

Peptidomics Methods and protocols Mikhail Soloviev (Ed) Humana press, Totowa, NJ (USA) Series: Springer Protocols Methods in Molecular Biology, Volume 615, 2010 Pages: 395; €93.55 ISBN: 978-1-60761-534-7

Nearly ten years ago the scientific community added another discipline to the big -omics family, peptidomics, i.e., "the study of the complement of peptides from a cell, organelle, tissue or organism". This fact derives from the exceptional capacity to produce data by highthroughput techniques and machines that allow us to pass from proteomics analysis of complex biological systems to the capacity to resolve their peptides content even at the single cell level. Thus, the time is set to have this Peptidomics: Methods and protocols edited by Mikhail Soloviev. I think the editor did a great job; I was reading a very usefull book, a great collection of protocols (that widely range as for the organisms studied, from Bacteria to Man!) both for those who are newcomer potential users, as I am, and for those already acquiented to the use of this very powerfull technique.

The book is divided in three sections. The first (one chapter), by the Editor himself, highlights the concept of peptidomics (and its methodologies) as it has been self-constructing from 1994 till today (see Figure 1.1) as a specific approach to the proteomic analysis: to purify and to separate at first glance the 10 -100 (- 1000!) peptides of a complex biological system (a cell, an organism) and then to characterize them both structurally and functionally. The second section ("from Bacteria to Man", 19 chapters) presents a long list of protocols dedicated to specific cases usefull to highlight specific features of this intriguing discipline. More than one chapter are devoted to the peptidomic analysis of spider venoms and four to the Insect's neuropeptides. The third section (6 chapters) is devoted to the necessary "Tools and approaches" for all the steps entailed by the peptidomics analysis (purification, isolation, structural and functional characterization of the peptides) plus a welcome bioinformatics (two chapters) approach to the novel identification of peptides that are not yet in a database, including plant peptides.

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