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Author <b>Ragnar Stolt</b>		
Title (English) <b>Peptide mapping by capillary/standard LC/MS and multivariate analysis</b>		
Title (Swedish)		
Abstract The potential of LC/MS peptide mapping combined with multivariate analysis was investigated using IgG1 as a model protein. Five batches of IgG1 were exposed to different levels of an oxidizing agent. A method to detect differences between the batches using solely MS data was developed and successfully applied. Four peptide fragments containing methionine residues were found to represent the most significant differences and characterized using MS/MS. In order to evaluate different computational strategies Principal Component Analysis (PCA) was used. Attempts were also made in order to use the information from the whole LC/MS space.		
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