

# Agilent 6546

Parameter	Measure	Specification
MS Sensitivity, positive	Signal-to-noise (S/N) for 1 pg injection of reserpine, while maintaining maximum mass resolution	>500:1 RMS in 10 replicates
MS/MS Sensitivity, positive	S/N 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 Sensitivity, negative	S/N for 1 pg injection of chloramphenicol, while maintaining maximum mass resolution	>500:1 RMS in 10 replicates
MS/MS Sensitivity, negative	S/N for 1 pg LC/MS injection of chloramphenicol, monitoring the most intense product ions ( <i>m/z</i> 152, 176, 194, and 257) while maintaining maximum mass resolution	>1,500:1 RMS in 10 replicates
MS Accuracy, positive	Measured at the (M+H) <sup>+</sup> ion of reserpine ( <i>m/z</i> 609.2807) using an internal mass reference	<0.8 ppm RMS in 10 replicates
MS/MS Accuracy, positive	Product ion <i>m/z</i> 397.2122 for reserpine	<2.0 ppm RMS in 10 replicates
MS Accuracy, negative	Measured at the (M-H) <sup>-</sup> ion of chloramphenicol ( <i>m/z</i> 321.0051) using an internal mass reference	<0.8 ppm RMS in 10 replicates
MS/MS Accuracy, negative	Product ion <i>m/z</i> 152.0353 for chloramphenicol	<2.0 ppm RMS in 10 replicates
Mass resolving power, positive	Full width half mass (FWHM) of spectral peak, with all instrument parameters set by autotune	>30,000 FWHM at <i>m/z</i> 118 >60,000 FWHM at <i>m/z</i> 2,722
Mass resolving power, negative	FWHM of spectral peak, with all instrument parameters set by autotune	>30,000 FWHM at <i>m/z</i> 113 >60,000 FWHM at <i>m/z</i> 2,834
Isotope fidelity	Relative isotopic abundance error (RIA error (%)) = $100 \times (RIA_{exp} - RIA_{theo}) / RIA_{theo}$ of the RMS for 10 ESI calibrant ions in positive polarity	<5 %
Mass range		<i>m/z</i> 50–10,000
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	In spectrum dynamic range on coeluting components while maintaining maximum mass resolution	Up to five 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
Agilent SWARM Autotune	Flexible automated optimization for different <i>m/z</i> ranges as well as fragile compounds	
Data Analysis for the following workflows	Target/Suspect Screening in MassHunter Quantitative Analysis with LC Q-TOF Screener, Qualitative flux analysis in VistaFlux, Food authenticity analysis in Mass Profiler Professional (MPP) and MassHunter Classifier, Metabolomics and Lipidomics analysis with MPP and MassHunter Lipid Annotator	
<b>Integrated calibrant solution</b>	Automated delivery of calibrant for tuning and mass calibration	
<b>Vent-free capillary removal</b>	Isolation valve to allow source and sampling capillary maintenance while maintaining system vacuum.	

All chemical sensitivity, chemical accuracy, and resolution specifications are achieved in manufacturing, and instrument performance data are 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.

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This information is subject to change without notice.

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