

Oznaczanie modyfikacji potranslacyjnych białek metodami spektrometrii mas

Łukasz Marczak

Instytut Chemii Bioorganicznej, Polska Akademia Nauk, Poznań

Analysis of protein posttranslational modifications using mass spectrometry

Summary

Identification of posttranslational modifications (PTMs) of proteins provides better understanding of their biological functions. Mass spectrometry has become a method of choice for the analysis of PTMs, both MALDI-ToF and tandem (MS/MS) mass spectrometers are perfect tools for assignment of PTMs. The latter due to their peptide fragmentation capability give better identification and information about localization of PTMs in protein molecule. In this paper, an overview of possible use of mass spectrometry and bioinformatic tools together with description of the basic features and limits of the analysis of post translational modifications by mass spectrometry are presented.

Key words:

mass spectrometry, posttranslational modifications, proteins, proteomics, peptide fragmentation, chromatography

Adres do korespondencji:

Łukasz Marczak, Instytut Chemii Bioorganicznej, Polska Akademia Nauk, ul. Noskowskiego 12/14, 61-704 Poznań