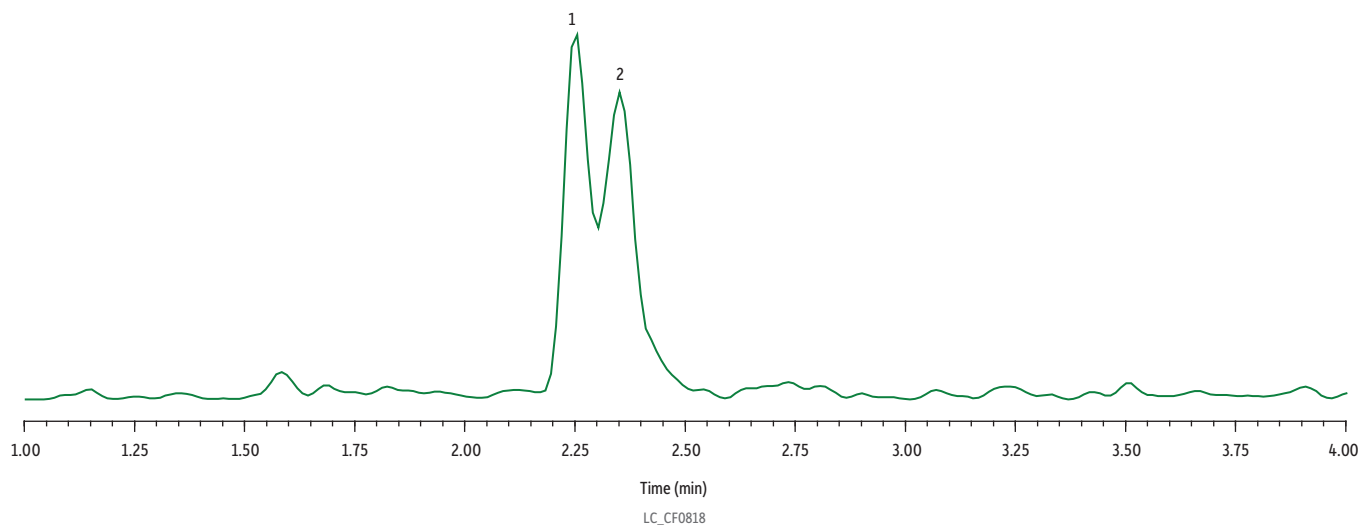


# Plasma Matrix Interference Co-Eluting with D4-UDCA in Patient Sample on Raptor C18



Peaks	t <sub>R</sub> (min)	Precursor Ion	Product Ion
1. Matrix interference	2.25	-	-
2. D <sub>4</sub> UDCA	2.35	395.40	395.40

**Column** Raptor C18 (cat.# 9304252)  
**Dimensions:** 50 mm x 2.1 mm ID  
**Particle Size:** 1.8 µm  
**Pore Size:** 90 Å  
**Guard Column:** UltraShield UHPLC precolumn filter 0.2 µm (cat.# 25810)  
**Temp.:** 60 °C

**Standard/Sample**  
**Diluent:** 65:35 Water:methanol  
**Inj. Vol.:** 3 µL

**Mobile Phase**  
**A:** 5 mM ammonium acetate in water, pH unadjusted  
**B:** Methanol:acetonitrile (v/v, 50:50)

Time (min)	Flow (mL/min)	%A	%B
0.00	0.5	65	35
2.00	0.5	60	40
2.50	0.5	55	45
3.50	0.5	50	50
4.60	0.5	45	55
5.70	0.5	20	80
5.90	0.8*	5	95
6.50	0.8*	5	95
6.51	0.5	65	35
8.50	0.5	65	35

**Max Pressure:** 275 bar  
**Detector** Shimadzu LCMS-8045 in ESI- mode  
**Instrument** Shimadzu Nexera X2  
**Sample Preparation** A 50 µL aliquot of patient sample was added to a microcentrifuge tube. Fifty microliters of internal standards was added to the tube and vortexed. The samples were protein precipitated using 800 µL of ice-cold acetonitrile. After vortexing and centrifugation at 4200 rpm for 10 min, the supernatant was transferred to a new vial and dried down at 60 °C under nitrogen. All samples were reconstituted in 200 µL of 35% methanol in water.

**Notes** \*The flow rate was increased to 0.8 mL/min to more thoroughly flush phospholipids from the analytical column, thereby reducing matrix effects.

The flow was diverted to waste before 1 minute and after 6 minutes to protect the mass spectrometer.