

Accepted Manuscript

Title: The role of protein and peptide separation before mass spectrometry analysis in clinical proteomics

Author: Serena Camerini Pierluigi Mauri

PII: S0021-9673(14)01941-4

DOI: <http://dx.doi.org/doi:10.1016/j.chroma.2014.12.035>

Reference: CHROMA 356108

To appear in: *Journal of Chromatography A*

Received date: 23-5-2014

Revised date: 9-12-2014

Accepted date: 11-12-2014

Please cite this article as: S. Camerini, P. Mauri, The role of protein and peptide separation before mass spectrometry analysis in clinical proteomics, *Journal of Chromatography A* (2014), <http://dx.doi.org/10.1016/j.chroma.2014.12.035>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



The role of protein and peptide separation before mass spectrometry analysis in clinical proteomics

Serena Camerini ^a and Pierluigi Mauri ^{b*}

^aDept of Cell Biology and Neurosciences Higher Institute of Health (ISS), Rome, Italy

^bInstitute for Biomedical Technologies (ITB-CNR), Segrate, and Institute of Life Science - Scuola Superiore Sant'Anna, Pisa, Italy

* Author's Contact Details: +39 02 26422728. Fax: +39 02 26422770. Email: pierluigi.mauri@itb.cnr.it.

Abstract

The purpose of clinical proteomics is to characterise protein profiles of a plethora of diseases with the aim of finding specific biomarkers. These are particularly valuable for early diagnosis, and represent key molecules suitable to elucidate pathogenic mechanisms. Samples deriving from patients (i.e. blood, urine, cerebrospinal fluid, biopsies) are the sources for clinical proteomics. Due to the complexity of the extracted samples their *direct* analysis is unachievable. Any analytical clinical proteomics study should start with the choice of the optimal combination of strategies with respect to both sample preparations and MS approaches. Protein or peptide fractionation (off-line or on-line) is essential to reduce complexity of biological samples and to achieve the most complete and reproducible analysis. The aim of this review is to introduce the readers to a functional range of strategies to help scientists in their proteomics set up. In particular, the separation approaches of proteins or peptides (both gel-based and gel-free) are reviewed with special attention paid to their advantages and limitations, and to the different liquid chromatography techniques used to peptide fractionation after protein enzymatic digestion and before their detection. Finally, the role of mass spectrometry (MS) for protein identification and quantification is discussed including emerging MS data acquisition strategies.

Keywords

Proteomics

Protein and peptide separation

Mass Spectrometry

Introduction

Clinical proteomics is one of the more recent and exciting frontiers of science. It aims to help clinicians to characterise the molecular profiles of diseases with particular attention to chronic diseases, cancer and neurodegenerative pathologies [1-4]. The keynote strategy of proteomics is based on the description of protein content present in samples coming directly from patients. However the actual purpose of clinical proteomics is not just a report of lists of proteins, rather obtaining relevant data that could find applications in the clinical practice. The aim of clinical proteomics is actually to find molecular signatures, describe affected pathways, possibly identify candidate biomarkers that can help in the diagnosis, prognosis and prediction of therapeutic outcomes and elucidate pathogenic mechanisms [5-7]. This means translating basic proteomic science into clinical research, from bench to bedside, as has been suggested already more than ten years ago [8]. Clinical proteomics by definition analyses the identity, the quality and the quantity of proteins residing in patients' samples. The origins

Download English Version:

<https://daneshyari.com/en/article/7612005>

Download Persian Version:

<https://daneshyari.com/article/7612005>

[Daneshyari.com](https://daneshyari.com)