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Agilent 6300 Series Ion Trap LC/MS Performance Specifications

Product Overview

The Agilent 6300 Series Ion Trap LC/MS systems deliver robust, sensitive, data-dependent MS/MS that makes structural confirmation and sample identification easier.

6310 – makes high performance and data-dependent MSⁿ economical for every lab

6320 – provides greater sensitivity, mass resolution, and scan speed

6330 – offers ultimate sensitivity for low-abundance analytes

6340 – adds electron transfer dissociation (ETD) for better PTM characterization and protein identification

Product Features

- State-of-the-art performance with Agilent's legendary reliability and ease of use
- A wide range of ionization choices for the analysis of everything from environmental toxins to metabolites to low-abundance peptides and proteins
- Intelligent, data-dependent acquisition ensures fast, efficient collection of the highest quality, most useful data
- Application-specific software tools increase productivity for every type of data analysis from quantitation to protein database searching

Technical Specifications:

Mass range, mass resolution, and scan speed				
	6310		6320, 6330, and 6340	
Mass Range <i>m/z</i>	Resolution FWHM (u)	Scan Speed (u/s)	Resolution FWHM (u)	Scan Speed* (u/s)
50 - 2200	≤ 0.6	13,000	≤ 0.6	26,000
	≤ 0.45	5,500	≤ 0.35	8,100
	≤ 0.35	1,650	≤ 0.25	800
200 - 4000	3 - 4	27,000	≤ 3	27,000

*Total scan cycle times for the 6330 and 6340 are approximately 1/3 the scan cycle time of the 6320, allowing the 6330 and 6340 to perform 3X as many scans at the same nominal scan speed. In the 6340, ETD and ETD+CID operating modes increase scan cycle times slightly compared to CID-only operation.

Mass Accuracy (All)

±0.2 u within the calibrated standard mass range at normal resolution in full scan mode, with proper calibration, ICC target and ion statistics, and thermal equilibrium of electronics and ion source.

Mass Axis Stability (All)

Within ±0.2 u of the observed calibrated value over 8 hours in standard mass range at normal resolution in full scan mode, with proper ICC target and ion statistics, and thermal equilibrium of electronics and ion source and ambient temperature of 21°C ± 3°C (70°F ± 6°F).

Monoisotopic Precursor Selection (All)

Monoisotopic precursor selection is possible throughout the standard mass range (m/z 50 - 2200) at an ambient temperature of 21°C ± 3°C (70°F ± 6°F).

Polarity Switching

6310 ≈ 0.5 seconds

6320 ≈ 0.5 seconds

6330 ≈ 0.5 seconds

6340 ≈ 0.5 seconds

PSensitivity Specification

Column – ZORBAX Rapid Resolution SB-C18 2.1×30 mm 3.5 micron

Mobile Phase – 25% water 75% methanol 5 mM ammonium acetate

Flow rate – 400 µl/min (200 µl/min for XCT)

Mode – full scan MS/MS

MS/MS – transition of the protonated molecular ion (m/z 609) to the sum of the two most abundant product ions

Product ion scan range – m/z 175 - 650

Mass range – standard (m/z 50 - 2200)

Resolution – normal/ultrascan (0.6 u)

Sensitivity				
	6310	6320	6330	6340
Quantity (reserpine - on column)	5 pg	1 pg	250 fg	TBD*
Signal-to-Noise Ratio (full scan MS/MS)	≥ 25:1	≥ 50:1	≥ 50:1	TBD*

*TBD - To be determined

Stages of MS

	Automated	Manual
6310	5	11
6320	5	11
6330	5	11
6340	5	11

Descriptions and specifications supersede all previous information and are subject to change without notice.



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