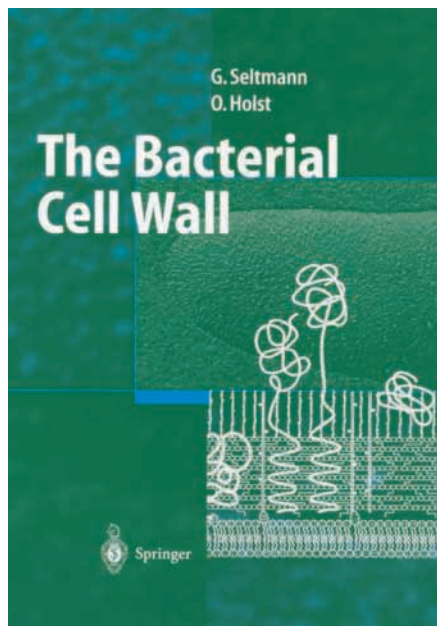


## Shadows and fog or zellwand and zellumschlag?



### The Bacterial Cell Wall

by Guntram Seltmann and Otto Holst

Springer-Verlag (2002) 280 pages. ISBN 3-540-42608-6  
£74/\$110

For their size bacterial cells are incredibly complex. They possess highly sophisticated cell envelopes that play critical roles in cell survival in diverse environments while at the same time functioning as selective permeability barriers. *The Bacterial Cell Wall* represents the second edition of a book originally published in German nearly 20 years ago [Seltmann, G., Kühnemund, O. and Reissbrodt, R. (1982). *Die Bacterielle Zellwand*. Stuttgart: G. Fischer]. In this new book, Guntram Seltmann and Otto Holst provide a completely revised and updated view of the architecture, chemical composition and function of bacterial cell envelopes in Gram-positive, Gram-negative and archaeal microorganisms.

I disagree with the authors on the use of the term 'wall' to define the bacterial surface envelope. Generally the term 'cell wall' would be best used for the rigid peptidoglycan layer, which

represents only one of the many components of the cell envelope ('zellumschlag'). Although it does justice to the English translation of the title of the first edition of this book, 'zellwand' cannot account for the outer membrane, capsules, S-layers and other cell surface components. These components provide the bacterial cell surface with a rich range of features that make the bacterial world and its research so fascinating. In the authors' defense, they indicate in the Preface that the term 'wall' is loosely applied, but it would have been better to replace it rather than to explain that it means something different. As Woody Allen said in *Shadows and Fog*, 'I know exactly what I think about all this, but I can never find words to put it in. Maybe if I get a little drunk I could dance it for you.'

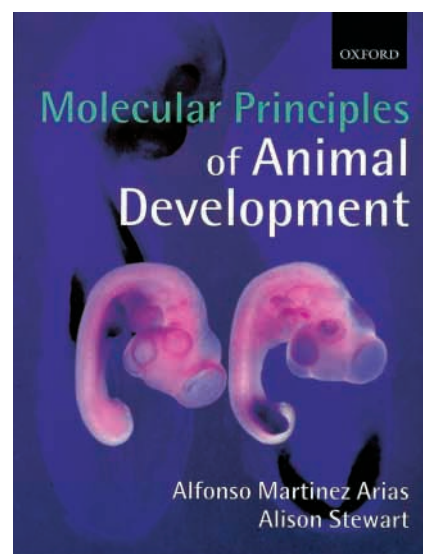
The book is divided into four chapters covering discussions of the components of the bacterial outer membrane, periplasm, cell wall peptidoglycan and cell-wall-associated proteins, and four additional chapters describing unique aspects of cell wall components in Archaea, cell surface polysaccharides, S-layers and cell wall functions in general. Each chapter has a very classical layout describing each of the components discussed in a systematic manner. Although this strategy clearly provides a logical structure it may be tedious for nonspecialists. The chapters are accompanied by a succinct bibliography that was carefully chosen to represent the major points discussed, but it is sometimes outdated. The diagrams, chemical formulae and tables are simple and useful additions to the text. Overall, the authors have made a great effort to be succinct and comprehensive in covering a topic that may very well fill several books. *The Bacterial Cell Wall* is a very useful and comprehensive introductory guide to the bacterial cell envelope that could be especially important for undergraduate students of microbiology, as well as graduate students and fellows.

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## Animal magic unclocked



### Molecular Principles of Animal Development

by Alfonso Martinez Arias and Alison Stewart

Oxford University Press (2002) 410 pages. ISBN 0-19-879284-0  
£28.99

The transformation of an egg into a living organism is one of the most magical processes of biology. Over the past 20 years, the application of genetic and biochemical techniques has given us a molecular outline for this biological miracle. The new book by Martinez Arias and Stewart sets out to summarize and identify common principles in the molecular processes that underlie the development of an animal. The book differs from others in that it focuses on commonalities in molecular mechanisms rather than on the embryological description of the processes they execute and control. The project is timely because many of the molecules involved in easily observed developmental processes have now been identified and found to function similarly in different animal species. I found that the book broadly achieved its aim of summarizing developmental principles, and it will be a valuable source of reference and inspiration for the researcher, teacher and final-year undergraduate.

The book is divided into four sections. The first few chapters deal with the

molecular basis of information transfer: signal initiation at the cell surface, signal transduction and transcriptional control are all discussed using examples relating to developmental biology. The second section then explains how the unit of development, the cell, responds appropriately to these signals: behaviours such as shape change, migration, division and death are all reviewed. These foundations are then used to build an understanding of developmental concepts, such as lineage determination and morphogen gradients. Finally, the authors provide a truly excellent overview of well-characterised developmental processes, such as myogenesis and neurogenesis. I found that this overall organisation made good logical sense. I particularly enjoyed the early chapters where the molecules are introduced not only in terms of how they function but also in terms of how they were discovered and how they are studied.

The text is up-to-date and well written, combining reasoned arguments with judicious use of appropriate metaphor. The numerous and colourful diagrams are helpful and one of the strengths of the book. I particularly applaud the abundant inclusion of original data, together with references, which make it easy for readers to find further detail. The molecules that are the focus of the book are clearly represented as linear modular structures according to their protein domain content. It would have been helpful, however, to have a glossary of these diagrams together with further information as an appendix for quick reference. Indeed, I felt that the book could be improved by placing a greater emphasis on structural explanations of molecular functions and then relating these to developmental outcomes. A chapter or section that described structural aspects of the protein domains present in the molecules would have been appropriate. In particular, an explanation of the specificity of the protein–nucleic-acid and protein–protein interactions that form the basis of biological function would have reinforced the value of looking at processes at a molecular level.

These latter points aside, this book makes an excellent job of presenting

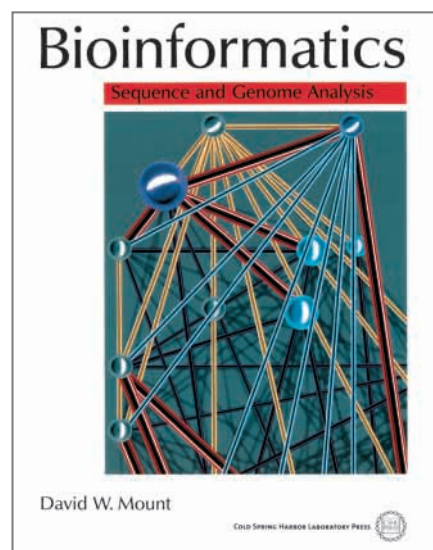
developmental biology in a fresh way, through the underlying molecular principles. Genome sequencing projects coupled with technical advances have driven an ever-growing interest in using a reverse-genetic approach to understanding gene function. Martinez Arias and Stewart show that textbooks, as well as research papers, can take this ‘molecule first’ approach to explaining biological processes. This may be the way of the future. I can wholeheartedly recommend this book to researchers, students and anyone else interested in discovering more about the wonderful process of animal development. For me, understanding the mechanics still doesn’t take away any of the magic.

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## A coming of age for bioinformatics



### Bioinformatics: Sequence and Genome Analysis

by David W. Mount

Cold Spring Harbor Laboratory Press (2001) 564 pages. ISBN 0-87969-608-7  
£70

The idea of making a living in sequence analysis in the early days of

bioinformatics risked provoking the incredulity and, often, the derision of one’s peers. Why line up letters when there are so many interesting experiments waiting? The growth of bioinformatics and, more importantly, of sequence databases, however, has made this new discipline an essential part of the biologist’s repertoire. Now, every experimental result can be cast in the light of evolutionary history to provide novel insights into homologous systems.

The maturation of a discipline requires degree courses, proselytizers, historians and text books. In each of these respects, David Mount’s *Bioinformatics: Sequence and Genome Analysis* reflects the coming of age of bioinformatics. It is a foundation text book that archives the early history of the field and describes the emergence of key analytical methodologies. If you have ever been curious about the inner workings of the BLAST algorithm, about what is meant by the threading of sequence onto structure, or about what Rosetta stone proteins are, then this book is for you.

In the first two chapters, the reader is gently introduced to the early history of computational biology and humdrum, but necessary, matters such as formats and data structures. Pair-wise and multiple alignment methods are then plumbed in depth with good pointers to many of the classic papers in the field. This reading is not for the fainthearted, especially those who seldom stray beyond the bounds of BLAST: the in-depth, and often step-by-step, algorithmic analysis is spread over two chapters and some 150 pages. Subsequent chapters describe a gamut of bioinformatics prediction methods relating to RNA structure, phylogeny, homology, genes and protein structures. The last chapter concentrates on the fast-moving field of genome analysis. Currently, such research is the preserve of the well-heeled bioinformatics research groups because it requires significant computational resources. However, as genome sequencing becomes more routine and computer prices tumble, this could be an area that might prove to be fruitful for smaller research groups.

The author and publishers have addressed the rapid evolution of bioinformatics methodologies by providing a website (<http://www.bioinformaticsonline.org>), which displays weblinks, examples and problems at no extra charge. The website also promises to keep the book's readers up-to-date in the future with the latest strategies and technologies. Although this book was first published in 2001, the fast pace of progress in the field guarantees that some of the material is already out of date. Advances in 2001 and 2002, such as refinements to PSI-BLAST (Schäffer et al., 2001), genome analysis tools such as BLAT (Kent, 2002) and gene prediction algorithms based on genome-genome alignments (Korf et al., 2001), would be necessary additions to any subsequent edition.

Some of the material in this book would have benefited from a more critical discussion of the respective merits of the various bioinformatics tools and their applicability to different biological problems. Nevertheless, much of the vocabulary and many of the 'rules-of-thumb' in bioinformatics are explained succinctly enough. Thus, *Bioinformatics: Sequence and Genome Analysis* should find a place in any advanced undergraduate or graduate bioinformatics degree course.

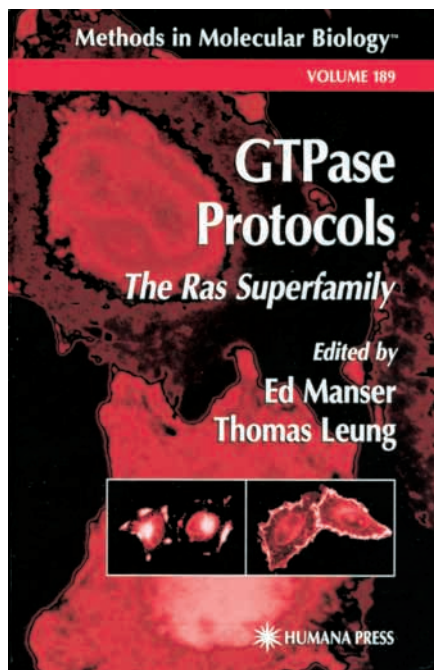
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## Super Ras



### GTPase Protocols: The Ras Superfamily

edited by Ed Manser and Thomas Leung

Humana Press (2002). 267 pages. ISBN 0-89603-934-X  
\$99.50

Few families of signalling proteins rival the Ras-related small GTPases in breadth of cellular function. Since identification of Ras as a key oncogene in human cancer 20 years ago, well over 100 related mammalian proteins have been recorded, together with a host of relatives in simpler eukaryotes. Cell biologists find these proteins particularly hard to avoid – small GTPases are key regulators of some of the most intensely researched problems in cell biology. The 50 or so human Rab GTPases alone are enough to keep membrane traffickers quiet for the foreseeable future.

In *GTPase Protocols*, Manser and Leung assemble the key protocols required for researchers venturing into this field, together with inspiration for those of us whose talk of 'heroic' pull-down purifications somehow never makes it into the cold room. The publishers state that the book is "written by international experts who, in many cases, have

pioneered the technique", and this is evident from both the impressive list of contributors and the quality and detail of the presented methods.

The book is organised into two parts: a shorter first section describing general protocols, followed by specific methods for each of the five small GTPase subfamilies. In some ways this feels like a slightly artificial division – Zhao and Lim's update of their classic blot overlay protocol is a great general method that deserves to be liberated from the Ras techniques section. Similarly, the excellent description by Takai and co-workers of the isolation of Rab3 effectors by affinity chromatography is one that could be usefully applied to any other small GTPase. These are minor quibbles that in part reflect the commonalities between the small GTPase subfamilies.

For most of us, our initiation into small GTPase work will involve throwing dominant-negative mutants at our system and hoping for the best. Fittingly, the book begins with a thorough introduction to these experimental tools in which Manser explains both the basis of their action and, most importantly, the caveats of their use. This is an example of where the book is at its strongest – the combination of clear practical detail with underlying theory provides the reader with the information required not only to perform the technique but also to interpret the resulting data. Other basic techniques are handled in this section with equal clarity. Smith and Rittinger provide an exhaustive description of the purification of recombinant small GTPases from bacteria. Here, it would have been nice to see some discussion of purification of post-translationally-modified small GTPases from insect cells, although this is dealt with briefly elsewhere. Ahmadian et al. give a precise account of fluorescent techniques for the kinetic analysis of small GTPases, including assays for guanine-nucleotide-exchange factors and GTPase-activating proteins. What can seem quite complicated assays are explained in a straightforward manner, with the fringe benefit of reducing unnecessary graduate student irradiation. After three of the 'bread and butter' techniques of small GTPase work, the

section closes with a general technique for the more adventurous: Van Aelst and colleagues giving a detailed description of cDNA-RDA screens for identifying genes regulated by small GTPases.

The subsequent sections deal with specific protocols for the Ras, Rho, Rab, Arf and Ran GTPases although, as mentioned before, there is plenty of potential for cross-pollination between these subject headings. For me, the standout specific techniques are the protocols for assaying Rho GTPases and for measuring cell migration and invasion, although this is probably

coloured in part by my own experimental frustrations. Workers on other small GTPase subfamilies will also find succour: there are detailed protocols for the post-translational modification of Rab and Arf GTPases and an excellent section on Ran GTPases. As with most books of experimental methods, there are occasional chapters that read like lightly revised methods sections from previously published work but these are few and far between.

In summary, this is a collection of detailed and precise experimental

methods from some of the leading research groups in this field. The authors are to be congratulated on the clarity brought to each technique, and thanked in advance for dealing with the flood of requests for reagents that their involvement will undoubtedly provoke.

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## Commentaries

**JCS Commentaries highlight and critically discuss recent exciting work that will interest those working in cell biology, molecular biology, genetics and related disciplines. These short reviews are commissioned from leading figures in the field and are subject to rigorous peer-review and in-house editorial appraisal. Each issue of the journal contains at least two Commentaries. JCS thus provides readers with more than 50 Commentaries over the year, which cover the complete spectrum of cell science. The following are just some of the Commentaries appearing in JCS over the coming months.**

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