

***Development of a bioanalytical method  
for the quantification of a  
phosphorothioated oligonucleotide in  
human plasma capillary micro-sample  
using LC-MS/MS***

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22 November 2013***

# Introduction

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- ❖ *Advantages of capillary micro-sampling*
- ❖ *Oligonucleotides*
- ❖ *Method development challenges*
- ❖ *Mass spectrometer infusion*
- ❖ *Liquid chromatography*
- ❖ *Extraction procedure*
- ❖ *Results*
- ❖ *Conclusion*

# *Aim*

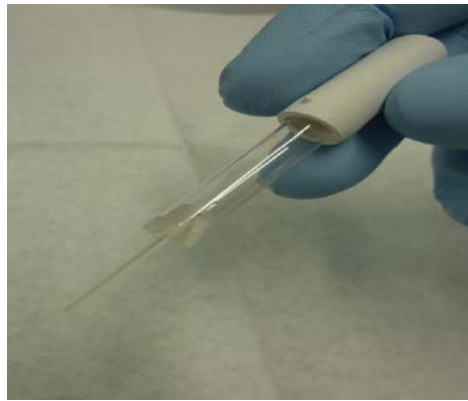
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*The aim of this research was to demonstrate the compatibility of capillary micro-sampling with a difficult and challenging class of compounds.*

# Capillary micro-sampling

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*A technique used to collect or handle blood, serum or plasma by drawing liquid into a glass tube by capillary action*



*Interest and use of the technique in bioanalysis has increased over the past few years*

# *Advantages of capillary micro-sampling*

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- ❖ Reduction in the amount of animals required.*
- ❖ Tail vein used rather than retro orbital sampling, hence no anaesthesia required.*
- ❖ Shorter restraint times, less need for warming rodents.*
- ❖ Less need for terminal bleeds.*
- ❖ Less consumption of test material*
- ❖ Less rodent facilities required*
- ❖ Less technicians required*

# *Method Development*

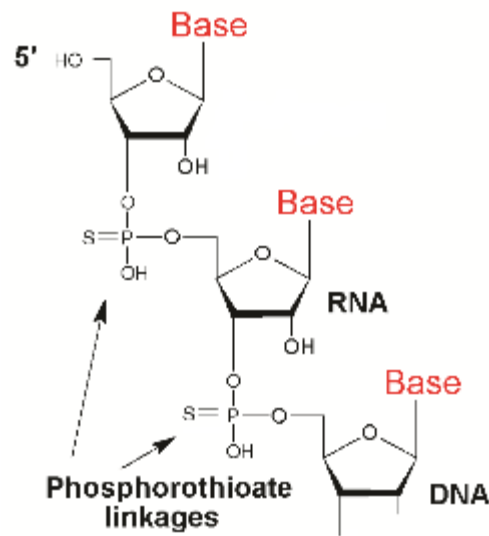
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*Step 1: Develop conventional plasma method.*

*Step 2: Modify extraction procedure for capillary micro-sample analysis.*

# Oligonucleotides

*Synthetic nucleic acid-based drug candidates (Typically 15-35 nucleotides in length)*



*Bind to target mRNA and prevent translation*

# *Oligonucleotides continued*

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*Analyte sequence*

*A\*T\*G\*C\*C\*T\*G\*G\*A\*T\*T\*G\*C\*G\*C\*G\*A\*T\*T\*G*

*Mass: 5825 Da*

*Internal standard sequence*

*A\*T\*G\*C\*C\*T\*G\*G\*A\*T\*T\*G\*C\*G\*A*

*\*Phosphorothioate linkage*

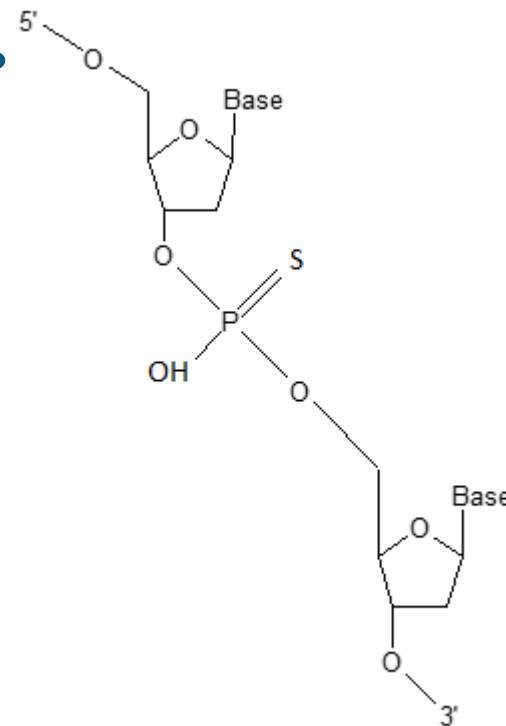
*Mass: 4832 Da*

*Simulates typical anti-sense therapeutic*



# Method development challenges for oligonucleotides

- ❖ *Highly charged poly-anionic backbone dominates the chemistry of nucleic acids.*
- ❖ *Susceptible to nuclease degradation*
- ❖ *Prone to adsorption*
- ❖ *Strongly protein bound*
- ❖ *Multiple charge states*
- ❖ *MS/MS selectivity challenge*



# Considerations for chromatographic separation

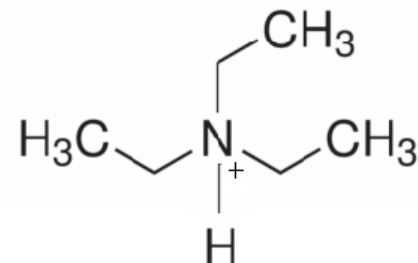
*Ion-pair reversed phase is the system of choice for LC-MS/MS analysis of oligonucleotide.*

❖ *Triethylamine (TEA)*

*Ion pair reagent for acidic compounds*

*Shields the acidic groups of the oligo*

*Typically active at 0.05-2%*

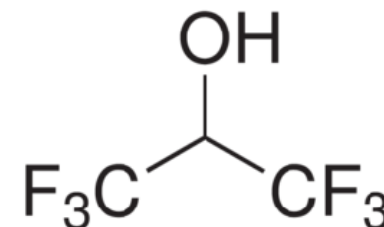


❖ *Hexafluoroisopropanol (HFIP)*

*Extremely volatile acidic solvent*

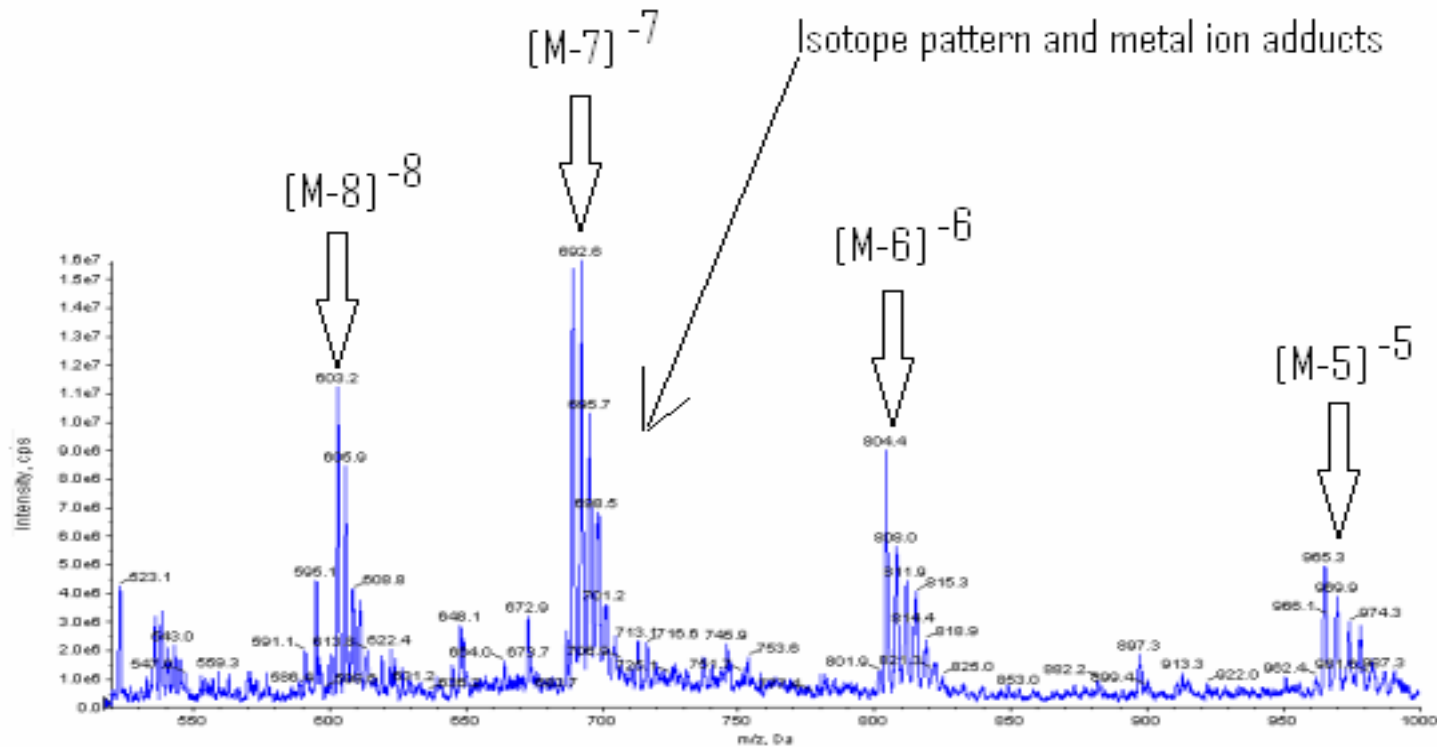
*Lowers the pH of TEA-containing mobile phase solvents, thus increasing the efficiency of the oligo-TEA ion pairing*

*Readily evaporated in the MS source.*



# Mass spectrometer Infusion

- ❖ Infused on an AB-Sciex API 4000 at 50 µg/mL
- ❖ Prepared in Water: MeOH:HFIP: TEA 70:30:1:0.1 v/v/v/v
- ❖ Infusion solution at 0.15 mL/min whilst under LC flow of 0.15 mL/min (H<sub>2</sub>O:MeOH:HFIP:TEA 70:30:1:0.1 v/v/v/v)



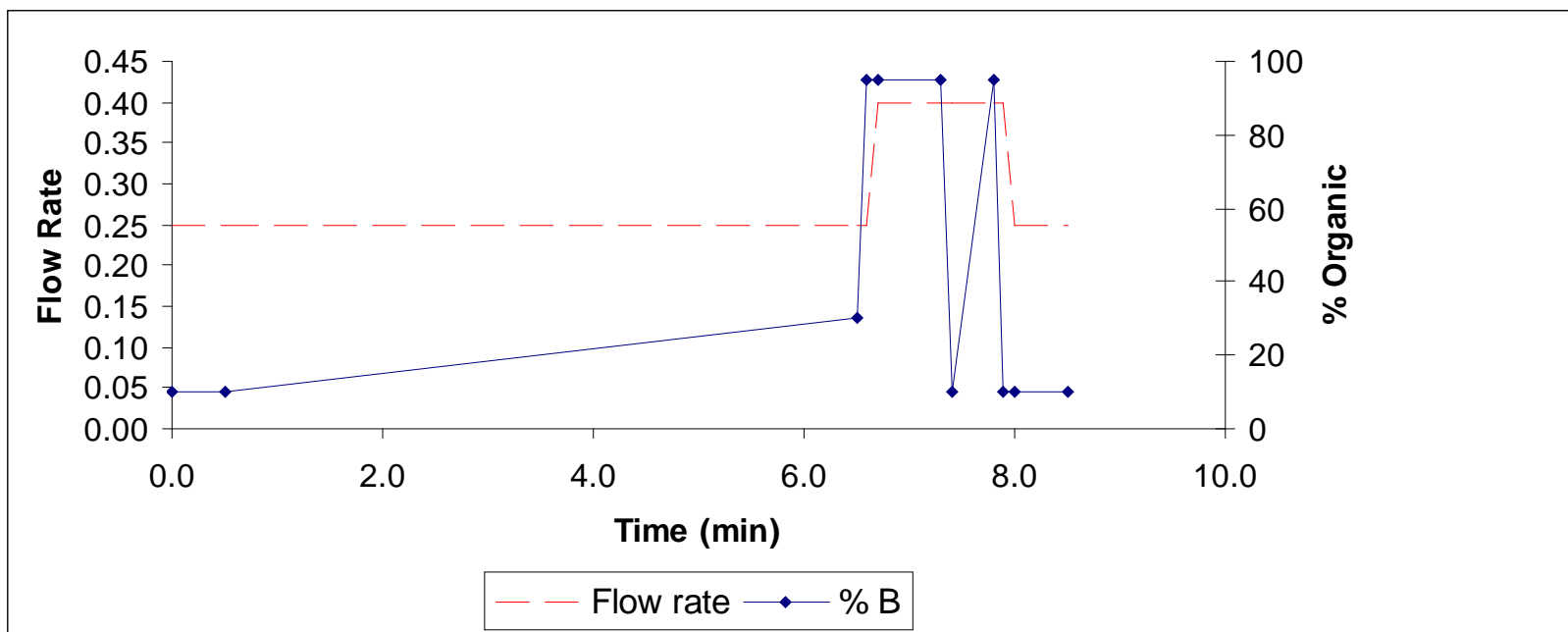
# Liquid chromatography

Mobile phase A= Water:HFIP:TEA 100:1:0.1 v/v/v

Mobile phase B= MeOH:HFIP:TEA 100:1:0.1 v/v/v

Column= Acquity BEH C18 1.7  $\mu\text{m}$  2.1 x 50 mm

Column temperature= 50 °c



# *Conventional plasma extraction procedure*

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*Liquid-Liquid extraction  
followed by reversed phase SPE*

# Step 1: liquid-liquid extraction

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1	<i>Aliquot 200 <math>\mu</math>L into 1.5 mL Eppendorf tubes</i>
2	<i>Add 500 <math>\mu</math>L of water: ammonia (95:5 v/v) to each tube and mix for 10 min.</i>
3	<i>Add 100 <math>\mu</math>L of phenol: chloroform: isoamyl alcohol (25 : 24 : 1, v/v/v)</i>
4	<i>Transfer 600 <math>\mu</math>L of the supernatant to a 2 mL 96 well plate.</i>
5	<i>Add 600 <math>\mu</math>L of Water: HFIP: TEA (100: 2: 0.2, v/v/v)</i>

## Step 2: Reversed phase SPE

6	<i>Prime SPE plate (HLB 10mg) with acetonitrile</i>
7	<i>Prime SPE plate with Water: HFIP: TEA (100: 1: 0.1, v/v/v)</i>
8	<i>Transfer entire sample to SPE plate</i>
9	<i>Wash plate with Water: HFIP: TEA (100: 1: 0.1, v/v/v)</i>
10	<i>Elute sample into 96-well plate with acetonitrile: water: TEA (60: 40:1, v/v/v)</i>
11	<i>Evaporate to dryness under stream of nitrogen at nominal 40 °C</i>
12	<i>Re-dissolve in methanol: water: HFIP: TEA (10 : 90 : 2 : 0.2, v/v/v/v)</i>
13	<i>Cap plate and vortex mix, centrifuge and submit for analysis</i>

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*Modification of conventional plasma method  
for capillary micro-samples*



## *Method development challenges for CMS*

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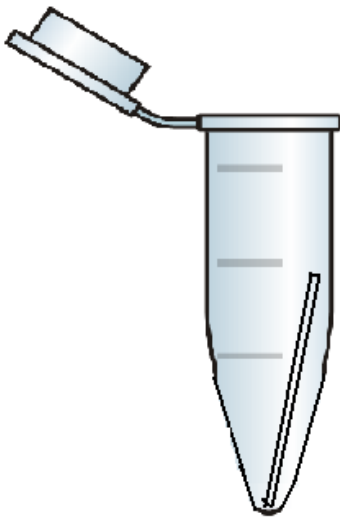
- ❖ Reduced sample volume compared with typical plasma analysis. 20  $\mu$ L plasma capillary sample*
- ❖ Requires a suitable washout solvent in which the analyte is soluble and will not precipitate proteins*
- ❖ General expectations for oligonucleotide analysis is to achieve low ng/mL LLOQs*
- ❖ Dilution of samples*

# Washout solution

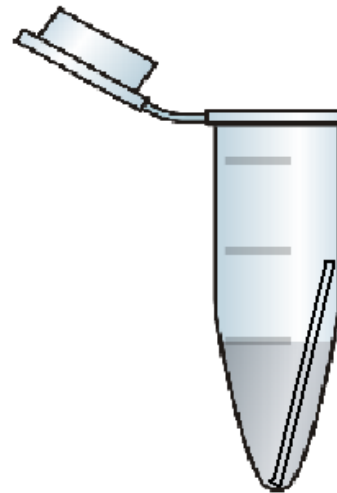
*Washout solution = 5% ammonia in water.*

*Should not precipitate the proteins in the capillary tube.*

*Oligonucleotide are soluble in aqueous solutions.*



Quality Control CMS samples stored at -20°C in Eppendorf tubes



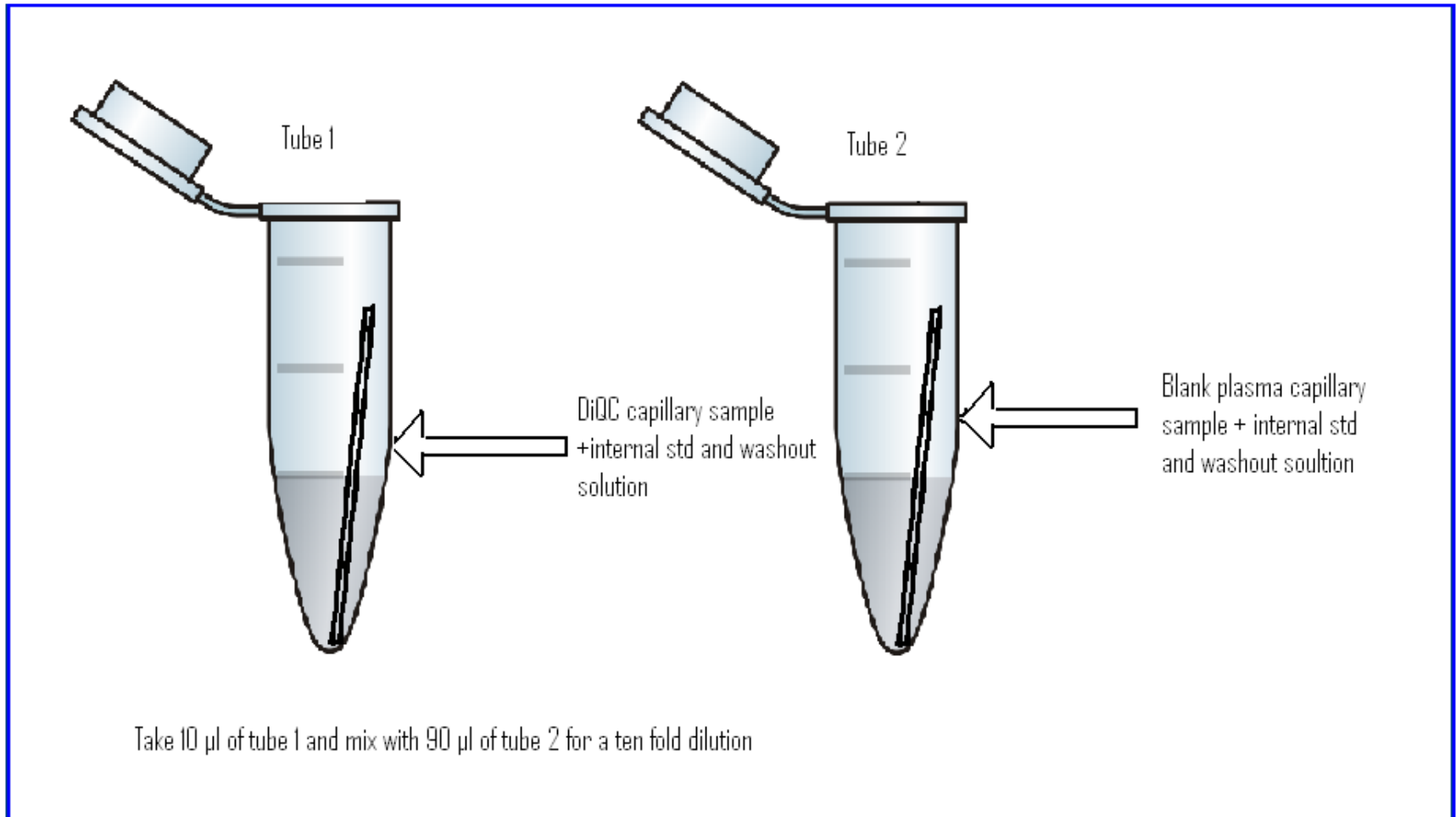
Washout solvent added once CMS have been thawed

# Plasma capillary micro-sample extraction procedure

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1	<i>Draw sample into a 20<math>\mu</math>L capillary and place into 1.5 mL Eppendorf tubes</i>
2	<i>Add 250 <math>\mu</math>L of water: ammonia (95:5 v/v) to each tube and mix for 20 min to ensure the sample has fully equilibrated.</i>
3	<i>Add 50 <math>\mu</math>L of phenol: chloroform: isomyl alcohol (25 : 24 : 1, v/v/v).</i>
4	<i>Transfer 300 <math>\mu</math>L of the supernatant to a 2 mL 96 well plate..</i>
5	<i>Add 300 <math>\mu</math>L of Water: HFIP: TEA (100: 2: 0.2, v/v/v)</i>

# Dilution method

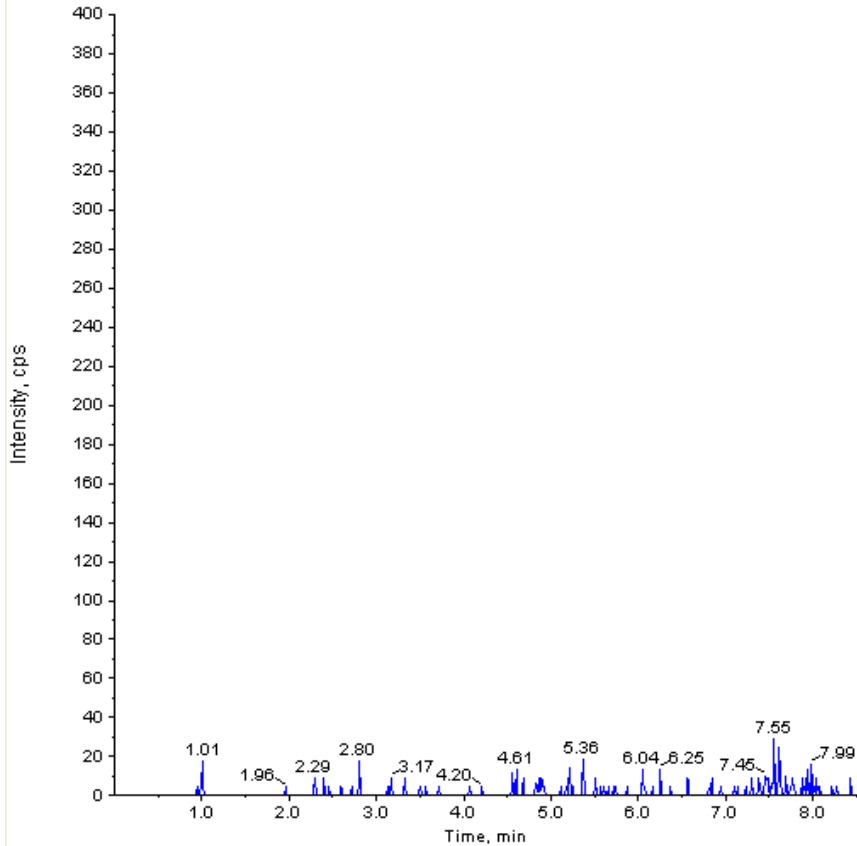


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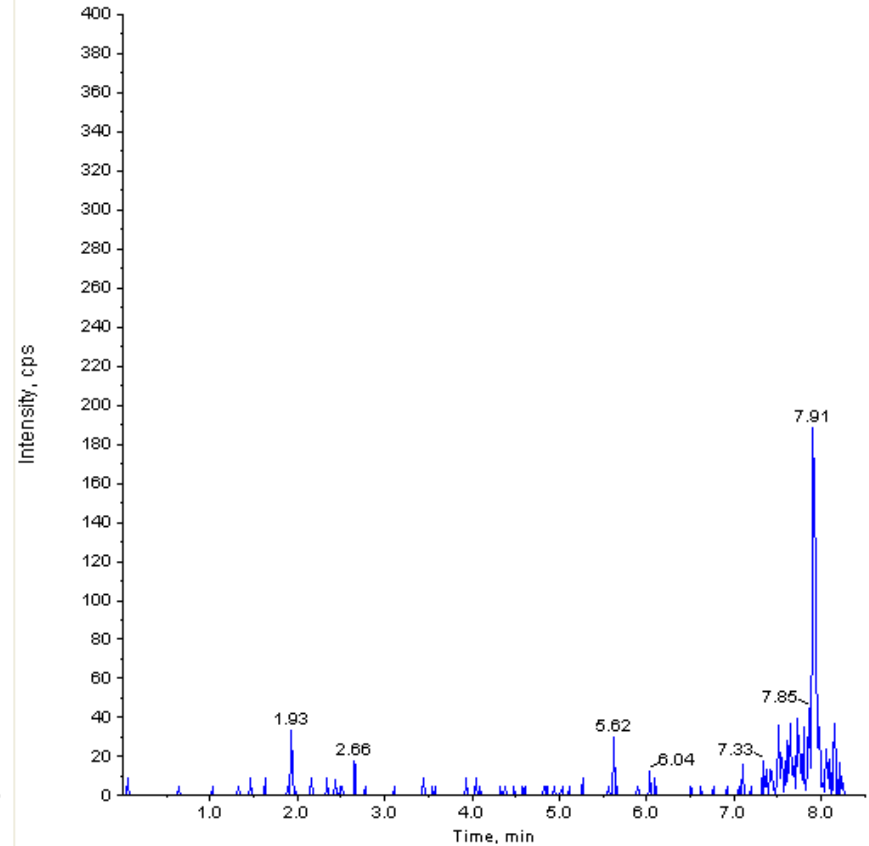
# *Results*

# Blank chromatogram

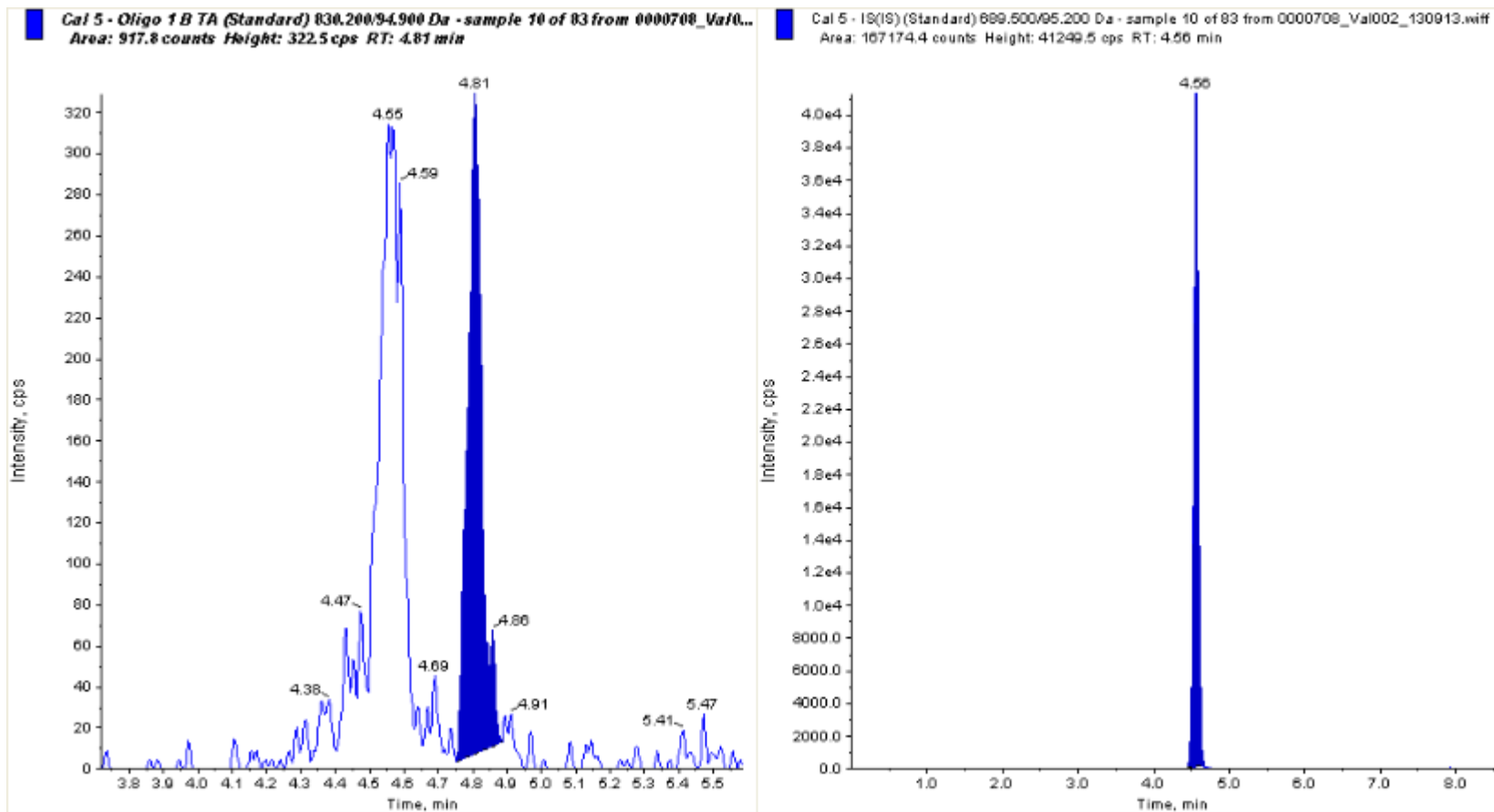
MB - Oligo 1 B TA (Unknown) 830.200/94.900 Da - sample 22 of 57 from 0000708\_Val001...  
(peak not found)



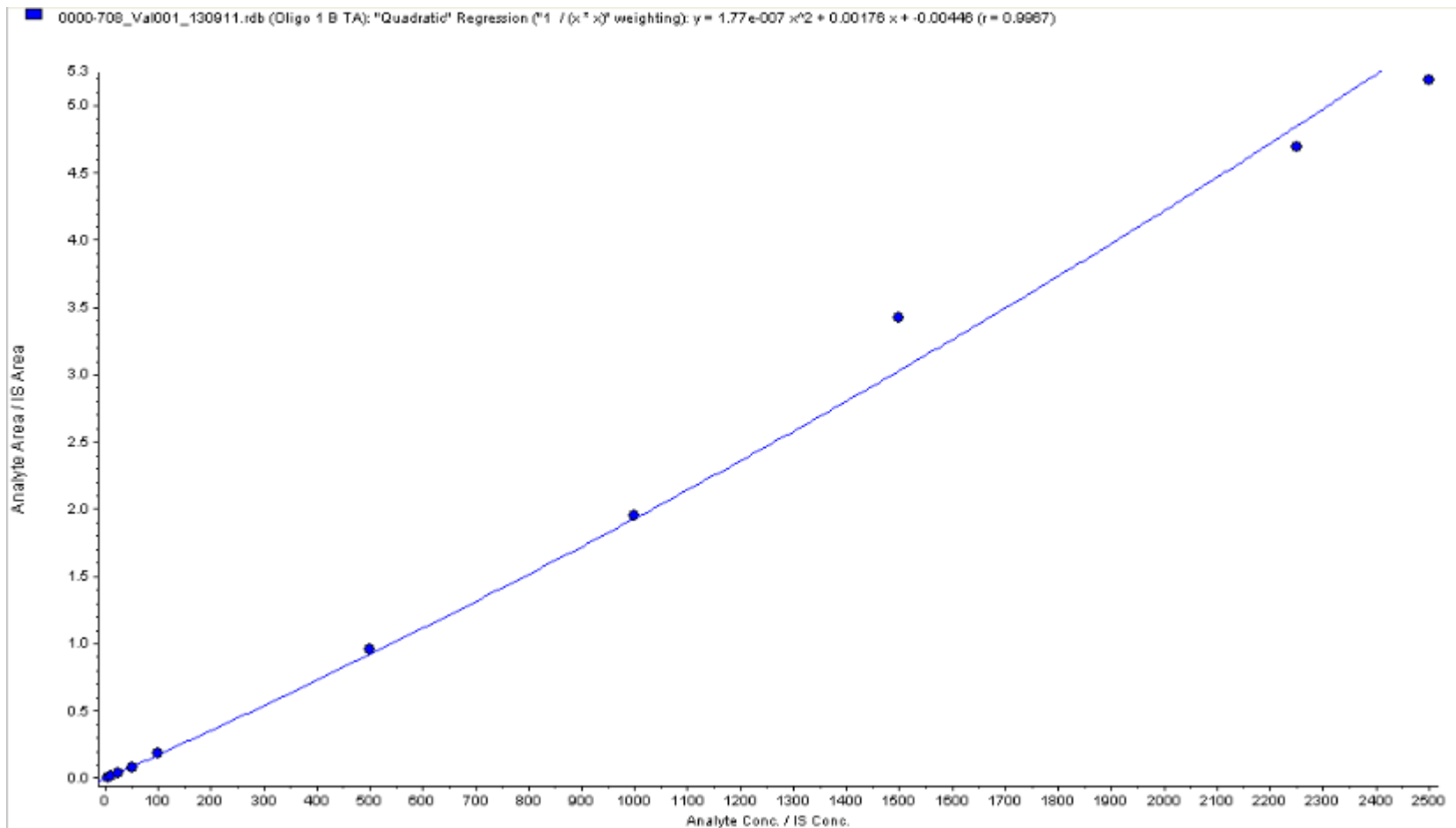
MB - IS(IS) (Unknown) 689.500/95.200 Da - sample 22 of 57 from 0000708\_Val001\_130912.wiff  
(peak not found)



# Lower limit of quantification 5ng/mL



# Calibration curve 5-2500 ng/mL





# Inter-assay accuracy and precision

	<i>LLOQ QC</i> <i>5 ng/mL</i>	<i>LoQC</i> <i>15 ng/mL</i>	<i>MeQC</i> <i>175 ng/mL</i>	<i>HiQC</i> <i>2000 ng/mL</i>	<i>DiQC</i> <i>12500 ng/mL</i>
<i>Mean ng/mL</i>	<i>5.62</i>	<i>14.3</i>	<i>192</i>	<i>1950</i>	<i>12900</i>
<i>SD</i>	<i>0.507</i>	<i>1.13</i>	<i>9.63</i>	<i>83.5</i>	<i>462</i>
<i>RSD %</i>	<i>9.0</i>	<i>7.9</i>	<i>5.0</i>	<i>4.3</i>	<i>3.6</i>
<i>Accuracy %</i>	<i>112.4</i>	<i>95.3</i>	<i>109.7</i>	<i>97.5</i>	<i>104.0</i>
<i>N</i>	<i>18</i>	<i>17</i>	<i>17</i>	<i>18</i>	<i>6</i>

# *Spiked individual data at LoQC level*

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	<i>Observed concentration ng/mL</i>	<i>Accuracy (%)</i>
<i>Ind 1</i>	<i>14.7</i>	<i>97.9</i>
<i>Ind 2</i>	<i>15.0</i>	<i>99.8</i>
<i>Ind 3</i>	<i>14.2</i>	<i>94.8</i>
<i>Ind 4</i>	<i>14.4</i>	<i>96.0</i>
<i>Ind 5</i>	<i>12.9</i>	<i>85.9</i>
<i>Ind 6</i>	<i>14.5</i>	<i>96.6</i>

- *Recovery 83 %*
- *24 hour RT stability demonstrated*

# Conclusion

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- ❖ *Practical application of CMS demonstrated.*
- ❖ *LLOQ of 5 ng/mL achieved from 20  $\mu$ L of plasma.*
- ❖ *Fully validated method that met FDA and EMA guidelines.*
- ❖ *Longer extraction time.*

# *Acknowledgements*

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*Dr Phillip Turpin*

*Dr Matthew Ewles*

*Dr Lee Goodwin*

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*Any Questions*