Waters QTOF Premier

Q-Tof Premier™ and SYNAPT MS/HDMS™ Mass Spectrometers installed with a MALDI source accessory provide you with a no-compromise solution for the exact mass characterization of compounds using MALDI-MS, MALDI-MS/MS, and MALDI MS/IMS/MS (Synapt HDMS) analyses.

Compound identification by mass spectrometry can be limited by the incompatibility of some molecules with electrospray ionization. Your Q-Tof Premier or SYNAPT MS/HDMS instrument can overcome this limitation with the addition of an exchangeable vacuum MALDI source offering:

- Dual ionization capability
- Significant increase in the number of compounds ionized and analyzed
- Compatible with 96/384 spot target plate formats
- MS and MS/MS analysis with high resolution, sensitivity and mass measurement accuracy

Additionally, the ion mobility separation capability of the SYNAPT HDMS system enables components previously invisible to traditional MALDI analyses to be revealed, allowing species of interest within complex biological extracts to be separated from isobaric co-eluting compounds, MALDI matrix ions or background interferences.

Rapid Changeover

Q-Tof Premier and Synapt MS/HDMS instruments feature a unique, motorized engagement system which enables rapid, tool-free changeover between API and MALDI modes of operation. Users exchange sources by first removing the API source and then with a motorized stage, raise the MALDI source before securing it in position.

The exact mass MALDI-MS/MS data provided by Q-Tof Premier and Synapt MS/HDMS instruments provide:

- Improved protein identification and protein sequence coverage
- Characterization of proteins and PTMs using exact MALDI-MS and MS/MS technology
- Significantly improved de novo sequencing compared to post-source decay (PSD) techniques
- Sensitive, accurate analysis of polymers, glycans, small molecules and oligonucleotides
- Metabolite identification and profiling
- Biomarker discovery
- Molecular imaging

The MALDI Synapt HDMS instrument with its additional ion mobility separation capability also offers the possibility of ground breaking experimentation in new areas of research.

Q-Tof Premier with MALDI Source installed (from rear).

Instrument Compatibility

Installation of the vacuum MALDI source is only recommended for Q-Tof Premier™, SYNAPT™ MS and HDMS™ instruments already equipped with at least an 8,000 amu mass range quadrupole analyzer. However, there are some small molecule MALDI applications where a 4,000 amu quadrupole analyzer is satisfactory. The MALDI source can also be added to Synapt MS/HDMS instruments already equipped with the 32,000 amu mass range quadrupole analyser.

On-site conversion of 4,000 amu quadrupole analysers to 8,000 amu mass range is also available for both Q-Tof Premier and Synapt series instruments.

A minimum of MassLynx ™ 4.1 Software is required.

Equipment and Installation

The vacuum MALDI source assembly includes a 200Hz solid state Nd:YAG laser system with dual axis sample inlet, providing full random access movement across each sample well. The high repetition rate laser, with an expected lifetime in excess of one gigashot, offers increased sample throughput together with excellent spatial resolution.

When configured for API operation, the MALDI source and vacuum system is fully retracted into the front of the new instrument enclosure.

For MALDI operation the new source is raised from its retracted position using an integrated motorized column, before being secured to the existing transfer housing using a tool free clamping system.

The source is compatible with all Waters sample plates and supports the option to incorporate lock mass sample wells for enhanced mass measurement accuracy. The source is also compatible with glass microscope slides and selected Applied Biosystems target plates through use of separate plate adaptors.

User controllable laser attenuation is included together with high magnification viewing optics that display a real-time image of the sample well on the instrument PC screen for acquisition purposes.

LC-MALDI

Specific proteins from within complex mixtures that are only ionized by MALDI, can also be accommodated by first carrying out liquid chromatography separations followed by MS analyses.

An off-line LC separation is carried out and a robotic spotting device is used to spot the eluting LC fractions directly onto a MALDI target plate. This is then introduced into the instrument for MALDI analysis.

This procedure is particularly effective for protein identification using peptide mass fingerprinting where low-abundance and high-abundance proteins are mixed together.

With other traditional methods low-abundance proteins are undetected due to ion suppression effects, instrumental dynamic range limitations and chemical noise interferences.

LC MALDI analyses provide:

- Chromatographic separation spatially preserved on the MALDI target
- Generation of high sensitivity, interference-free, off-line LC-MS and LC-MS/MS data by MALDI
- Peptide mass mapping of low-abundance proteins in mixtures containing high-abundance proteins