ribozymes and the leadzyme are presented. Details about the dynamics and metal ion-binding sites are also included.

The final section, Section VIII, is devoted to the therapeutic applications of ribozymes. Chapter 20 (Daniela Castanotto, Michaela Scherr, Nan-Sook Lee and John. J. Rossi) first addresses the importance of finding the optimally accessible RNA target site. Here, a clever mix of secondary structure predictions and experimental conditions based mainly on RNase H assays is recommended. Vector design as well as transduction protocols are discussed. Chapter 21 (Caroline G. L. Lee, Kuan-Teh Jeang and Michael M. Gotteman) adds the advantage of a selection marker, the mdr1 gene in their example, for long-term expression. Chapter 22 (Hiroaki Kawasaki, Shiori Koseki, Kazunari. K Yokoyama and Kazunari Taira) stresses the importance of polIII-derived tRNAval as an expression system. The expected colocalisation with the target in the same compartment should ensure the optimal use of the ribozyme administered. Finally, Chapter 22 (Masahiro Kizaki, Hiromichi Matsushita and Yasuo Ikeda) adds a defined example of targeting a leukaemia-causing translocation (8;21). Here, a hammerhead-derived ribozyme inhibits the growth of myeloid leukaemic cells via induction of apoptosis.

The authors of this book are mostly highly regarded experts in their fields and the book is well edited. As pointed out, the scientist interested in ribozymes in general would be recommended to start with Chapters 14–16. As for the individual chapters, even experts in one ribozyme area will find interesting details about other examples of the ribozyme world. The price may restrict a wide distribution, but any scientist interested in catalytic RNA can certainly learn from this book and should have access to a copy.

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A Primer of Genome Science
Greg Gibson and Spencer V. Muse

This book reviews technologies used in functional genomics and proteomics. The intended audience are (final year) undergraduates of life science degrees. We feel this book could be a useful primer for scientists wanting an overview of these technologies. The primer has six chapters. At the end of each chapter is a summary of the main points, a short list of discussion questions and cited literature. The book has a website (http://www.sinauer.com/genomics/). Chapters 2–5 have a short list of website exercises. A useful glossary can be found at the end of the book. The quality of the illustrations is very high and this adds value to the explanations given in the text.

The book covers in some detail a wide range of technologies and related analytical techniques. Topics covered include: microarray systems and serial analysis of gene expression to investigate gene expression and transcriptomes; mass spectrometry, protein identification, yeast two-hybrid, protein structure determination and prediction to study proteomes; SNPs to study genetic variation within the human population; and integrative genomics to study metabolic networks. These disciplines are described well, and in sufficient detail for the reader to appreciate their important aspects. Illustrative examples have been well chosen, both in terms of the points that the authors are making and also for their intrinsic interest. Detailed discussions of specific areas are isolated in boxes in instances where they would otherwise interfere with the main text — a tried and tested technique that has been well executed in this book. On the whole, the authors do not avoid difficult issues where glossing over them might give rise to misconceptions, but
have gone to considerable effort to provide careful explanations; neither do they shy away from discussing the issues and limitations of the various technologies.

On the downside, the publicly funded human genome sequencing project is presented as mainly an affair of the USA, and, according to this book, Ensembl is the only connection that the Wellcome Trust and the Sanger Centre in the UK have with it. In fact, both organisations have a long association with the project and have played a crucial role in its success, not least in May 1998 when the Trust decided to increase funding and raise the target for its contribution to one-third of the whole human genome (see http://www.wellcome.ac.uk/en/genome/hgp.htm for more information). This unfortunate faux pas is bound to irritate knowledgeable readers. There are other places where the international collaborations that underpin the production and management of biological data are not described. For example, it would have been useful to explain briefly the nature of the International Nucleotide Sequence Collaboration and the relationship between GenBank, EMBL and DDBJ (DNA DataBank of Japan; http://www.dd.bj.nig.ac.jp/intro-e.html).

Potential purchasers should be aware that this is not a book of protocols, but a good introduction into the principles and application of various technologies in adding functional information to genomic data. Also, this book focuses on the principles of laboratory techniques and statistical analysis used in genome science. Bioinformatics is not dealt with in the same depth. Having said that, this book is very strong on the discussion of scientific and technical issues — and what it sets out to do, it does well. It also fills a gap between general biological sciences textbooks and more specialist works, and for this it is very welcome.

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