



Agilent 6545XT AdvanceBio LC/Q-TOF

Data Sheet



Parameter	Measure	Specification
MS Sensitivity, positive	Signal-to-noise for 1 pg injection of reserpine, while maintaining maximum mass resolution	>500:1 RMS in 10 replicates
MS Accuracy, positive	Measured at the (M+H) ⁺ ion of reserpine (<i>m/z</i> 609.2807) using an internal mass reference	<0.8 ppm RMS in 10 replicates
MS Sensitivity, negative	Signal-to-noise for 1 pg injection of chloramphenicol, while maintaining maximum mass resolution	>500:1 RMS in 10 replicates
MS Accuracy, negative	Measured at the (M-H) ⁻ ion of chloramphenicol (<i>m/z</i> 321.0051) using an internal mass reference	<0.8 ppm RMS in 10 replicates
MS/MS Sensitivity	Signal-to-noise for 1 pg LC/MS injection of reserpine, monitoring the most intense product ions (174, 195, 397, and 448 <i>m/z</i>) while maintaining maximum mass resolution	>1,500:1 RMS in 10 replicates
MS/MS Accuracy, positive	Product ion <i>m/z</i> 397 for reserpine	<2.0 ppm RMS in 10 replicates
MS/MS Accuracy, negative	Product ion <i>m/z</i> 152 for chloramphenicol	<2.5 ppm RMS in 10 replicates
Intact protein accuracy	Deconvolved mass assignment of intact trypsinogen protein	<10 ppm RMS in 10 replicates
Mass resolving power	Full width half mass (FWHM) of spectral peak, with all instrument parameters set by autotune	>50,000 FWHM at <i>m/z</i> 2,722
Mass range		50–30,000 <i>m/z</i>
Temperature stability	Temperature: 15 to 35 °C (59 to 95 °F) at constant temperature	Maintain 1 ppm mass accuracy (variations <3 °C from calibration temperature)
Dynamic range	Intrascan dynamic range on coeluting components	Up to 5 decades
Spectral acquisition rate, MS	Acquisition speed while maintain maximum resolving power (mode dependent)	50 spectra/second
Spectral acquisition rate, MS/MS	Acquisition speed while maintain maximum resolving power (mode dependent)	30 spectra/second
Polarity switching	Complete cycle of positive and negative spectral acquisition	1.5 seconds with proper configuration
Agilent SWARM Autotune	Flexible automated optimization for protein, peptide, and small/labile molecule analysis.	
Automated data analysis for the following workflows	Intact Protein Analysis, Peptide Sequence Mapping, Glycan Profiling	
Vacuum system	Single foreline pump with dual split-flow turbo pumps capable of reaching flight tube vacuum of 10 ⁻⁹ torr under standard operating conditions	
Integrated calibrant solution	Automated delivery of calibrant for tuning and mass calibration	
Vent-free capillary removal	Isolation valve to allow source and sampling capillary maintenance while maintaining system vacuum.	

All sensitivity, chemical accuracy, and resolution specifications are achieved in manufacturing, and instrument performance data is supplied with shipment. All specification values are achieved after autotune, and do not require manual optimization. These specifications are not standard installation specifications for the Agilent Q-TOF. The Agilent high-resolution accurate mass Q-TOF instruments are tested and installed in accordance with standard performance tests as described in the Agilent installation manual.

www.agilent.com/chem

For Research Use Only.
Not for use in diagnostic procedures.

This information is subject to change without notice.

© Agilent Technologies, Inc., 2017
Published in the USA, October 2, 2017
5991-7957EN



Agilent Technologies