



METHOD FOR THE ABSOLUTE QUANTIFICATION OF PEPTIDES BY TANDEM MASS SPECTROMETRY

TECHNOLOGY OFFER



COMPETITIVE ADVANTAGES

- ✓ **Market:** this technology has applications in different fields (agriculture, chemistry, pharmacy, biomedicine or food safety).
- ✓ **Growing scope of market:** the application in Clinical Chemistry is particularly relevant, since the number of proteins that serve as biomarkers of diseases grows exponentially.
- ✓ **Unlike current methods:** minor isotope effects, lower detection limits, increased accuracy and precision, and reduced analysis time.

PATENTS

- ES patent granted.
- PCT application, international phase.

TYPE OF COLLABORATION

- Licence agreement.

INNOVATIVE ASPECTS

- ✓ It allows to directly obtain the mole ratio between the peptide to be determined and its isotopically-enriched analogue.
- ✓ It allows the accurate and precise measurement of the isotopic distribution of the endogenous peptide, the labelled peptide and the isotope diluted peptide.
- ✓ It is applicable to the determination of proteins when tryptic digestion is used.
- ✓ The mole ratio is obtained from the ratio of mole fractions instead of the peak area ratio providing better accuracy and precision in comparison with other approaches.
- ✓ It is not necessary to perform a methodological calibration, so the analysis time is considerably reduced.

ABSTRACT

This method allows to quantify peptides (defined as amino acid chains with fewer than 50 units) in an absolute, accurate and precise way. The method can also be used for determining proteins in biological samples by quantifying their characteristic peptides after the protein hydrolysis.

The method is based on the determination of peptides in a sample by: i) adding to the sample a known amount of the isotopically-enriched analogue that present spectral overlap with the natural abundance peptide ("Mass Overlapping Peptide"); ii) measurement of the isotopic distribution of the isotope diluted peptide by Selected Reaction Monitoring at low resolution in the first quadrupole of a tandem mass spectrometer (Full Width at Half Maximum between 2 and 20); iii) calculating the molar fractions of the natural and labelled peptide by multiple linear regression; and iv) calculating the amount of natural peptide from the molar fractions and the added amount of labelled peptide.

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