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ABI QStar XL
Hybrid LC/MS/MS System
Performance Specifications

Computer Requirements (PC):

System Requirements: Windows NT® Data Acquisition Workstation (Included with QSTAR® XL System)

CPU: Dell Precision 530 Workstation

Memory: 512 MB

CD-ROM : 4X/10X/40X CDRW

Hard Disk: 2 x 36 GB

Performance/Throughput:

- 10,000 (FWHM) at m/z 1,165 (triple charge peak of insulin B chain in positive ion mode)
- 10,000 (FWHM) at m/z 1,163 (triple charge peak of insulin B chain in negative ion mode)
- 8,000 (FWHM) at m/z 829 in positive ion MS
- 8,000 (FWHM) at m/z 569 in positive ion MS/MS

Mass Accuracy: 5 ppm

Mass Range: m/z 5-40,000

Physical Specifications:

Width 160 cm (63 in)

Height 107 cm (42 in)

Weight 592 kg (1,302 lb)

Depth 79 cm (31 in)

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The QSTAR® XL Hybrid LC/MS/MS System is a high-performance, hybrid quadrupole time-of-flight mass spectrometer designed for proteomics, drug discovery, metabolomics, and drug development.

- Enhanced ion optics provide the highest sensitivity and reliability.
- Unique pulsing/trapping capabilities and patented LINAC® collision cell technology enable you to scan precursor and product ions sensitively.
- Excellent mass accuracy and stability ensures you obtain unequivocal molecular weight and high-quality structural information.

- Extended MS and MS/MS mass range (6,000 and 40,000 m/z) broadens the reach of your protein and peptide studies.
- OMALDI™ 2 ion source enables LC MALDI workflow for sensitive peptide-based and metabolite identification experiments.
- Comprehensive selection of interchangeable, application-specific ion sources--from atmospheric pressure ionization (API) to matrix-assisted laser desorption ionization (MALDI)--offers you optimal flexibility.

Groundbreaking Technologies

As the highest-sensitivity hybrid quadrupole time-of-flight mass spectrometer, the QSTAR® XL LC/MS/MS System enables you to determine unequivocally the molecular weight and high-quality structural information of drug metabolites, as well as the type and location of post-translational modifications (PTMs). Our unique pulse/trapping capabilities, patented Q0 collisional focusing, and LINAC® collision cell technology enable you to get sensitive and superior MS and MS/MS scans with a maximum duty cycle.

A Powerful Combination

Together with our Analyst® QS software, the QSTAR® XL system offers a full complement of features to simplify every aspect of methods development, data acquisition, and processing, including flexible control of popular LC platforms. The system design enables you to exchange ionization sources easily to accommodate a wide range of applications and flow rates. Finally, to obtain more useful information per sample, you can pull it all together with advanced application software, including Metabolite ID, BioAnalyst™, Pro ID, Pro BLAST, Pro ICAT, Pro QUANT, oMALDI™ Xpert, and MALDI Imaging.

Accurate Mass for Metabolite Identification

The QSTAR® XL system provides the detailed accurate mass information you need in drug discovery and development to analyze the elemental composition of unknown drug metabolites. With accurate MS/MS-spectra-based mass assignments and structural information, you can confidently identify and fully characterize impurities as well as known and unknown metabolites. Further, you can take advantage of the LC MALDI workflow to re-analyze your complex metabolite samples to uncover even more information.

The Solution for Challenging Protein Analysis

The QSTAR® XL system is the best solution for challenging proteomics and protein analysis experiments such as de novo sequencing, intact protein analysis, PTMs, and relative quantitation. Together with our tagging chemistries, electrospray and MALDI ion sources, and applications software, this tandem MS system offers the sensitivity, robustness, and versatility you need to solve your protein problems.
For Research Use Only. Not for use in diagnostic procedures.

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