

# PROTEOMICS, STATE OF ART AND FUTURE PERSPECTIVES. ARE WE GOING IN THE RIGHT DIRECTION?

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Proteomics has now been around for almost two decades. During this period it has undergone a dramatic development. The number of genomes sequenced, which is the basis for proteomics, has expanded exponentially. New generations of mass spectrometers and LC-equipments dedicated to the use in proteomics have been developed. New bioinformatics tools to handle the huge amount of data produced are constantly emerging. Presently several thousands of proteins are routinely identified and quantified in a high throughput proteomics experiment and the information stored in databases. Elegant techniques for enrichment of modified peptides have been developed and many modifications can be routinely site specifically assigned and quantified *e.g.* phosphosites. There has been a strong focus on the search for mechanisms behind diseases and for reliable diagnostic biomarkers. However, there are still limitations. The dynamic range of the proteins in the cells is  $10^7$ - $10^8$  and in serum around  $10^{11}$  and no analytical technique can handle such a dynamic range. In spite of the huge investments in search for reliable biomarkers only a few if any have been identified using proteomics. Better understanding of the basic biology and new concepts for identification of the relevant markers or combinations of markers are needed. Improved methods for enrichment of specific low abundant proteins must be developed. The present state of art of proteomics will be described and the need for rethinking the perspectives of the present trends in proteomics discussed.