

Gene expression profiling, 2nd edition Methods and protocols Lorraine O'Driscoll (ed), Methods in molecular biology; vol. 784, 2011 Humana Press – Springer Verlag, Heidelberg, Germany ISBN: 978-1-61779-288-5 Pages: 210 pp; Figures: 37; €94,95

There must be some good reasons to last for a second edition on the very same topic: likely, the topic is crucial to basic and applied science, it is a very rapid evolving topic and there must occurred some breakthroughs meanwhile the two editions. Well, I think that all of these reasons are here to justify this very wellcome second edition of Gene expression profiling, a topic that is crucial for the understanding of the basic principles of cellular and molecular biology. In other words the study of gene expression profiling actually is the master study from which it depends our ability to understand the gene networks activities keeping alive living organisms and to manipulate their life cycles. The reader will immediately appreciate that the fourteen chapters are written in an extremely detailed manner and the covered themes span the molecular, cellular and histological levels of animal organization in both healthy and patological conditions. It descends that even the techniques highlighted span from advanced PCR protocols (real-time and reverse transcriptase) till the most advanced microscopical methods and techniques (laser scanning confocal and atomic force microscopies) to dissect the relationship existing among networks of networks controlling gene expressions. Interestingly enough, Prof. Lorraine O'Driscoll (School of Pharmacy, trinity College Dublin) contribute several

chapters as coauthor of five among those of high interest: just to mention one of the most challenging situation in which to study gene expression profiles, that of working with minimal amounts of biological reagents, i.e. starting from extracellular material to study gene expression profiling and to be able to get the best results from such specimens. Microarray analysis of mRNAs are obviously a must and actually there are two chapters devoted to explain how the experimental design is crucial to well perform with this methodology and the software and other analytical tools to dataminig the enourmous quantity of data provided by microarray experiments.

The studies of gene expressions in both the most devastating and intricated biological (patological) process (cancer) and those carried out thanks to the use of formalin-fixed and paraffin embedded tissues provide a window over the clinical issues. The microRNAs role in controlling and finely tuning the gene expression profiles is already well known but still the hunt is open to assigne a functional role to many of those already identified in humans (1523 as for 03/11/2012, http://www.mirbase.org): a full chapter is explaining how to perform such studies, in particular considering the intercellular and extracellular microRNAs. The study of the gene expression products cannot be forgot and in fact several chapters are dealing with proteins which are studied by Western blotting, 2D gel electrophoresis and mass spectrometry, tissue microarrays and immunohistochemical techniques.

> Manuela Monti Scientific Department San Matteo Foundation for Research, Hospitalization and Health Care, Pavia, Italy

