Journal of Chromatography A, 1217 (2010) 892

Contents lists available at ScienceDirect

Journal of Chromatography A

journal homepage: www.elsevier.com/locate/chroma

Editorial

Editorial on "Plucking, pillaging and plundering proteomes with combinatorial peptide ligand libraries" by P.G. Righetti, E. Boschetti, A. Zanella, E. Fasoli and A. Citterio

The proteome is complex in size, composition, and function, including interactions of its members with each other and with other types of biomolecules. The post-translational modifications add considerable structural heterogeneity. Further, all of this is dynamic. The complexity of the proteome means that many analytical tools are needed to make progress in knowing how it all works, and in discovering the variations that we call biomarkers when they answer questions about health and disease. The analytical challenges are many. Some of the proteins are very abundant and their removal can entail losses of the minor ones that you want to study. The proteome is so delicate that small variations in the conditions of sample collection and storage can lead to different analytical results. The analyses often give a deluge of data. We are in an era when analytical tools are being developed to overcome these challenges while, at the same time, contribute valuable information about the proteome.

The review by Pier Righetti and his coworkers brings us up to date about a leading technique in the field of proteomics. Affinity chromatography with peptide ligands is at the heart of this method. In a clever way, the technique greatly enriches the part of the proteome that, while vast in its composition, is very low in abundance. This achievement is extremely important because minor proteins in general (ranging down to rare ones) are responsible for most of the function of the proteome. The method is a wonderful complement to an alternative strategy in which affinity is used to pull out the abundant proteins so that they do not obscure the minor ones in chemical analysis.

Righetti and his coworkers are leaders for this exciting method, and we thank them for this update on its status that provides perspectives, insights, and eye-opening examples with a focus on recent developments both in the methodology and in fundamental protein discovery.

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0021-9673/$ – see front matter
doi:10.1016/j.chroma.2009.08.074