Tag-Based Next Generation Sequencing

M. Harbers, G. Kahl eds. Chichester: Wiley-Blackwell, 2012
ISBN 978-3-527-32819-2. 581 pp. £150.

This book is a comprehensive guide aimed at anyone entering the field of next-generation sequencing. It provides a deep yet broad overview on recent developments and techniques using tag-based approaches, along with background information, detailed protocols, applications and perspectives. It is a multi-author book divided into 30 chapters, where the expertise of almost 100 experts in their field lead the reader through the various techniques. Each chapter follows a similar style, commencing with an introduction, an overview, step-by-step methods and protocols, applications, and ending with a useful perspective.

Over the past five years there have been huge leaps in DNA sequencing technologies (so-called 'next-generation'). This has led to a vast increase in the data generated, coupled with plummeting costs required to generate these data. The increased accessibility and affordability of sequence data is now enabling experiments once thought unimaginable. Continued advances have rendered these technologies omnipresent, and the number and variety of applications for which these data can be used continues to grow. As a consequence, the need for the development of tools capable of handling large numbers of samples in application-specific processes is quickly becoming the bottleneck in realising the opportunities toward advancement of diagnostics, personalised medicine, and new therapeutics poised to overcome the increased challenges of modern healthcare.

Tag-sequencing approaches using high-throughput sequencing technologies are now regularly employed to identify specific sequence features. Such techniques will maintain their important role in life and biomedical science, because longer read lengths are often not required to obtain meaningful data for many applications. For instance, while whole genome sequencing may benefit from increasingly powerful sequencing methods, analytical applications can be performed by tag-based approaches, where the focus shifts to better means of data acquisition and analysis.

The chapters contained in this book open up the complete repertoire available to tag sequencing both at the practical and analytical levels. The book begins with detailed methods of techniques in which tag-based principles are applied to gene-expression studies such as serial analysis (Deep super-SAGE) and cap analysis of gene expression (Deep-CAGE and CAGE-scan), rapid amplification of cDNA ends (Deep RACE), full-length mRNA analysis (RNA-PET), RNA-seq, differential RNA-seq, non-coding RNA methods and Helicos single-molecule sequencing using various different platforms.

Further sections cover DNA analyses using massively parallel tag sequencing and applying this to various tissues and organisms, such as mammalian cells to microbes, or bacterial artificial chromosomes and the detection of polymorphisms, structure analyses and epigenetic marks. Protein-DNA (ChIP-seq) and RNA (RIP-CHiP) and chromatin (ChIA-PET and FAIRE) interaction tools are also described in the same detailed formats. All these methods are covered using various technologies from pyrosequencing, sequencing by synthesis, by ligation, real-time and electronic sequencing, while additional sections give further details on the numerous platforms currently available, and also those under development. Finally, various computational and data management tools are introduced, again following a detailed hands-on style.

As one reads through the sections one is left with a detailed understanding and confidence in the various tools. Rather than simple background explanations, the book offers a real practical introduction with clearly explained methods. Importantly, the book is edited in an extremely clear and uniform style. This makes the book very easy to understand and move between reading the various sections.

As both an introduction and expert methodological source to the various tag-based techniques used in next-generation sequencing, this book is invaluable. With expert tuition from introductory backgrounds to detailed step-by-step protocols written by experts in the field, this text is a highly important addition.

C. Murgatroyd

Medical Biochemistry at a Glance (3rd edn)

J. G. Salway. Chichester: Wiley-Blackwell, 2012.
ISBN 978-0-470-65451-4. 171 pp (softback). £26.99.

One of the reasons I do this job is that, as a young man, I was seduced by the splendour of metabolic pathways. It is therefore an absolute pleasure to read this book and wonder again at the beauty of biochemistry. The pathways laid out in this slim volume are themselves multicoloured, and are peppered with amusing cartoons emphasising features such as excretion, mutations, and the transfer of chemical groups such as a methyl residue.

The author draws the reader along a journey from the smallest particles (protons, in the section on acids and bases) through increasingly larger molecules (amino acids, carbohydrates) to the largest (DNA). The pure 'chemistry' part of each section is complemented with a medical aspect – an excellent example of this is that metabolic and respiratory acidosis and alkalosis follow renal function and pH. The 'at a glance' aspect is fully adhered to – in many cases the descriptive text in and around the fabulous diagrams exceeds the notes. In other parts, such as that dealing with lipid metabolism, roughly the same diagrams are reproduced over several pages so the reader can see how the complex pathways overlap

As you can probably guess, I enjoyed reading this book immensely and will keep it close to me. Those who will benefit from this book will be undergraduates and postgraduates in basic and in biomedical science. It will also be essential reading for those preparing for professional qualifications such as FIBMS and FRCPath, possibly even MRCP, and will serve as an excellent resource for the more senior researcher, lecturer and academic.

A. D. Blann

Transfusion Medicine (3rd edn)

J. McCullough. Chichester: Wiley-Blackwell, 2012.
ISBN 978-1-444337051. 595 pp (softback). £54.99.

This is quite a chunky and comprehensive volume of 20 chapters, providing all you need to know about the subject. The opening chapters describe the history and technical aspects of blood transfusion. The first provides a very interesting historical perspective; the second and third consider the donation and collection of blood, and its preparation and storage. Chapters that follow discuss autologous transfusion, apheresis and the laboratory testing of donated blood, mostly for infectious diseases.

The next section is what might be considered 'classical' blood transfusion, being on the molecular basis of blood groups, and then the major laboratory methods of group and save, and then the crossmatch. With regard to the former, it is good to see all the 'antigens' listed according to the new standard numerical notation defined by the International Society of Blood Transfusion, and also their function. For example, the Kidd antigenic system is designated number 009, and functions as a transporter of urea. The section is completed with a discussion of clinical aspects and a focus on the patient; for example, requirements in special conditions, complication of adverse reactions, and transmissible diseases.

The book concludes with chapters on human leucocyte antigens (HLAs), use of growth factors, future developments and quality control. Overall, everything the practitioner needs is included. Each chapter is heavily referenced and there are the usual copious tables, diagrams and graphs. There may of course be some differences in practice between the USA (home of the author) and the UK, but where these are present they are relatively minor. Those who will benefit from this book will be undergraduates and postgraduates in basic and in biomedical science, and therefore the book enters a reasonably crowded market place. It will also be useful reading for those preparing for professional qualifications such as FIBMS and FRCPath.

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