

Preface

In February 2001, the draft sequence of the human genome was published. While at the time of writing many of the details still remain to be worked out, broad consensus now exists on the architecture of our genetic makeup. Understandably, therefore, the focus of cutting-edge research is now on functional genomics, *i.e.* the study of gene expression, and of its regulation, at the mRNA and the protein level.

Techniques for studying gene expression have burgeoned. However, as far as we are aware there does not yet exist a single comprehensive work devoted to this topic. This is what inspired us to compile and co-author this book. Our aim was two-fold. First, to provide a compendium of current methods of analysing gene expression with sufficient detail to allow the novice to decide what technique is most suitable for a particular application. Second, to put these different methods into perspective with relation to each other and to highlight the relative advantages and disadvantages associated with each.

We have divided this book into seven chapters, not because of the biblical charm of the number seven, but because we found this to be the most logical way to organise the content. Chapter 1 describes the fundamental biology of gene expression and chapter 2 outlines the tools needed to prepare samples and carry out gene expression analysis. Chapter 3 describes methods of mRNA expression analysis that can be implemented in the normal research setting, while chapter 4 is devoted to high-throughput methods more suitable to the industrial environment. Chapter 5 describes methods for analysing protein expression, chapter 6 is devoted to methods for analysing gene expression *in situ* and in the living organism at the mRNA and protein levels. Finally, chapter 7 rounds off the book by describing currently available bioinformatics approaches and internet databases.

To our knowledge, this work represents the most complete text currently available devoted solely to the topic of analysing gene expression. We have done our best to make it as up-to-date as possible. Most contributions represent the state of the art in March/April 2002. Although the two volumes of this book run to nearly 1,000 pages, it is still not possible for them to provide all the experimental detail needed for the researcher to implement the protocols in his or her laboratory. For that reason, we have made a special effort to comprehensively cite relevant literature, and to ensure that the papers and books cited are as recent as possible.

This is reflected in the large number of citations from 2001 and 2002. Despite our best efforts, it is possible that this book has overlooked important techniques or approaches. We apologize for any egregious gaps, responsibility for which is entirely our own. Wherever possible, we have tried to eliminate redundancy in the text. However, in a compendium of this nature, a degree of repetition is unavoidable, and we ask readers to overlook any particularly irritating examples that still remain.

No scholarly endeavour can today ignore the impact of the internet. In deference to this fact, we have included as much information as possible on currently available internet resources. One of the drawbacks of the world wide web is its ephemerality, and we hope that readers will excuse us if some of the links cited no longer function, or if their content is not as described.

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Throughout the text, we have referred to researchers in the masculine form only. This is purely a convention to save space and is in no way intended as a slight on our female colleagues.

Finally, we would like to thank all the contributors who made this work possible. We hope that it proves useful to our fellow-scientists in their attempt to navigate the choppy seas of the post-genomic era.

Stefan Lorkowski and Paul Cullen
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