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Preface

When during the sixties of the last century polyacrylamide gel electrophoresis joined the armamentum of laboratory separation techniques, hardly anybody expected that it could became (in its two dimensional version) one of the mightiest separation techniques available. Of course its applicability regards macromolecular species, in particular proteins, glycoproteins and nucleic acid fragments. With the advance of genome analysis and with understanding which proteins are encoded in a particular gene, the term proteome was introduced to describe this protein set. However, today the definition of proteome is a bit different and more vague than originally intended. Currently proteomics refers to the set of proteins presented in a particular biological compartment (typically a cell or a set of cell of defined function), in a well defined tissue or its parts (for instance muscle proteomics) or a series of proteins ensuring a particular biological function (for instance all proteins of the respiratory chain) to enumerate just a few examples. Consequently the term functional proteomics was born.

One may say that with the advanced two-dimensional gel electromigration techniques and their hyphenation to a separation system working on a different physico-chemical principle through which arrangement it is possible to discern several thousand proteins, we have reached the goal and we have in our hands a tool how to analyze complex protein mixtures (which is nearly the synonymum for proteomics today). However, this is a theory and the applications are still hindered by a lot of problems in practice. One example for many others: how to discern a protein modified by a single posttranslational modification (for instance glycation) that is present once over total molecular mass of 10^5? This is where different fragmentation techniques step into the game. In these situations we deal with a set of peptides, which generally are more easy to separate, however, we pay for this possibility by having an already complex mixture made even more complex. Another crucial point is that in spite of the available image analysis (if two-dimensional flat gel separation is taken for the basis) we always have a set of spots, about which (even if well separated, which is not always the case) we can hardly say that they represent pure entities and their quantitation is still a difficult task. In summary multiple hyphenations, additional selective (bioaffinity) procedures and analysis of fragmented molecules are typical areas to be worked out in the future and this list is far from being complete.

In order to create a basis of current knowledge in the proteomics field we are presenting this volume which, as it is always the case with Topical Volumes, is not exhaustive. The reason is twofold. Either there is still not enough information about a particular set of proteins or for a given topic we failed to find a suitable author willing to overview the subject. We would deeply appreciate any comments of the potential readers as well as their suggestions for further development of this area in our Journal.

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