



Case Study

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Project Goal

To explore the unique features of high-resolution mass spectrometry (HR-MS) and ask: What are the advantages over the traditional nominal mass approach to quantifying signature peptides and intact proteins?

The Challenges

- Plasma digestion creates many other peptides from the sample matrix that can interfere with quantification of the signature peptide
- The instrument system must be able to resolve the different isotopes of the intact protein
- Frequent calibration is necessary to maintain the essential high mass accuracy of HR-MS

The Solution

- Leveraging the high resolution and mass accuracy of the TripleTOF® 6600 system in MRM mode to narrow the mass extraction window and focus more closely on the signature peptide. The narrow window removes interferences from the range and improves the signal to noise ratio
- Easily revisiting the original data from the TripleTOF 6600 system in TOF mode to examine interferences or to do complementary studies of things like oxidation products

The Outcomes

- Reliable quantitation of signature peptides, even in the presence of matrix peptides that complicate the spectra
- A powerful and versatile way to gather comprehensive data on intact proteins that allows you to go back and examine interferences or to perform complementary studies

“HR-MS can be used as a tool for quantification of biopharmaceuticals as an alternative to a triple quad, both after digestion and for intact protein analysis.”

Type of Organization

Contract research organization (CRO) that provides clinical development services

Applications

Quantitative analysis of biopharmaceuticals using high-resolution mass spectrometry

SCIEX Products

- TripleTOF 6600 Quadrupole Time-Of-Flight (QTOF) mass analyzer

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