METHODS IN MOLECULAR BIOLOGY™

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Cancer Gene Profiling

Methods and Protocols

Edited by

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Preface

Science is the agent between imagination and reality

(Anonymous)

During the last few years, the methods for analysing cancer-related genes on a molecular level have changed rapidly. With the advent of automated sequencing, new and faster investigations have become possible. This has led to the collection of a large number of DNA samples, such as Expressed Sequence Tag (EST) libraries whose entries run into millions. The advances in DNA sequencing technologies resulted in rapid improvements in oligonucleotide synthesising technologies, which has allowed researchers to produce oligonucleotides for each and every imaginable sequence at a low cost. Finally, the method of polymerase chain reaction (PCR), and other improvements in enzymatic *in vitro* amplification of nucleic acids, gave researchers the opportunity to use low amounts of nucleic acids for analysis. This enabled the research community to investigate the populations of cells in a given tissue.

Sometimes it takes only a few advances for a technology to be successful – for example, the concept of arraying biological probes in a reproducible manner, and the use of these arrays instead of a single probe, greatly advanced biomedical research, especially as it was discovered that everything is arrayable. It has also changed the landscape of science in another way: a reduction of costs. The costs of generating such an array are high, but the costs of replicating such arrays are not. This key fact has led to a growth in the number of biotech companies that design and produce arrays, and that today more and more researchers have access to and use. Such unrestricted access to these resources has really been the key to the biomedical research revolution we see today.

In this book, we have brought together the experiences of leading scientists in the discipline of cancer gene profiling. We have included several microarray techniques, as well as methods for arraying tissues and proteomics, because cancer genes can be profiled in different ways. Such different approaches are needed to understand the key stages of cancer development, because using only one technique would be insufficient. Therefore, we attempt to give an overview of the state-of-the-art methods that will enable the reader to perform these experiments successfully. It has been written for any student or practitioner with an interest in cancer gene profiling, and can be used in any well-equipped research laboratory. It may also serve as a demonstration of the kind of analysis that is possible today and will be complementary to other textbooks in the area of biomedical research.

This book has been divided into five main sections. The first section covers techniques to get clinically relevant cancer material through the best methods of sample collection and storage.

The second part begins with an overview of gene expression technology and gives an introduction to the latest cancer gene profiling technologies. Because cancer gene profiling is more than just the profiling of cancer gene expression, we have also included techniques for comparative genomic hybridisation (CGH) arraying and single-nucleotide polymorphism (SNP) analysis, and proteomic techniques.

The third section contains real-life examples for the different technologies, and shows the full potential of cancer gene profiling today. This potential can only be utilised by the use of adequate bioinformatics tools. These tools are covered in the fourth part of the book. Because a cancer gene profiling experiment will most often lead to numerous candidate genes, which, in turn, have to be further validated and analysed, examples of performing post profiling experiments can be found in the final section of the book. It should be noted that all of the chapters in the book are linked by the description of particular successful experiments that were performed within the field of gene expression profiling.

We offer our gratitude to all of the contributing authors and the staff of Humana Press – without their help, this book would not have been possible. We also thank our families for their love and patience. Finally, we are indebted to our mentor Hans Detlev Saeger for his unwavering support.

Science is not just a profession – it should also be fun. This fun comes from the inception of an idea that goes on to be proven through experimentation, or, as we found in a Chinese fortune cookie: “The impossible is only the untried.”

We hope that you will not only be successful, but will also have fun using our book in your research.

Dresden, Germany

*Robert Grützmann
Christian Pilarsky*

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