Bacterial Genetic Systems (Methods in Enzymology, Vol 204); edited by J.H. Miller; Academic Press; San Diego, New York and Londen, 1991; xxiv + 706 pages; $85.00

The 706 densely typed pages of Methods in Enzymology's 204th volume contain a rich deposit of invaluable information for the practising bacterial geneticist. The chapters have been contributed by acknowledged experts in the field. Almost all of the authors are based in the United States, a bias which does not reflect accurately the international distribution of expertise in bacterial genetics.

The book is in two parts. Section I, approximately half of the book, is devoted to *Escherichia coli, Salmonella typhimurium* and their bacteriophages — systems about which a great deal is known. Section II is concerned with 'Other Bacterial Systems' and consists of chapters on *Agrobacterium, Bacillus subtilis, Caulobacter crescentus*, Cyanobacteria, *Haemophilus influenzae, Mycobacteria, Myxobacteria*, Neisseriae, *Pseudomonas, Rhizobium melilotti*, Rhodospirillaceae, Staphylococci, Streptococci, *Streptomyces* and *Vibrio* i.e. fifteen prokaryotes with less well-understood genetic systems. While one might argue that there are important omissions (e.g. *Bordetella* and *Erwinia*), the editor deserves praise for ensuring a uniformly high standard in the textual presentation of the selected material. However, since the format of the Methods in Enzymology series has remained largely constant since 1955, readers who have become used to large-format laboratory manuals may question the suitability of the traditional book layout of this volume, particularly for use at the bench. Furthermore, the quality of the illustrations in the book is variable, suggesting a need for standardisation in the editing of the these. Some of the figures have a distinct 'back-of-the-envelope' look about them while others are old friends from earlier reviews. Conversely, those associated with the chapter on *Vibrio* genetics are of a very high quality.

While this is a very readable book, it is not one for the novie because it presupposes a detailed background knowledge of the biology of the bacteria covered. For experienced workers, the volume contains a great deal of useful information on classical and molecular genetic techniques combined with authoritative discussion of their associated merits and potential pitfalls. As one would expect, mutagenesis techniques (for in vivo and in vitro use) are covered, together with selection and screening methods. The use of transposon Tn*10* in *E. coli* is described in detail and mutagenesis strategies for other transposons in more exotic bacteria are also described. The importance of gene fusion techniques to modern bacterial genetics is illustrated by a specialist chapter on this subject and by descriptions of the use of reporter gene fusions in chapters devoted to particular bacteria. Classical gene transfer and mapping techniques such as bacterial conjugation and transduction continue to be highly relevant and chapters on these topics are included. The use of bacteriophages λ, Mu, P1, P2, P4 and P22 in genetic analysis is covered in detail, with the Mu chapter providing excellent background information for those wishing to exploit the Mu-based gene fusion vehicles described elsewhere in the book. Bacteriophages which can be exploited in genetic analysis of the bacteria in Section II are also described in the chapters dealing with their host organisms. There is a fifty-page chapter on plasmid transformation that will reward careful reading by even the most experienced molecular geneticist. The inclusion of a chapter on how to set up and manage a bacterial culture collection is an excellent idea. In addition to practical advice, this chapter rightly sets out the obligations placed on all workers in the field to ensure that strains and other materials described in the literature are made available to others in a timely and efficient manner.

This book fills an important gap in the available literature and while some of its material has appeared recently in monographs or as part of other books, it represents the first time that such a comprehensive survey of bacterial genetics has been attempted in a single volume. *Bacterial Genetic Systems* is a very worthwhile acquisition which no self-respecting bacterial genetics laboratory will wish to be without. Its niche lies between books devoted to the relatively well-served topic of bacterial molecular and cellular biology and the ubiquitous 'cut-and-paste' molecular genetics recipe books. Its appearance in the Methods in Enzymology series is a clear indication of the convergence of research interest which is characteristic of modern biology.

C.J. Dorman

Biologicals from Recombinant Microorganisms and Animal Cells: Production and Recovery; Edited by M.D. White, S. Reuveny and A. Shafferman; VCH Verlag; Weinheim, 1991; xvi + 568 pages. £104.00, DM 280.00

This compendium of conference papers is the product of the 34th OHOLO conference held at Eilat, Israel in December 1990. It consists of papers grouped into a number of clearly defined areas. These may be summarised as:

1. Improvements to prokaryotic expression systems from the point of view of secretion of product, terminal amino acid processing and design of the gene to maximise transcription and translation.
2. The bioreactors and bioreactor systems (generally perfusion based) for the production of materials from animal cells in culture. Particular attention was also given to oxygenation and shear in such systems.
3. A section devoted to insect cell expression systems
4. An extensive set of papers which were centered upon the prokaryotic type of microorganism covering the various unit operations involved in the liberation of the product from the cells and the subsequent concentration and purification.
5. The last two sections were based on papers describing specific products which derived from either bacterial expression systems (4) or animal cell recombinant systems (3).

There is much of value in this volume. Not all the papers are to the same standard or of the same length. Yet workers in the two fields of prokaryotic and animal cell production systems will find much that they can use in their practical and theoretical

Sinai School of Medicine, The Rockefeller University, New York, New York 10021. M . K A Y E T R E M B A T H (2 0) , Department of. Biochemistry, Monash University, ClayÂ ton, Australia. A L E X A N D E R T Z A G O L O F F (2 0 , 4 2) , Public. Health Research Institute, The City of New York, Inc., New York, New York 10016.Â The friendly cooperation of the staff of Academic Press. is gratefully acknowledged. Sidney fleischer lester packer. xxi. Methods in enzymology. Edited by. Sidney P. Colowick and Nathan O. Kaplan. Vanderbilt university school of medicine. Nashville, tennessee. Department of chemistry university of california. At san diego la jolla, california. I. II. Academic Editor: Barbara H. Iglewski. Copyright Â© 2010 Veronica Casas et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.Â Many exotoxin genes are carried on mobile genetic elements, including bacterial viruses (bacteriophage or phage).Â [41] C. A. Mims, Mimsâ€™ Pathogenesis of Infectious Disease, Aca-demic Press, San Diego, Calif, USA, 4th edition, 1995.Â [48] V. Casas and F. Rohwer, â€œPhage metagenomics,â€ Methods in Enzymology, vol. 421, pp. 259â€“268, 2007. Here, using whole-genome shotgun metagenomic and untargeted metabolomic methods, we identified 3 bacteriophages, 47 bacterial species, and 50 fecal metabolites showing notable differences in abundance between MDD patients and healthy controls (HCs). Patients with MDD were mainly characterized by increased abundance of the genus Bacteroides and decreased abundance of the genera Blautia and Eubacterium.Â The gut microbiome, a vital and direct environmental contributor to central nervous system development, consists of a vast bacterial and viral community that can significantly influence host health and disease (5, 6). The gut bacterial microbiome has gained the greatest attention. A striking example is the recent San Diego patient who was infected by multi-drug resistant Acinetobacter baumannii stain during travelling to Egypt. The patient went into a coma for nearly 2 months but awoke 2 days after intravenous injection of a phage cocktail that lyses this bacterium and finally completely recovered (Schooley et al., 2017).Â Phages were used to treat bacterial infections since their discovery in the early 20th century (Lu and Koeris, 2011; Wittebole et al., 2014; Moelling et al., 2018).Â Engineering modular viral scaffolds for targeted bacterial population editing. Cell Syst. 1, 187â€“196. doi: 10.1016/j.cels.2015.08.013.