Foremost among these is the format of the references. Firstly, I would have preferred one set of references collated from all the chapters and placed at the end of the book. Secondly, references should include the titles of papers. It is infuriating to have to hunt down a paper before discovering it has only tangential relevance to the topic being pursued. The index also has the quirk of repeating the words 'plasmid' and 'phage' before every example of these, when simple indentation would have sufficed – as indeed it does elsewhere. Each chapter is subdivided into small numbered sections: these might usefully have been collected into a contents listing, in the style of the *Annual Reviews*. But these are minor quibbles. Overall, 'Vectors' merits a place in any library catering for cloners. I am sure that many noteworthy vectors have been omitted, but I believe that most of the current vector concepts are covered. It is, however, a rapidly moving field: I look forward to the next edition, which will need to appear in about five years.

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Maximising Gene Expression. Edited by WILLIAM REZNIKOFF and LARRY GOLD. London: Butterworths. 1987. 375 pages. £65. ISBN 0 409 90027 3.

This book in the Biotechnology Series from Butterworths, which has Julian Davies as general editor, has the practical aim, kept in rather distant view, of helping the biotechnologist to achieve maximal expression of genes of special interest in suitably artificial genetic and environmental backgrounds. The eleven chapters in the book will not make the biotechnologist's task seem easy, but they contain much of interest to geneticists and molecular biologists who are not busy modifying some genome for the genefit of the human race.

In the first two chapters William Reznikoff and William McClure discuss the promoters of *E. coli* and Kevin Struhl examines the comparable elements of yeast, as the best-known representatives of prokaryotes and eukaryotes, and this sets the scene for the later studies. Transcription initiation in *E. coli* occurs at frequencies ranging from one per 5–10 seconds (for rRNA genes) to once per generation (*lacI*) or even less, a difference of near 10000-fold. Analysing this variation has raised many difficult problems, e.g. relating *in vitro* and *in vivo* data and sorting out the so-called tight-binding sites which behave as promoters only *in vitro*, determining the precise 5′ end of each mRNA, analysing the successive chemical steps in initiation, predicting promoter strength from DNA sequence, and so on. The importance of conservation of certain bases in the −10 and −35 regions of the promoter are well documented from comparisons of 112 *E. coli* promoters; and I was disappointed not to find an explanation of the very slow rate of *lacI* gene expression. In this context a comparison of the *E. coli* *lacZ* and *lacI* promoter sequences with those of Klebsiella, recently sequenced by Buvinger & Riley (*J. Bacteriol.* **163**, 858–862 (1985)), should be of interest in view of the very different levels of activity of these two operons.

Yeast genes are not organized in operon-like clusters, and their promoters (if that is the correct word for them) are hardly comparable with those of *E. coli*. They are larger, variable in size, and can be as far as 450 base pairs upstream of the RNA start; and the molecular mechanism of transcription initiation and its regulation must be qualitatively different in yeast. Yeast cells must have many specific transcription factors because upstream elements are required for transcription but can consist of different DNA sequences, can act at long and variable distances upstream and can act even when inverted with respect to the TATA box and the initiation site.

B. Wasylyk discusses promoter elements and *trans*-acting factors of protein coding genes in higher eukaryotes, where the situation is even more complex than in yeast and includes data on SV40 and adenovirus promoters. The promoter region consists of several components: the cap site element at the start site of transcription, the TATA box at around −30, the upstream elements between about −40 and −110, and enhancer elements that are located either farther upstream or even downstream of the initiation site. The TATA box directs initiation to the correct position 30 base pairs downstream, and also affects promoter efficiency. Upstream elements determine efficiency but not accuracy of initiation, and upstream elements are interchangeable between different promoters in some cases. Enhancers appear to form, quantitatively, the most important promoter elements and have no fixed position relative to other promoter elements. Wasylyk discusses current models of their action.

David Kennell examines an old mystery, the mRNA instability in bacteria. In *E. coli* each message decays at a unique rate, with functional half-lives ranging from 30 seconds to more than 8 minutes at 37 °C and rather longer times at lower temperatures. These rates form a marked contrast to the relative stability of many messengers in higher eukaryotes, but are clearly what the bacterium needs to enable it to adapt to rapid environmental changes. One way of increasing gene expression would be to reduce the decay rate of one or a group of messenger RNAs, but this has not been achieved experimentally and no specific enzymes for mRNA degradation have been identified. Kennell has been unable to detect any characteristics of sequenced messengers which could make them more, or less, resistant to the many RNAses present in the cell.

Barry Polisky discusses replication control of ColE1-type plasmids and Robert Knowlton considers copy number and stability of yeast plasmids, in the next two chapters; and in both systems the implications for maximising expression of cloned genes are examined. These form important current areas of applied research and the authors examine the problems which each system presents.

Gary Stormo discusses translation initiation in both prokaryotes and eukaryotes. Some laboratories have begun to collect data on the efficiencies of particular initiation sites, and Stormo concentrates on the effects of mRNA sequence on translation efficiency. This, of course, brings up the very difficult problem of structural features of the mRNA, which are difficult to predict from its sequence but can have an important effect on initiation rate. The *E. coli* data lead to the following rules for maximizing the yield of a particular protein: (1) AUG is the best initiation codon; (2) A Shine-Dalgardo sequence of at least four nucleotides, taken from the sequence AGGAGG, should be used; longer may help some messages; (3) The optimum spacing between the S-D sequence and the initiator codon is about nine bases. Some additional rules are also given. Stormo finds that the requirements for efficient expression of eukaryotic proteins are quite different from those for prokaryotes, but only some less general proposals can be made for increasing gene expression.

In by far the longest chapter in the book, de Boer and Kastelein present data on biased codon usage, and show that genes coding for abundant proteins have a marked bias towards major tRNA species compared with poorly expressed genes, which make much more use of minor tRNA species. Data on translation time (amino acids per second) for strongly and poorly expressed genes are also given, and evolutionary aspects of biased codon usage are discussed.

In the last three chapters Goldberg & Goff describe the selective degradation of abnormal proteins in *E. coli* and the eight soluble proteases responsible; Dobner & Villa-Komaroff discuss the detection of proteins produced by recombinant DNA techniques; and Buell and Panayotatos consider how knowledge described in the previous chapters has been used for the overproduction of proteins, specifically in *E. coli* which has been the major source of information. Each chapter has a comprehensive list of references, and there is a detailed index.

Many of the studies presented in this book were no doubt motivated by practical or commercial aims, but they have often made novel and valuable contributions to basic molecular genetics, and this should make the book of considerable interest to a wide readership. The book, in spite of its sixteen contributors (thirteen from USA, two from Geneva and one from France), reads as a unified whole, and the two editors are to be congratulated. I have to give the book a very warm recommendation, only mitigated by the high price, which will limit its siting to library rather than personal bookshelves.

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Molecular Evolutionary Genetics. By MASATOSHI NEI. New York: Columbia University Press. 1987. 512 pages. U.S. $50.00. ISBN 0 231 06320 2.

The rapid accumulation of data at the molecular genetic level, from protein and DNA sequencing, restriction enzyme analysis and electrophoretic variants have given us much information on the tempo and structure of the evolutionary process and on variability within populations. Major theoretical developments have ensued in order to interpret all the new data. It is now about a quarter of a century since Zuckerkandl and Pauling first drew attention to the steady molecular clock of protein evolution, over 20 years since Harris' and Lewontin and Hubby's demonstration of substantial polymorphism within species inferred from gel electrophoresis, and 20 years since Kimura's proposal of the neutral theory to explain these data. There have been other fundamental discoveries, such as of different rates of evolution at silent and coding sites and of concerted evolution of multiple genes, and developments in theory such as in measures of genetic distance, phylogenetic tree structure using molecular data and of models to describe evolution of gene families. As a consequence evolution and variation are now considered mainly by geneticists at the molecular level. Although this may seem to ignore the importance of adaptation and of an understanding of the evolution and maintenance of variation of continuous traits, this reductive stance does reflect the amount of new data coming forward and the power of molecular analysis.

Masatoshi Nei and his group at Houston have been major contributors and stimulators of this work, for example, on methods for distance measurement, for tests of neutral and alternative theories, and for synthesising theory and observations. It is not, therefore, surprising that his *Molecular Evolutionary Genetics* is a most useful book which brings together molecular data, methods for their analysis, and the theoretical basis of their interpretation. It will serve as a reference book on both methodology and results, and should be of value both to population geneticists and to those molecular geneticists prepared to extend their horizons to anything but the most superficial evolutionary interpretation of their data.

The greater part of the text deals with the kind of molecular data which has been collected: initially protein and subsequently DNA sequences between species, on electrophoretic, DNA sequence and restriction fragment length variation within species and how