Project Requirement:

To develop an LC-MS/MS method for quantification of a highly polar, and rarely encountered peptide, for a biotech company's discovery process.

The Peptide:



- All D-amino acids
- 10 Arginines & 5 Lysines
- C-terminal acid and N-terminal amine
- Highly polar positively charged peptide



The challenges and Aurigene's solutions:





a. LC conditions were modified and different columns were used

Here are the trial results towards the optimization of LC parameters -

Trial 01



SPE-HLB; SB Phenyl 4.6 X 150 mm 3.5 µm; Isocratic; 70:30 Formic ā in H2O + Formic ā in MeOH

Good peak shape and response. Analyte eluted in void volume in 50 & 150 mm columns **Trial 02**



SPE-HLB; SB Phenyl 4.6 X 150 mm 3.5 µm; Isocratic; 50:50 Formic ā in H2O + Formic ā in MeOH

Split peak observed

Trial 03

Trial 04



SPE-HLB; SB Phenyl 4.6 X 150 mm 3.5 µm; Gradient; Formic ā in H2O + Formic ā in MeOH

Poor peak shape and low response. Tailing observed



SPE-HLB; Waters Xbridge BEH; 4.6*50mm; 3.5µm; Isocratic; Formic ā in H2O + Formic ā in ACN

> Good peak shape and response. Analyte eluted in void volume.



Trial 05

SPE-HLB; Waters Xbridge BEH; 4.6*50mm; 3.5µm; Gradient; SPE-HLB; Waters Xbridge BEH; 4.6*50mm; 3.5µm; Gradient; Formic ā in H2O + Formic ā in ACN

Split peak observed





Formic ā in H2O + Formic ā in MeOH

Good peak shape and response Analyte retained; LLOQ 20 ng/mL