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## Waters 3100 Mass Detector

The Waters® 3100 Mass Detector is an advanced benchtop single quadrupole mass detector designed for high performance analytical and preparative LC/MS applications. With a wide range of ionization options including Atmospheric Pressure Photo Ionization (APPI) and the Atmospheric Solids Analysis Probe (ASAP), the 3100 Mass Detector is ideally suited for a wide range of qualitative and quantitative applications. The system includes IntelliStartTM Technology, for automated system optimization and status monitoring, ensuring that the highest quality data is routinely available to users of all levels.

## SYSTEM HARDWARE SPECIFICATIONS

API sources and ionization modes	High performance ZSprayTM dual-orthogonal API sources: 1) ESI (standard) 2) Multimode source – ESI/APCI/ESCi® (standard) 3) Dedicated APCI (optional) 4) Dual mode Atmospheric Pressure Photo Ionization (APPI)/APCI source
	(optional) 5) Atmospheric Solids Analysis Probe (ASAP) (optional) Vacuum isolation valve Tool free access to customer serviceable elements Plug and play probes
Ion source	De-clustering cone gas Software control of gas flows and heating elements  High efficiency hexapole ion guide
transfer optics	Ingli efficiency nexapore for guide
Mass analyzer	Single high resolution quadrupole analyzer, plus prefilter to maximize resolution and transmission while preventing contamination of the main analyzer.
Detector	Low noise, off axis, long life photomultiplier detector Digital dynamic range up to 4 x 106
Vacuum system	Single, split-flow air-cooled vacuum turbomolecular pump evacuating the source and analyzer One rotary backing pump
Dimensions	Width: 34.5 cm (13.8 in.)
	Height: 53.3 cm (20.8 in.)
	Depth: 65.5 cm (25.6 in.)

Electrical	CE and NRTL
safety/EMC	
testing	

## **SYSTEM SOFTWARE SPECIFICATIONS**

Software	Systems supported on MassLynxTM 4.1 or EmpowerTM 2 software (and later versions)
IntelliStart Technology	System parameter checks and alerts Integrated sample/calibrant delivery system plus programmable divert valve Automated mass calibration Automated sample tuning Automated SIR method development LC/MS System Check – automated on-column performance test
Quantification methods database*	QuanpediaTM – a database for storing and sharing user defined LC/SIR acquisition methods and associated processing methods for the targeted quantification of named compounds. Database entries for a number of applications are also provided. Quanpedia is an optional software item included with the purchase of the TargetLynxTM Application Manager.
SIR acquisition rate assignment*	Dwell time, inter-channel delay time, and inter-scan delay times for individual channels in a multiple SIR experiment can be automatically assigned (using the Auto-Dwell feature) to ensure that the optimal number of SIR data points per chromatographic peak are acquired. The Auto-Dwell feature can dynamically optimize SIR cycle times to accommodate retention time windows that either partially or completely overlap. This greatly simplifies SIR method creation, irrespective of the number of compounds in a single assay, while at the same time ensuring the very best quantitative performance for every experiment.
SIR acquisition window assignment*	Multiple SIR experiments can be scheduled (manually or automatically using the Quanpedia database) using retention time windows to optimize the cycle time for each SIR channel monitored. If required, SIR retention time windows can overlap partially or completely. This ensures that SIR data acquisition rates will be optimal for the quantification of all analytes in a given assay.
AutoPurification software capabilities	The following capabilities are provided with the optional FractionLynxTM Software and may rely on preparative scale LC hardware being part of the system: Solvent monitoring system for solvent and waste reservoirs Automatic collection time delay calculation Early run termination Total flow and gradient calculator Direct Inject

## PERFORMANCE SPECIFICATIONS

Acquisition	Full scan MS
modes	Selected Ion Recording (SIR)
Mass range	2 to 2048 m/z

Scan speed	Up to 10,000 Da/s Examples of achievable acquisition rates:
Scan Speca	10 scans per s (m/z 100 to 1000) 20 scans per s (m/z 50 to 500)
Mass stability	Mass drift is < 0.1 Da over an eight hour period
Linearity of	The linearity of response relative to sample concentration for a specified
response	compound is five orders of magnitude from the limit of detection
Polarity	20 ms to switch between positive and negative ion modes
switching time	20 ms to switch between positive and negative fon modes
ESCi mode	20 ms to switch between ESI and APCI
switching time	20 ms to switch between Est and AFCI
	Maximum acquisition rate of 100 CID data naints nor second
SIR acquisition	Maximum acquisition rate of 100 SIR data points per second
rate	Minimum dwell time of 5 ms per SIR channel
	Minimum inter-channel delay of 5 ms
Number of SIR	Up to 16,384 SIR channels (512 functions, 32 channels per function) can be
channels**	monitored in a single acquisition; up to 1024 SIR channels when operating in
	GLP/secure mode (32 functions, 32 channels per function).
Mass resolution	Automatically adjusted (IntelliStart) to desired resolution; The valley
	between the 2034.63 Da and 2035.63 Da peaks is <12% of the average
	height of the two peaks.
SIR sensitivity	A 1 pg loop injection (5.0 $\mu$ L of 0.2 pg/ $\mu$ L) of reserpine, with a mobile phase
(ESI+)	flow rate of 300.0 μL/min will give a chromatographic signal-to-noise for
(-2-)	m/z 609 > 100:1.
SIR sensitivity	A 1 pg loop injection (5.0 $\mu$ L of 0.2 pg/ $\mu$ L) of reserpine, with a mobile phase
(APCI+)	flow rate of 300.0 μL/min will give a chromatographic signal-to-noise for
( )	m/z 609 > 100:1.
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<sup>\* \*\*</sup> Feature is only available on systems controlled by MassLynx 4.1 SCN#714 or later. 512 function operation is only available with systems controlled by MassLynx 4.1 SCN#714 or later. Empower 2 controlled systems monitor a maximum of 1024 SIR channels (32 functions, 32 channels per function).

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