

## Evaluation of the Quattro Premier for the Quantification of Sulfadimethoxine in Hanks Balanced Salt Solution

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### Abstract

The newly designed ZSpray source for the Quattro Premier contains several improvements from earlier versions. The source is a vertical design similar to the Quattro micro with a smaller ion block that reduces the volume of the source chamber. An isolation valve allows the sample cone to be easily removed for cleaning without breaking the vacuum. A new feature of this source is an exhaust trap. This trap is positioned directly opposite the ionization probe ensuring that non-ionized materials entering the source are rapidly removed from the ionization chamber. Again this can be easily removed and cleaned if necessary.

### Benefits

The new ZSpray source design has enabled the rugged analysis of pharmaceutical compounds with excellent reproducibility.

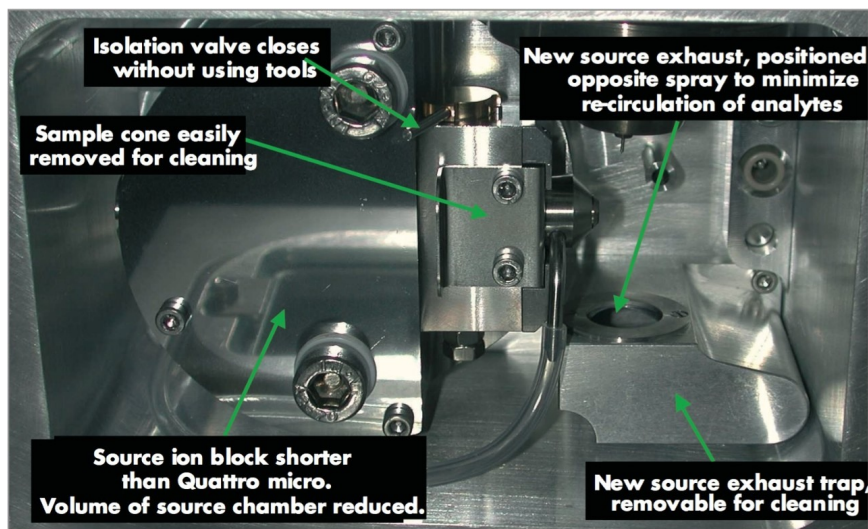
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### Introduction

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The Waters Micromass Quattro Premier Tandem Quadrupole Mass Spectrometer incorporates new developments to the ZSpray dual orthogonal API interface designed to meet the demands of the pharmaceutical industry. In this environment robustness and sensitivity are the driving forces for successful bioanalysis.

The following study has been developed to evaluate source robustness by injecting samples of sulfadimethoxine spiked into Hanks Balanced Salt Solution (HBSS) directly into the source without any dilution. The study ran over a 24-hour period in negative ion atmospheric pressure chemical ionization mode (APCI-ve).



*Features of the new ZSpray source for Quattro Premier.*

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## Experimental

### LC Conditions

HPLC system:	Alliance 2695
Column:	Atlantis dC <sub>18</sub> , 5 $\mu$ m, 2.1 x 100 mm 3 $\mu$ m
Flow rate:	0.8 mL/min

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Mobile phase composition:	Water/ACN, 30/70, v/v
Run time:	3.0 mins
Injection volume:	10 $\mu$ L

## MS Conditions

Mass spectrometer:	Waters Micromass Quattro Premier
Ion mode:	APCI-ve
Corona:	25.00 $\mu$ A
Cone:	50.00 V
Source temp.:	140 $^{\circ}$ C
Desolvation temp.:	550 $^{\circ}$ C
Collision energy:	35 eV
Gas cell pressure (mbar):	$3.58 \times 10^{-3}$ mbar (argon)
MRM transition:	309.2>154.1

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## Results and Discussion

The data were acquired over a 24-hour period with 300 samples of sulfadimethoxine spiked into HBSS directly injected onto an Atlantis dC<sub>18</sub>, 5  $\mu$ m, 2.1 x 100 mm Column. This eluent was sprayed directly into the Quattro Premier ionization source.

Figure 2 shows the plot of absolute area against injection number resulting in a relative standard deviation

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(RSD) of 4.1% across all samples.

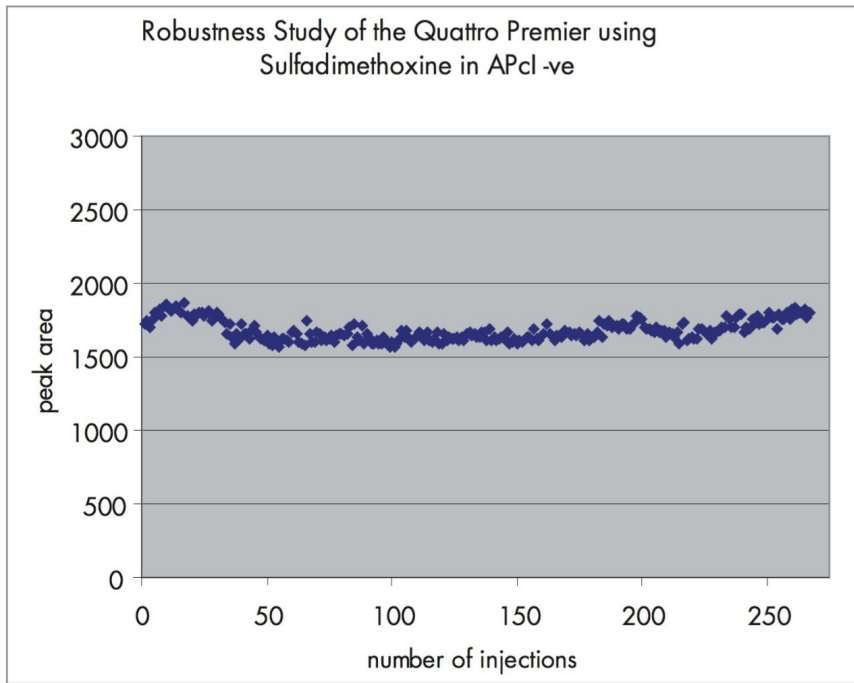


Figure 2. Peak Area of Sulfadimethoxine plotted against number of injections to show the stability of the new Quattro Premier ZSpray source over a 24-hour period.

The calibration range of 10 to 50000 pg/ $\mu$ L showed excellent linearity with a correlation coefficient of >0.99 using a linear fit with 1/x weighting. All the calibration points gave back-calculated values within  $\pm 15\%$  of the theoretical concentrations.

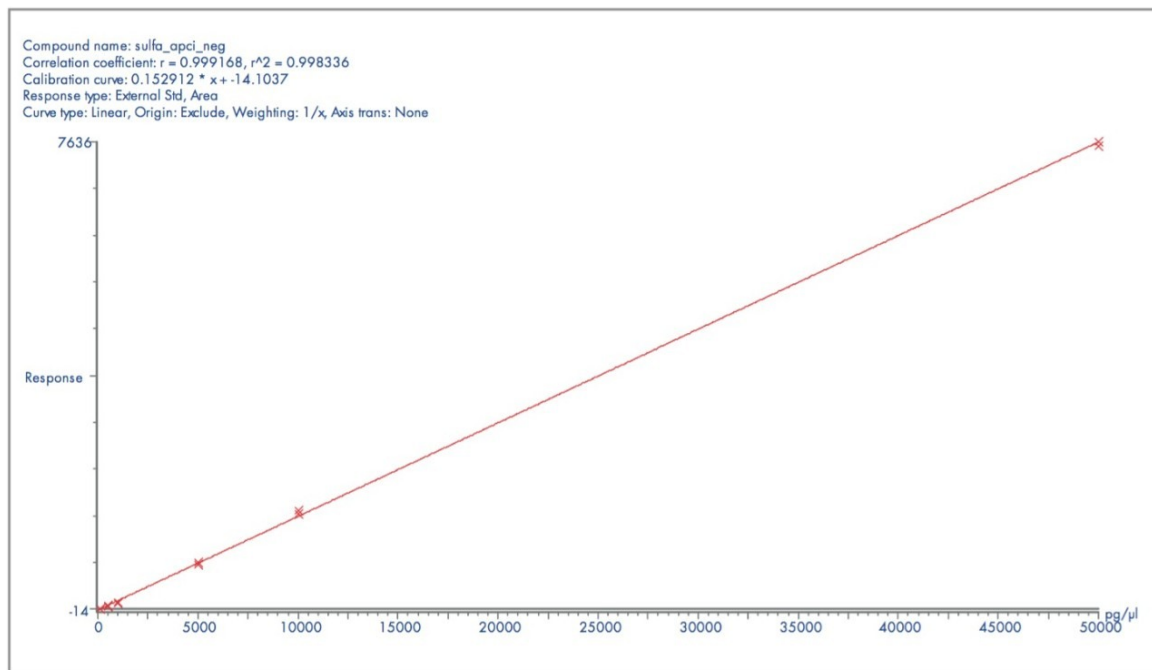


Figure 3. A Calibration line over the range of 10 to 50000 pg/μL for Sulfadimethoxine in HBSS acquired in APCI negative mode.

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## Conclusion

The Quattro Premier Tandem Quadrupole Mass Spectrometer has been developed for quantitative LC-MS/MS. The new ZSpray source design has enabled the rugged analysis of pharmaceutical compounds with excellent reproducibility. The instrument was evaluated by injecting undiluted HBSS spiked with sulfadimethoxine over a 24-hour period (300 injections).

The results showed that the sensitivity of the sulfadimethoxine analysis was maintained with a relative standard deviation of 4.1%. The calibration line resulted in a linear plot over the range 10 to 50000 pg/μL with a correlation coefficient of >0.99 highlighting excellent linearity. This demonstrates the robustness of the new ZSpray interface for complex matrices.

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