

LC-MS/MS Analysis of Amyloid Beta Peptides in Artificial Cerebrospinal Fluid Using the Xevo™ TQ Absolute Mass Spectrometer for Clinical Research

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This is an Application Brief and does not contain a detailed Experimental section.

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Abstract

Amyloid-beta (A β) peptides with sequences containing 36–43 amino acids are the main component of amyloid plaques deposited in the brains of individuals with neurodegenerative disorders, therefore, these peptides are of interest in clinical research. In this application brief, we demonstrate the suitability of the ACQUITY™ Premier UPLC I-Class System with Xevo™ TQ Absolute Mass Spectrometer as a tool in clinical research for analytically sensitive and selective quantitation of multiple A β peptide isoforms (1–38, 1–40, 1–42) in artificial Cerebrospinal Fluid (aCSF).



Figure 1. Waters ACQUITY™ Premier UPLC I-Class System with Xevo™ TQ Absolute Mass Spectrometer.

Introduction

Amyloid-beta ($A\beta$) peptides with sequences containing 36–43 amino acids are the main component of amyloid plaques deposited in the brains of individuals with neurodegenerative disorders, therefore, these peptides are of interest in clinical research of pharmacodynamics investigations of new therapeutics. Historically, quantification of $A\beta$ peptides in biological fluids has relied mainly on the use of immunoassays, such as ELISA.^{1,2} These techniques can suffer from cross-reactivity, contributing to batch-to-batch variation of the methods, which can impact confidence in results. In addition, for assessments that involve multiple biomarkers, an individual ELISA

method is required for each peptide, increasing overall analysis time and cost. Therefore, a single robust method providing greater analytical selectivity would help overcome these challenges. Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) could be a beneficial technique in the clinical research of A β peptides. These benefits include improvements in analytical selectivity, and the capability of multi-analyte quantitative detection in a single run. Utilizing the surrogate matrix methodology, the A β peptide isoforms can be measured with selectivity achieved through sample preparation, chromatographic separation, and Multiple Reaction Monitoring (MRM) mass detection.

Herein, we demonstrate the suitability of the ACQUITY™ Premier UPLC I-Class System with Xevo™ TQ Absolute Mass Spectrometer as a tool in clinical research for analytically sensitive and selective quantitation of multiple intact A β peptide isoforms (1–38, 1–40, 1–42) extracted from 200 μ L of artificial Cerebrospinal Fluid (aCSF) over the concentration range 0.1–10 ng/mL.

Sample Preparation and LC-MS Analysis

The sample preparation and LC-MS analysis details from the Application Note [720006517](#) were used with some minor changes highlighted in this section to improve analyte retention.³

Calibration and Quality Control (QC) working solutions at each level were spiked into the blank artificial CSF with 0.4% (w/v) Bovine Serum Albumin (BSA). An internal standard working solution was added to 200 μ L of spiked samples, which was diluted with 200 μ L of 5 M guanidine-HCl and 200 μ L of 4% (v/v) phosphoric acid. After incubation at room temperature for one hour the samples were loaded onto an Oasis™ MCX SPE μ Elution plate. The plate was washed and subsequently eluted using the protocol in [720006517](#) in Figure 1. The eluate was evaporated with nitrogen to dryness and reconstituted with 50 μ L of 20:80:1 (v:v:v) acetonitrile:water:ammonia.

An ACQUITY Premier UPLC I-Class FTN System was used to separate the A β peptide isoforms using a ACQUITY UPLC BEH Peptide C₁₈ 300 Å, 2.1 x 150 mm, 1.7 μ m Column with a 0.3% NH₄OH/water/acetonitrile gradient from 10–55% mobile phase B and analysed on a Xevo TQ Absolute Mass Spectrometer using the MRM transitions and precursor scan parameters listed in Table 1. Mobile phases were prepared freshly on daily basis.

| Analyte | Precursor ion (<i>m/z</i>) | Product ion (<i>m/z</i>) | Cone voltage (V) | Collision energy (V) |
|---------------------|---------------------------------|-------------------------------|---------------------|-------------------------|
| A β (1-38) | 1033.8 | 1000.5 | 50 | 19 |
| IS-A β (1-38) | 1046.4 | 1012.5 | 50 | 19 |
| A β (1-40) | 1083.4 | 1053.8 | 60 | 20 |
| IS-A β (1-40) | 1096.4 | 1066.8 | 60 | 20 |
| A β (1-42) | 1129.5 | 1078.8 | 60 | 23 |
| IS-A β (1-42) | 1142.8 | 1091.8 | 60 | 23 |

Table 1. The MRM transitions used to analyse the intact A β peptide isoforms and their internal standards (IS).

Results and Discussion

Analytical sensitivity of the lowest calibrator at 0.1 ng/mL was demonstrated with S/N (PtP) > 10:1 for all A β peptide isoforms (1-38, 1-40, 1-42) across the five analytical runs (Figure 2).

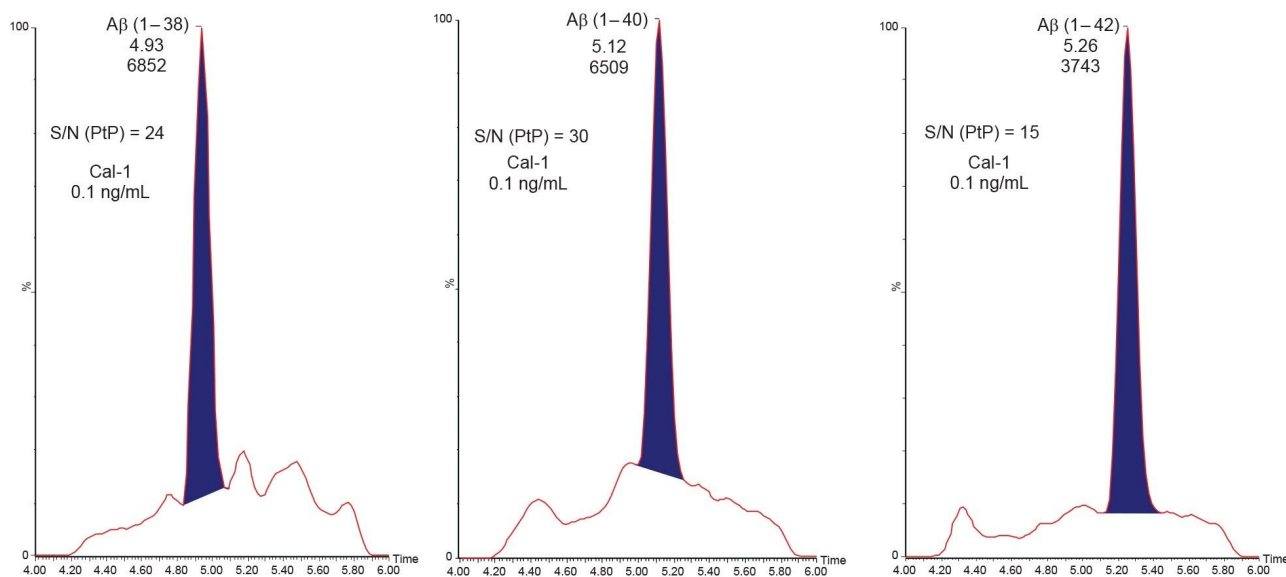


Figure 2. Analytical sensitivity of the method at 0.1 ng/mL for the Aβ peptide isoforms (1-38, 1-40, 1-42) using the ACQUITY™ Premier UPLC I-Class with Xevo™ TQ Absolute Mass Spectrometer (20 μL injection).

The calibration lines over five analytical runs were linear with $r^2 > 0.999$ for each of the peptides over the range 0.1–10 ng/mL.

Total precision and repeatability across the Aβ peptides on the Xevo™ TQ Absolute Mass Spectrometer was evaluated using QCs at three concentrations (0.2, 1.0, and 7.5 ng/mL), in replicates of five over five analytical runs ($n = 25$). Total precision and repeatability were determined to be $< 5\%$ CV, the accuracy of the QCs compared to nominal concentrations ranged from 96.1–100.4% across the Aβ peptide isoforms (Table 2).

| | Amyloid β (1-38) | | | Amyloid β (1-40) | | | Amyloid β (1-42) | | |
|--------------|---------------------|---------------------|----------------------|---------------------|---------------------|----------------------|---------------------|---------------------|----------------------|
| | QC low 0.2 ng/mL | QC mid 1.0 ng/mL | QC high 7.5 ng/mL | QC low 0.2 ng/mL | QC mid 1.0 ng/mL | QC high 7.5 ng/mL | QC low 0.2 ng/mL | QC mid 1.0 ng/mL | QC high 7.5 ng/mL |
| Mean | 0.1962 | 0.9989 | 7.4379 | 0.1969 | 1.0019 | 7.3909 | 0.1922 | 1.0038 | 7.4539 |
| StDev | 0.0037 | 0.0320 | 0.0997 | 0.0072 | 0.0292 | 0.1363 | 0.0087 | 0.0249 | 0.1704 |
| CV (%) | 1.9 | 3.2 | 1.3 | 3.7 | 2.9 | 1.8 | 4.5 | 2.5 | 2.3 |
| Accuracy (%) | 98.1 | 99.9 | 99.2 | 98.5 | 100.2 | 98.5 | 96.1 | 100.4 | 99.4 |
| (n) | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 | 25 |

Table 2. Total precision and repeatability performance for the Aβ peptide isoforms.

Conclusion

A LC-MS/MS method for the analysis of A β peptide biomarkers in artificial CSF was developed for clinical research. Through the use of the ACQUITY Premier UPLC I-Class System and Xevo TQ Absolute Mass Spectrometer excellent inter-day linearity, analytical sensitivity, precision, and accuracy can be achieved, providing confidence in the results obtained for quantification of A β peptide isoforms (1–38, 1–40, 1–42) in clinical research.

References

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3. Salcedo J, Ph. L, Davey L, Lame M, Dunning C, Chambers E: Amyloid Beta Peptides Quantification by SPE-LC-MS/MS With Automated Sample Preparation for Preclinical Research and Biomarker Discovery. *Waters Application Note*, [720006517](#).

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