Method for the determination of sequence variants of polypeptides

Abstract

The current invention is directed to a method for determining amino acid sequence mutations in a produced polypeptide, comprising the following steps of a) providing a sample of a produced polypeptide, b) incubating the polypeptide in the sample with a protease, c) performing a two dimensional analysis using reversed phase chromatography coupled with a high resolution mass spectroscopy (FT-ICR / FT-orbitrap) and MS/MS analysis of the amino acid sequence fragments of the peptides, d) data evaluation by comparing the LC-MS data sets obtained for the samples side by side with the data set of a reference sample, by searching for differences in the signal intensities at given retention times and by evaluation of differential signals with respect to amino acid sequence mutations. The reference sample for data evaluation (d) can be either a well characterized standard or one of the samples to be analyzed.

Fig. 5