Spektrometria mas w analizie białek i peptydów : znaczniki jonizacyjne = Mass spectrometry in analysis of peptides and proteins : ionization markers.

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Streszczenie

High sensitivity, accuracy, and ability to provide structural information makes mass spectrometry (MS) the method of choice for both qualitative and quantitative analysis in proteome research. Peptide sequencing by tandem mass spectrometry (MS/MS) was successfully applied to discover new peptide sequences and modifications. Insufficient ionization of some peptides is one of the main limitations of MS-based peptide identification. The development of sensitive detection techniques for the efficient analysis of such samples is very important. Differences in ionizability cause difficulties in quantification studies, which could be overcome by derivatization of peptides to improve both the detectability and the selectivity of an analysis. Incorporation of ionization markers and isotopic labels (particularly the isobaric tags) is often used for this reason. Isobaric labeling reagents (including commercially available iTRAQ, TMT, DiLeu and DiART) have found a wide application in quantitative proteomics. Mass spectrometry is a very good tool for the determination of posttranslational modifications (PTMs), but the modified proteins are usually present in low concentrations. The development of ionization tags specific to a particular PTM and suitable for sensitive analysis of the modified proteins is required. For the analysis of phosphorylated peptides, a combination of β-elimination and the reaction of resulting α,β-dehydroamino acid residues with the nucleophilic thiol group could be used to detect a labile PTM. Such reaction may be used to introduce derivatizing reagents at the original site of phosphorylation, to enhance ionization in MS analysis. Glycation and glycosylation of proteins are other very important PTMs associated with many natural processes as well as diseases. We have designed and synthesized bifunctional quaternary ammonium salt derivatives of phenylboronic acids for selective detection of carbohydrates and peptide-derived

Typ publikacji

Artykuł

Amadori products by ESI-MS. The attachment of a fixed charge (e.g. in a form of a quaternary ammonium salt) to the amino groups in peptides leads to the enhancement of a precursor ion signal in mass spectra. We have developed several new QAS-containing ionization reagents including bicyclic tags with DABCO, ABCO or azoniaspiro groups. It is worth noting that 2,4,6-substituted pyrylium salts react with amino groups in peptides introducing a stable positive charge and improve peptide detection by MS. The newly developed ionization tags were successfully applied for the analysis of OBOC combinatorial libraries as well as for studying possible biomarkers of preeclampsia, a pregnancy disorder.

Słowa kluczowe

mass spectrometry, posttranslational modifications, ionization markers, phosphorylation, glycation, combinatorial libraries

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