the simplest route to the highest quality data by MALDI mass spectrometry and features from a novel parallel PSD ('PSD MX') capability for confirming protein identification and analysing post-translational modifications. Benefiting from high mass accuracy, resolution and sensitivity, the MALDI micro MX generates excellent results from low abundance samples with a unique range of target plate technologies, specific to your application. This compact 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.

## High quality MALDI-MS data can be rapidly acquired for;

- Protein Identification
- Post-translational modification analysis
- Intact protein analysis
- Bacterial identification and speciation

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- Small molecule analysis
- DNA/oligonucleotide analysis

#### 'Parallel PSD' - Multiplexed Fragmentation Analyses

Parallel PSD is an innovative solution for structural analysis of peptides and overcomes many of the limitations associated with conventional PSD. In conventional PSD, precursors are selected for PSD analysis in series (e.g. with the use of an ion gate), which results in the need for one experiment per precursor. In 'parallel PSD' all of the precursors are fragmented in-parallel, which results in faster, more sensitive analyses, which consume less sample! Each experiment is completely automated with a Wizard-driven set-up and MassLynx 4.0 (Waters proprietary Mass-Informatics platform) has been enhanced to present the analyst with deconvoluted PSD-MX spectra for each precursor ion in the mixture – making the power of PSD-MX easily accessible. Parallel PSD is designed specifically for - , but not limited to:

- Confirming protein identity e.g. from 2D PAGE spots
- Protein identification from LC-separated peptide mixtures
- Analysis of post-translational modifications e.g. Phosphorylation

#### **MassPREP DIOS-targets**

Introduced at IMSC 2003, the Waters® MassPREP<sup>TM</sup> DIOS-target<sup>TM</sup> significantly increases the selectivity of laser-desorption/ionization time-of-flight mass (LDI-TOF) spectrometry and MS/MS instrumentation for small molecules. The increase in selectivity makes the analysis of small molecules by this rapid and simple matrix-free TOF technique feasible

#### **MassPREP PROtargets**

Sample preparation for MALDI mass spectrometry has taken a giant step forward. Now you can prepare your samples faster and easier than ever before and significantly improve the sensitivity of your MS analyses. By incorporating the innovative ActiveWell<sup>TM</sup> Sample Preparation Plate Technology, Waters<sup>®</sup> MassPREP<sup>TM</sup> PROtarget<sup>TM</sup> Plates enable high-volume sample loading and on-target cleanup for simplified sample preparation and improved detection limits for lower abundance proteins.

#### **MassPREP** Chemistries

Specifically developed for use with Waters mass spectrometry system solutions for the analytical laboratory, the new high-quality reference standards and purified matrices are for scientists performing a wide range of liquid chromatography (LC), liquid chromatography/mass spectrometry (LC/MS), and mass spectrometry (MS) analyses. These specialty products have been designed to monitor and optimize the performance of Waters proteomics system solutions

#### High Quality MS and PSD-MX Data in a Matter of Minutes

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Attention to detail is key in designing a precision instrument, right from the time the target plate is loaded into the MALDI source, we have designed measures to ensure data quality and reproducibility are maximized.

## The MALDI micro mass spectrometry system features the following:

- **Reflectron mode** (software selectable) 2.3 m effective flight path in reflectron mode designed for high resolution analyses over lower m/z ranges, e.g. for peptide mass fingerprinting applications
- Linear mode (software selectable) The linear detector configuration has a 1.2 path length, and is complemented by the use of a post acceleration detector (PAD), which enables a wide m/z range to be visualized concurrently, e.g. for intact protein analysis
- **Parallel PSD** Novel Innovation for multiplexed Post-source decay (PSD) PSD MX permitting multiple precursor ions to be fragmented and analysed in parallel. Compared to conventional PSD, this novel approach enables faster, more sensitive analyses and significant improvements in data quality all with reduced sample consumption.
- **PSD software** Wizard-driven automation ensures that throughput is maximized, sample consumption is minimized and results easily obtained. MassLynx 4.0 has also been enhanced to automatically provide de-convolute PSD-MX spectra for each precursor ion in the mixture making the power of PSD-MX easily accessible.
- **Target plate product range** Includes the novel MassPREP PROtarget Plate for up to 10 x sensitivity in the analysis of peptides and the MassPREP DIOS-target for the highly selective analysis of small molecules. 96 and 384 spot stainless steel target plates available for biomolecular and bacterial analyses.
- Sub femtomole detection The high sensitivity system is designed to analyze sub femtomole quantities of biological and synthetic molecules with molecular weights ranging from 500 Da to greater than 500 KDa
- Mass measurement accuracy The system acquires high resolution (10,000 FWHM) spectra and ensures good mass measurement (10ppm RMS) accuracy to provide high quality data. On-plate Near-point lock mass correction enables routine high mass accuracy
- Negative ion capability Extends MALDI applications beyond proteomics, to include genotyping, oligonucleotide and polysaccharide analysis
- High magnification camera– Allows clear sample viewing from your acquisition PC
- Fully automated acquisition With laser system tuning, and automated instrument calibration utilizing a real-time data selection algorithm

- High instrument stability and robustness For continuous operation and maximum up-time
- Floated delayed extraction source optics enhance resolution, mass accuracy and sensitivity, and allow the analysis of more thermally labile samples
- **Performance qualification** Your whole MS system is validated on install for total assurance and satisfaction
- Scalable system Can be integrated with Waters comprehensive range of automated sample preparation devices, reagents, columns and chemistries Easy software-guided set up and routine operation MassLynx<sup>™</sup> 4.0 employs the latest user interface and web-enabled technologies to provide customisable, application-specific functionality



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