

Multiplexing SIMs on a Novel Benchtop Orbitrap MS with a Quadrupole Mass Filter to Increase Sensitivity for Peptide Quantitation P1064

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Overview

Purpose: To develop multiplexed selected ion monitoring (SIM) methods on a novel benchtop quadrupole-Orbitrap™ hybrid mass spectrometer for biopharmaceutical applications.

Methods: We employed a ten-minute LC method at 150 µL/min. Mass spectrometry analysis was performed using quadrupole-Orbitrap hybrid LC-MS/MS systems equipped with a heated electrospray ionization (HESI) source. Wide SIM was used.

Results: A generic method development approach was used to analyze insulin, exendin-4 and GLP-1 peptides, between 10 ng/mL and 100 ng/mL with good linearity and reproducibility.

Introduction

In bioanalysis, triple quadrupole MS systems have been predominantly used for peptide quantitation. Although triple quadrupole systems generally offer the most sensitive and robust quantitation, the poor fragmentation and multiple charge states of large peptides can result in weak selected reaction monitoring (SRM) signals.

In this investigation, we demonstrate the accurate and precise quantification of peptides in a biological matrix using a new approach that utilizes multiplexed SIMs capability provided on a benchtop quadrupole-Orbitrap hybrid mass spectrometer.

Multiplexed SIMs refers to multiple fills of the instrument's C-trap with quadrupole-filtered ions, prior to a Orbitrap mass analyzer scan.

Methods

Sample Preparation

Calibration curves were prepared in rat plasma.

Liquid Chromatography

A Thermo Scientific Accela UHPLC and Thermo Scientific Open Accela Autosampler were used to reproduce linear gradients on a 100 × 1 mm, 1.9 µm particle size Thermo Scientific Hypersil GOLD column at 150 µL/min. The mobile phase was 0.1% formic acid in water and acetonitrile.

Mass Spectrometry

MS experiments were conducted on a Thermo Scientific Q Exactive high-performance benchtop quadrupole-Orbitrap system (Figure 1) operated in multiplexed SIM mode using 70,000 resolution (maximum 140,000 resolution at m/z 200). Targeted multiplexed SIM fills the C-trap with multiple packages of ions from the selected scan ranges.

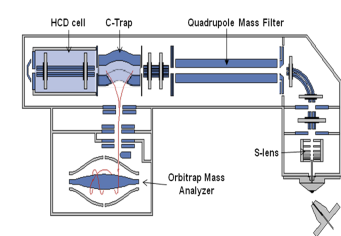
The C-trap collects the ions, and the Orbitrap mass analyzer analyses the ions previously collected. The isolation window used for the three peptides was 20 amu. To achieve maximum sensitivity, the AGC target values were optimized for each peptide.

Source conditions: heater temperature 200 °C, capillary temperature 275 °C, spray voltage 3.5 kV, sheath gas 40, aux gas 10.

Data Analysis

The data were processed with Thermo Scientific LCQUAN quantitation software version 2.7 using a 5-ppm mass window.

FIGURE 1. Schematic of the Q Exactive benchtop quadrupole-Orbitrap mass spectrometer.



Results

As shown in Figures 2 through 10, and Tables 1 through 4, all three peptides showed excellent sensitivity and reproducibility, over large dynamic ranges.

Insulin

FIGURE 2. Spectra of the acquired mass peaks of human insulin at 70,000 resolution.

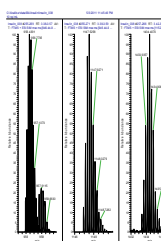


FIGURE 3. Chromatogram of 250 µg/mL human insulin (LLOQ).

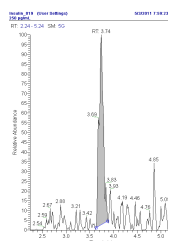
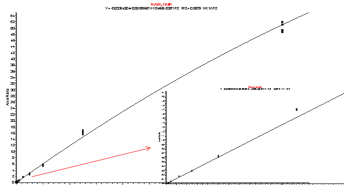


TABLE 1. Insulin summary table; dynamic range from 250 µg/mL to 1000 ng/mL.

Nominal Concentration (ng/mL)	Replicate #	Mean Calculated Concentration	Stdev	% CV
0.25	4	0.260	0.0000	11.5
0.5	4	0.434	0.0501	11.5
1	4	0.906	0.0540	5.96
2.5	4	2.81	0.0568	2.02
5	4	4.79	0.112	2.33
10	4	10.3	0.284	2.77
25	4	27.9	0.247	0.89
50	4	44.0	1.35	3.08
100	4	92.8	4.29	4.62
250	4	276	9.99	3.62
1000	4	979	36.7	3.75

FIGURE 4. Insulin calibration curve, dynamic range from 250 µg/mL to 1000 ng/mL.



Exendin-4

FIGURE 5. Spectra of the acquired mass peaks of exendin-4 at 70,000 resolution.

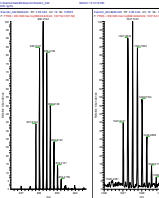


FIGURE 6. Chromatogram of 5 ng/mL exendin-4 (LLOQ).

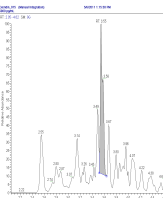
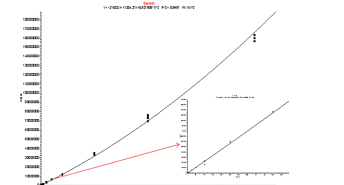


TABLE 2. Exendin-4 calibration table; dynamic range from 5 ng/mL to 10000 ng/mL.

Nominal Concentration (ng/mL)	Replicate #	Mean Calculated Concentration	Stdev	% CV
5	4	5.143	0.418	8.13
10	4	9.693	0.520	5.36
25	4	24.37	1.22	5.00
50	4	45.46	0.705	1.55
100	4	92.83	13.0	14.0
250	4	261.7	5.31	2.03
500	4	507.3	2.03	0.40
1000	4	966.0	25.2	2.61
2500	4	2675.6	60.7	2.27
5000	4	5205	169	3.24
10000	4	9740	150	1.54

FIGURE 7. Exendin-4 calibration curve, dynamic range from 5 ng/mL to 10 µg/mL.



GLP-1

FIGURE 8. Spectra of the acquired mass peaks of GLP-1 at 70,000 resolution.

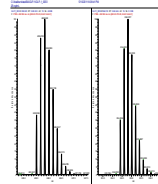


FIGURE 9. Chromatogram of 5 ng/mL GLP-1 (LLOQ).

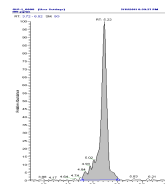
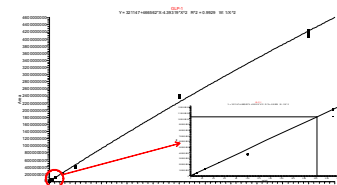


TABLE 3. GLP-1 summary table; dynamic range from 0.1 ng/mL to 10000 ng/mL.

Nominal Concentration (ng/mL)	Replicate #	Mean Calculated Concentration	Stdev	% CV
0.1	4	0.029	0.0026	8.91
0.25	4	0.251	0.0025	8.18
0.5	4	0.534	0.0337	6.31
1	4	0.905	0.0226	2.50
2.5	4	2.69	0.0578	2.15
5	4	5.36	0.126	2.36
10	4	9.99	0.120	1.20
25	4	26.6	0.664	2.50
50	4	50.6	0.563	1.11
100	4	80	0.692	0.86
250	4	243	14.2	5.86
500	4	462	15.5	3.35
1000	4	860	7.90	0.92
5000	4	5383	62.8	1.17
10000	4	9796	164	1.67

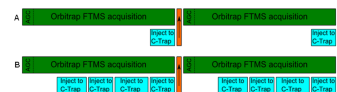
FIGURE 10. GLP-1 calibration curve; dynamic range from 5 ng/mL to 10 µg/mL.



Principle of Multiplexing

Figure 11 compares the standard operation mode with the spectrum multiplexing approach in the scan-to-scan AGC (automatic gain control) mode. In both modes, the instrument is operating in parallel mode. While one scan is acquired, the ions for the next scan are already collected. In the standard operation mode, only one precursor ion species is injected. With spectrum multiplexing, the idle time is used to inject several precursor ion species, resulting in higher throughput.

FIGURE 11. Standard operation mode (A) versus spectrum multiplexing (B).



Conclusion

- The Q Exactive™ high-performance benchtop quadrupole-Orbitrap mass spectrometer is a sensitive quantitation instrument that displays equal or better LOQs than those reported in the literature for high-end triple quadrupole instruments.¹ The Q Exactive mass spectrometer was found to be the instrument of choice for high-sensitivity quantitation with the following LOQs:

- Insulin to an LOQ of 250 µg/mL
- Exendin-4 to an LOQ of 5 ng/mL
- GLP-1 to an LOQ of 0.1 ng/mL

- The use of multiplexed SIMs is very effective for the quantitation of larger peptides such as insulin, exendin-4 and GLP-1. This technology makes the Q Exactive mass spectrometer highly selective.
- Because the instrument's multiplexing capability is coupled with advanced signal processing, its scan speed is fast enough to capture data across narrow UHPLC peaks. For example, 12 - 15 scans were recorded across the 6 second-wide exendin-4 chromatographic peak.
- These experimental results portend the applicability of the Q Exactive mass spectrometer for the quantitation of peptides, small proteins and oligonucleotides.

References

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- Jonathan R Kehler, Chester L Bowen, Sharon L Boram & Christopher A Evans. Application of DBS for quantitative assessment of the peptide Exendin-4; comparison of plasma and DBS method by UHPLC-MS/MS. *Platform Technology and Science, Drug Metabolism and Pharmacokinetics, GlaxoSmithKline Pharmaceuticals*
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