

## Optimized Extraction and Cleanup Protocols for LC-MS/MS Multi-Residue Determination of Veterinary Drugs in Milk

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Michael S. Young, Kim Van Tran

Waters Corporation



### Abstract

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In order to insure public health and safety, a reliable screening analysis is necessary to determine veterinary drug residue levels in milk samples. The compounds of interest range from highly polar water-soluble compounds to very non-polar fat-soluble compounds. There exists very effective extraction and cleanup procedures for individual compounds or compound classes, but these methods are not well suited for a multi-class, multi-residue screening analysis.

- Solvent extraction (with excess acetonitrile or methanol) can be effective for many veterinary drug residues in milk, but highly water-soluble drugs, such as salbutamol, are not well recovered using this approach.
- Aqueous buffer extraction can also be effective for many compounds, but fatsoluble compounds, such as dexamethasone, are not well recovered using this approach.
- Traditional solid-phase extraction (SPE) enrichment and cleanup (retention/ wash/elution) has limited utility for multi-residue analysis. Because the range of acidity/polarity/solubility among the compounds is so broad, dispersive or pass-through SPE is preferred for multi-residue methods

## Benefits

- Efficient, timesaving multi-class/ multi-residue methodology
- Straightforward sample preparation for diverse range of analytes
- Fast, sensitive UPLC/MS analysis

## Introduction

Optimized sample preparation and analysis protocols were developed for tandem LC-MS/MS determination of a wide variety of veterinary drug residues in milk samples. Samples are initially precipitated and extracted with an equal volume of acetonitrile. After the resulting extract is treated with acidified acetonitrile to precipitate remaining proteins, a simple SPE cleanup is performed using a Sep-Pak C<sub>18</sub> cartridge. After evaporation and reconstitution, the sample is analyzed using tandem LC-MS. Representative compounds were chosen from major classes of veterinary drugs including tetracyclines, fluoroquinolones, sulfonamides, macrolides, beta-lactams, NSAIDS, steroids, and beta-andrenergids.

## Experimental

## LC Conditions

LC system:	ACQUITY UPLC system
Column:	ACQUITY UPLC CSH C <sub>18</sub> , 1.7 µm, 100 mm x 2.1 mm (i.d.)
Mobile phase A:	0.1% formic in water
Mobile phase B:	0.1% formic acid acetonitrile
Injection volume:	7 µL
Injection mode:	Partial loop injection
Column temperature:	30 °C
Weak needle wash:	10:90 acetonitrile:water (600 µL)
Strong needle wash:	50:30:20 water:acetonitrile:IPA (200 µL)
Seal wash:	10:90 acetonitrile:water

## Gradient:

Time(min)	Flow(mL/min)	%A	%B	Curve
Initial	0.4	85	15	6
2.5	0.4	60	40	6
3.9	0.4	5	95	6
4.9	0.4	5	95	6

Time(min)	Flow(mL/min)	%A	%B	Curve
5.0	0.4	85	15	6
7.0	0.4	85	15	6

## MS conditions

Mass spectrometer: Waters ACQUITY TQD

Source temperature: 150 °C

Desolvation temperature: 500 °C

Desolvation gas flow: 1000 L/Hr

Cone gas flow: 30 L/Hr

Collision gas flow: 0.15 mL/min

Data management: MassLynx v4.1

Table 1 summarizes the MRM transitions and instrument parameters used for this study. Also presented in Table 1 are matrix-matched calibration data for each compound (calculated using the primary transition).

Compound	MRM	Cone (V)	Collision (eV)	Calibration Range (ng/g)	Correlation ( $r^2$ )	LOQ (ng/g)
Carbadox	263>231	15	17	25-200	0.9901	50
	263>145	15	25			
Ciprofloxacin	332>288	20	20	25-200	0.9911	25
	332>314	20	20			
Chloramphenicol	321>152	10	15	25-200	0.9903	25
	321>257	20	12			
Chlortetracycline	479>444	25	25	25-200	0.9945	25
	479>462	25	15			
Dexamethasone	393>355	18	13	25-200	0.9955	25
	393>373	18	10			
Enrofloxacin	360>316	15	15	50-400	0.9917	50
	360>342	15	15			
Erythromycin	734>158	25	25	2.5-20	0.9979	2.5
	734>576	25	20			
Lincomycin	407>126	15	35	12.5-100	0.9903	12.5
	407>359	15	15			
Oxacillin	402>160	30	15	25-200	0.9948	25
	402>243	30	10			
Oxytetracycline	461>426	22	20	25-200	0.9914	25
	461>381	22	20			
Penicillin-G	335>160	15	15	12.5-100	0.9961	12.5
	335>176	15	15			
Phenylbutazone	309>160	15	25	25-200	0.9908	25
	309>146	15	27			
Ractopamine	302>107	25	20	75-600	0.9935	75
	302>284	25	10			
Salbutamol	240>148	25	10	25-200	0.9902	25
	240>222	25	20			
Sulfamerazine	265>92	25	33	25-200	0.9951	25
	265>156	25	15			
Sulfamethazine	279>92	15	33	25-200	0.9915	25
	279>186	15	15			
Sulfanilamide	173>156	20	12	25-200	0.9910	50
	173>92	20	20			
Tetracycline	445>154	25	25	25-200	0.9929	25
	445>410	25	20			

Table 1. MRM transitions and calibration data.

## Sample Preparation Protocol

### 1. Initial Extraction/Precipitation:

<b>Transfer</b> 2 mL sample into a 15 mL centrifuge tube
<b>Add</b> 2 mL acetonitrile (ACN) and vortex for 30 seconds
<b>Centrifuge</b> 8000 x g for 4 minutes <sup>1</sup>

<sup>1</sup> This step gives good extraction of most compounds of interest but also extracts significant amounts of protein and some fats that may interfere with the LC/MS analysis.

### 2. Residual Protein Precipitation:

<b>Transfer</b> 2 mL of supernatant (from step 1) to a second centrifuge tube
<b>Add</b> 3 mL of acidified acetonitrile (0.2 % formic acid)
<b>Centrifuge</b> 30 seconds <sup>2</sup>

<sup>2</sup> This step effectively precipitates the residual protein.

### 3. SPE Cleanup:

Take 1 mL of the supernatant (from step 2) for SPE cleanup using a Sep-Pak C <sub>18</sub> cartridge (see SPE details in Figure 1). <sup>3</sup>
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<sup>3</sup> This step removes fats and non-polar interferences.

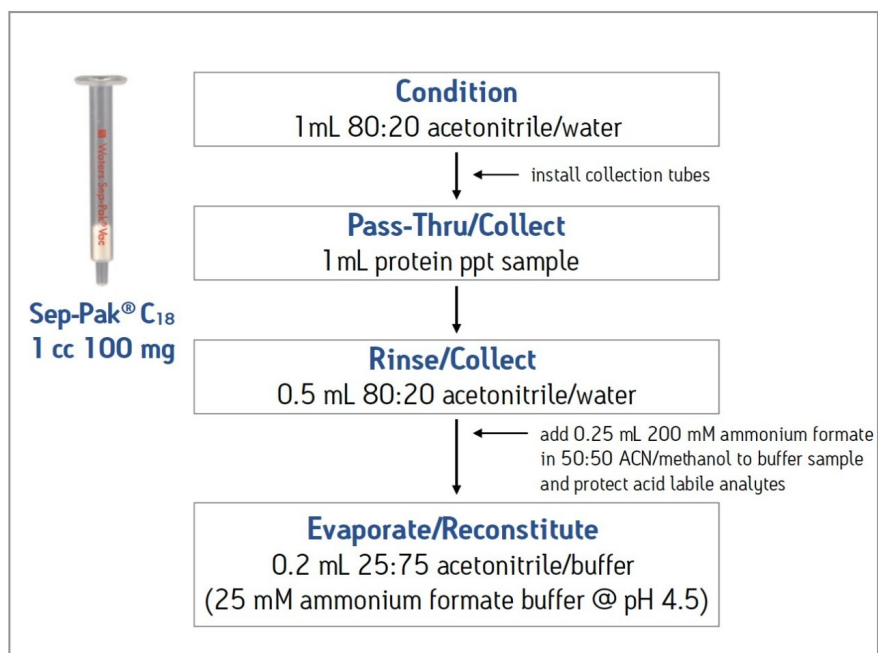


Figure 1. SPE cleanup protocol.

## Results and Discussion

Figure 2 shows a typical LC-MS chromatogram obtained from analysis of a matrix matched standard of erythromycin at 6.7 ng/g. Performance of the other compounds was similar. Table 2 shows the recovery and matrix effects observed for multiresidue milk analysis.

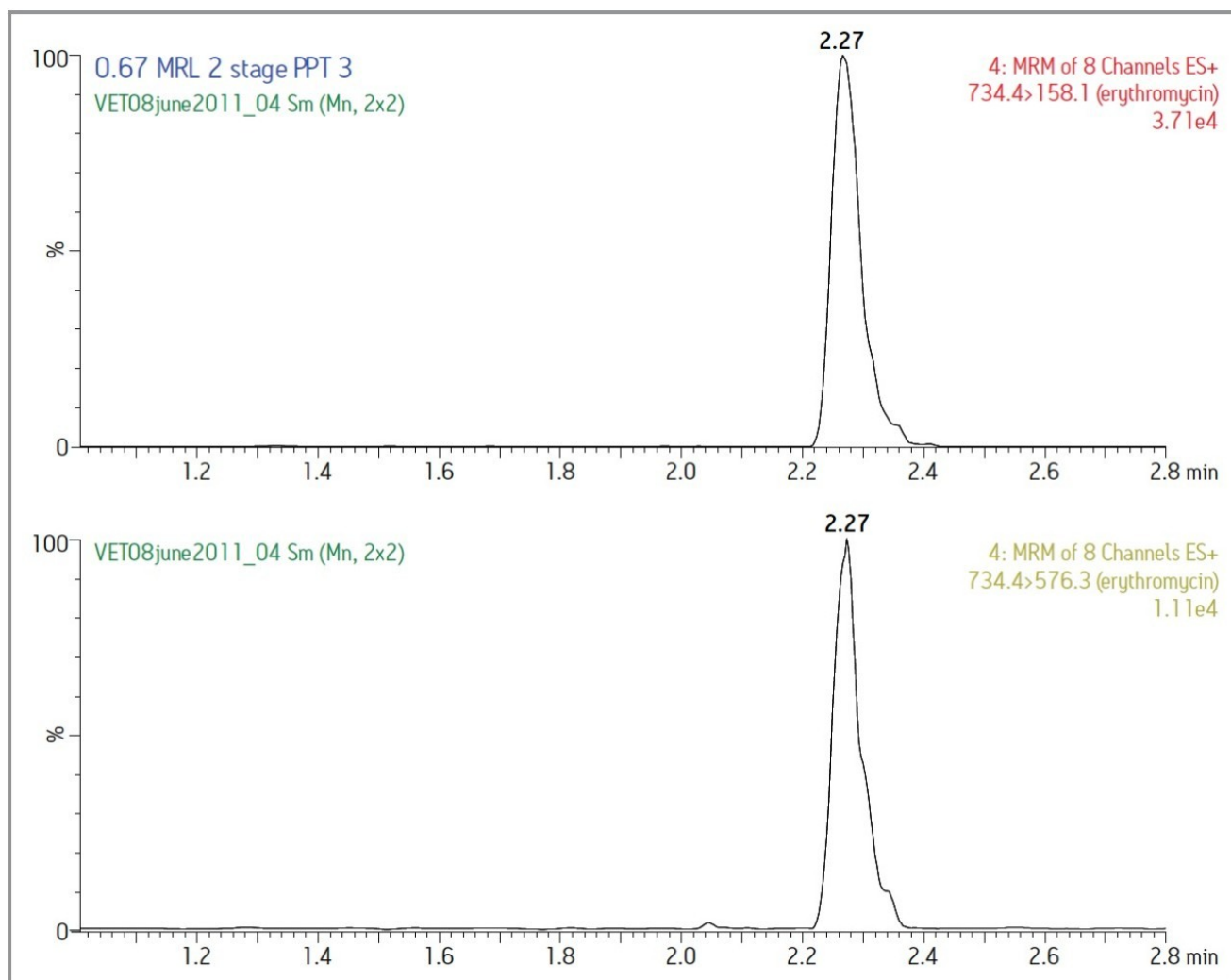


Figure 2. Typical LC-MS/MS Chromatogram obtained from milk spiked with erythromycin at 6.7 ng/g (primary MRM transition on top).



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	445>410	25	20			

Table 2. Recovery and matrix effects.

\* Negative number signifies matrix enhancement

The procedure chosen for the milk analysis was to initially extract and precipitate a milk sample with an equivalent amount of acetonitrile and then to precipitate the remaining protein from the supernatant with

acidified acetonitrile. A single step procedure was also considered by which the milk sample was directly precipitated with 0.2% formic acid in 80% acetonitrile. This procedure was more straightforward and produced a final extract of similar cleanliness compared with the chosen protocol. However, there was significantly lower recovery for the most polar compounds, such as sulfanilamide, and virtually no recovery of chlorotetracycline. Another approach was considered, by which two separate extractions were performed. The first extraction, for the water soluble compounds, was accomplished using aqueous succinic buffer. The second, performed on the re-suspended pellet, was with acetonitrile. This approach requires that each fraction be worked up independently before ultimately combining fractions for a single injection. Performance was marginally better than the chosen procedure but at a much greater cost of time and materials. Although the chosen procedure requires two precipitation steps, it provided the best balance of preparative time with good method performance.

## Conclusion

- A two step extraction/protein precipitation procedure was developed and demonstrated for milk analysis

The procedure was suitable for screening for a wide range of veterinary drug residues

Recoveries averaged 67% (22-110) with the lowest values for tetracyclines.

- A pass-thru SPE cleanup protocol using Sep-Pak C<sub>18</sub> was utilized for effective removal of residual fats.
- The sample preparation methodology for milk produced an extract for LC/MS that was free of particulates and required no subsequent filtration prior to LC-MS analysis.

## Featured Products

- [MassLynx Mass Spectrometry Software <https://www.waters.com/513164>](https://www.waters.com/513164)
- [ACQUITY UPLC System <https://www.waters.com/514207>](https://www.waters.com/514207)
- [Xevo TQD Triple Quadrupole Mass Spectrometry <https://www.waters.com/134608730>](https://www.waters.com/134608730)

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