



FE Feeling trapped between choosing accuracy or sensitivity?

To successfully identify proteins, sequence peptides *de novo* or characterize post-translational modifications, you require exact mass measurement and sensitivity. Why should you be forced to choose? Waters® benchtop LC/MS/MS solutions featuring Micromass® Q-ToF™ technology deliver automated exact mass measurement, full mass range sensitivity, and the acquisition mode versatility you demand for your proteomics applications. To learn more about LC/MS/MS Systems for Exact Mass Measurement, visit www.waters.com/micromass.

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Exact mass. Combine accuracy and sensitivity.

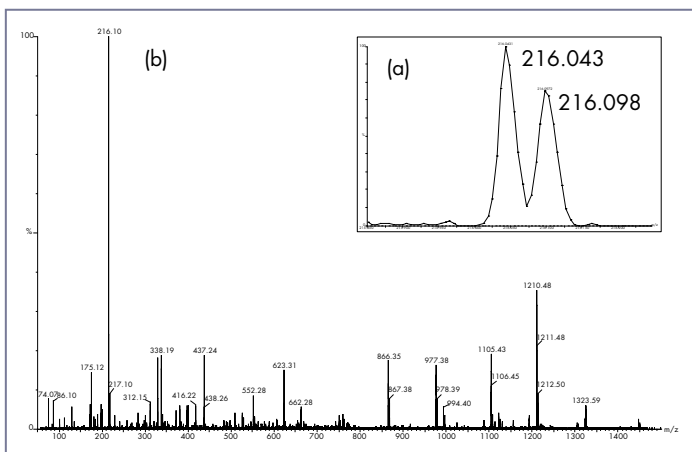
Whether you want to identify proteins or post-translational modifications, the Waters® LC/MS/MS Systems for exact mass measurement deliver the flexibility and precision you demand without forcing you to choose between mass accuracy or sensitivity.



Sequence	Mean mass error/ppm
(CM)GD(PM)ADECAMTQ	-150
(CM)GDFGADAQGASG(DT)	-100
HPGDFGADAQ(GA)MTQ	-50
HPGDFGADAQGAMTK	0
HPGDFGADAKGAMTK	+50
HP(AT)FGADAKKMTK	+100
HP(TA)FKDAKKMTK	+150

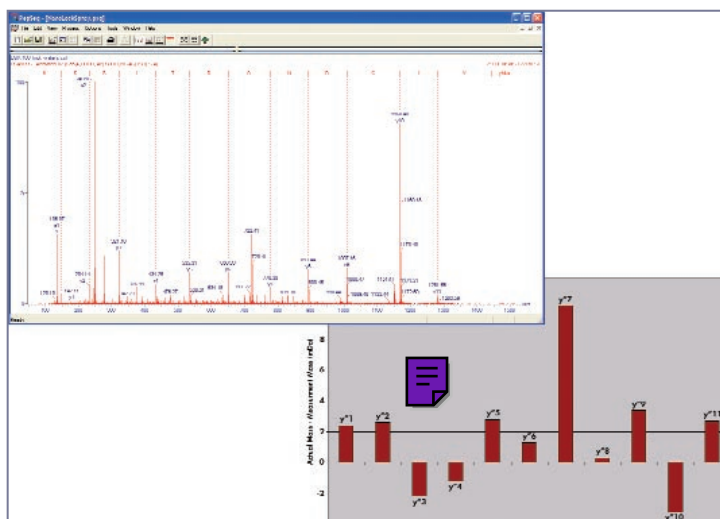
Green: Confident assignment
Red: Incorrect assignment
Yellow: Ambiguous assignment

An example of de novo sequencing using ProteinLynx™ 2.0. Correct assignment of the complete sequence is dependent upon the absolute mass measurement obtained on the MS/MS fragments.



Detection of a phosphotyrosine containing phosphopeptide by precursor ion discovery. (a) The high energy survey spectrum shows resolution of the b2 ion of 216.098 m/z resolved from the phosphotyrosine immonium ion of m/z 216.043. (b) MS/MS of the phosphopeptide precursor allowed full sequence determination.¹

This benchtop total solution integrates the Micromass® Q-ToF micro™ Mass Analyzer and NanoLockSpray™ with the Waters CapLC® pump and autosampler using MassLynx™ 4.0 Software. Extend the capabilities of your system by adding MassLynx Application Managers that streamline application-specific data acquisition and processing.



The Q-ToF micro, with simultaneous detection of ions across the full mass range, provides unparalleled power for peptide sequencing. Strong y¹¹ ions are present throughout the MS/MS spectrum from m/z 722.817 (2+) allowing unambiguous identification of the complete amino acid sequence. Exact mass measurement enables greater confidence and speed in protein identification by databank searching and de novo sequencing. In addition, it allows nominally isobaric amino acids, such as glutamine and lysine, to be successfully differentiated.

¹Bateman et al. JASMS (2002) 13, 792-803.

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