enough to warrant their genetic conservation throughout evolution'.

This is a clearly written, very readable, well referenced volume with good use of original data. It is also bang up-to-date; much of the data referred to as 'in preparation' is only now appearing in the primary literature. Individual chapters are complete in themselves, allowing them to be read as single review articles. However, this does lead to an inordinate amount of repetition of the generally accepted facts. An expanded introduction, covering the common ground, would have minimized repetition and highlighted those areas where the consensus has yet to emerge. The main emphasis of the book is on viral superantigens rather than bacterial superantigens. The editors do not comment on whether this is simply a reflexion of levels of activity in the two areas, or an indication that the role of viral superantigens is more profound – or more controversial – than that of bacterial superantigens. On the plus side, the editors have clearly encouraged the contributors to hypothesize and to spell out the links between their own work and the rest of the field. It is gratifying to find that questions raised in one chapter are seriously addressed in subsequent chapters. In summary, this is a stimulating journey through the rapidly unfolding superantigen saga which will be a rewarding read for anyone interested in the ontogeny of the immune system, the immune response to infection or the evolution of host–pathogen relationships.

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Transcriptional Regulation. Two volumes. Edited by STEVEN L. MCKNIGHT and KEITH R. YAMAMOTO. Cold Spring Harbor Laboratory Press. 1993. 1334 pages. Price Hard cover $160. ISBN 0 87969 4106. Soft cover $95 ISBN 0 87969 425 4.

The vectorial process of gene expression, which can be described in terms of four main stages, DNA transcription, RNA processing, RNA translation, and protein processing, is the sole means by which the genetic information contained within nucleic acids is realized. It is a truism, but one worthy of repetition, that this multifaceted process is by no means passive: It is by responding to different stimuli – whether internal or external – that both unicellular and multicellular organisms (and their genetic elements) in nature are able to survive. Gene regulation, in short, is the 'stuff of life'.

A primary target in such regulation, but by no means the sole one, is transcription by the DNA-dependent RNA polymerase(s). There are two main forms of this essential enzyme, one is multisubunit in composition and is present as a single species in eubacteria, archea, and chloroplasts, and as three species in the nuclei of eukaryotes; the other form is a single polypeptide chain as exemplified by the T3/T7/SP6 bacteriophage-encoded enzyme and that found in mitochondria. Given the strong conservation and widespread nature of the multimeric RNA polymerase, it is particularly fitting that this new publication from Cold Spring Harbor should attempt to consider transcriptional regulation in a single monograph (number 22 in the series). Note that in addition to the hardback there is a competitively priced paper edition.

Transcriptional Regulation comes from a long line of excellent monographs, and it is by no means surprising to find that the standards of this pedigree are maintained. Indeed, a veritable wealth of information is packed into this two-volume set, ensuring that both the pundits and lay people are well catered for. It is impossible to do justice to such a *magnum opus* and the following description is intended as a 'snap-shot', summarizing the basic details.

As with other CSH monographs, *Transcriptional Regulation* is written by key figures in this large field; it is very much a North American affair.

The topics covered in *Transcriptional Regulation* can be separated into three major areas: RNA polymerase itself, transcription factors, and regulatory networks, and although the emphasis is on eukaryotes, there is generally a healthy proportion of eubacterial material. (I was somewhat surprised to see no coverage of eubacterial RNA polymerases *per se*, especially bearing in mind its role as a simple paradigm for the more complex eukaryotic counterparts; the archaeal enzymes are also not considered.)

Let us look at the contents of the monograph in a little detail. For this purpose, given the eukaryotic bias, it is convenient to separate the topics on a species basis (chapter numbers are given in parenthesis).

Eukaryotic RNA polymerases. Other than an extensive review of the current status of the genetics and biochemistry of the three yeast enzymes, the focus is on RNA polymerase II (2), including, in addition to the general details, the intriguing CTD and its phosphorylation (3–5), and information on the three-dimensional structure at 15 Å (3).

Eubacterial transcription. Here we have both sigma factors and rho (6, 14), the termination cycle in quantitative and topological terms (7, 46), and the control of termination through antitermination mechanisms and various forms of attenuation (8, 15, 16). A number of individual transcription factors are considered separately in some detail: repressors – LacI, TrpR, lambdoid (23, 18, 17); activators – AraC, Crp, signal transduction response regulators (24, 19, 25).

Eukaryotic transcriptional initiation. In addition to considering the role of chromatin structure (47, 48), there are several chapters describing the well-characterized initiation factors acting on the three different RNA polymerases: TFIIs, TFIIIs, TATA-

box-binding protein (TBP), UBF/SLI, and the mediator (9–13, 20–22). A number of more specific activators/transcriptional regulators are also included: yeast GCN4, GAL4 & GAL11 (31, 35); *Drosophila* heat shock protein HSF (34); rat CCAAT/enhancer binding protein (29); serum response factor SRF which has a novel DNA binding domain (33); the leucine-zipper containing Fos/Jun components of AP-1 (30); and viral activators (26).

Eukaryotic regulatory networks. A considerable portion of book two of the monograph is devoted to this important and fascinating aspect: mating-type interconversion in yeast (36, 37); *Drosophila* development (45); retinoid and steroid receptors (42, 43); myogenesis and endodermal development (39, 40); and the multifaceted regulation of viral-induced human interferon synthesis (44).

If pressed to choose a 'favourite' amongst this impressive compendium, I would have to plump for the article by Charles Yanfosky, both for the historical perspective and the treatment of transcriptional regulatory mechanisms in prokaryotes and eukaryotes (1). Nevertheless, it is really not appropriate to single out a *pièce de résistance* given the high standard of *Transcriptional Regulation* throughout.

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Molecular Genetics of Drosophila Oogenesis. By PAUL F. LASKO. CRC Press and R. G. Landes Company, Georgetown, Texas. 1994. 120 pp. Hard cover price £74. ISBN 1 57059 032 X.

The differentiation of the oocyte is one of the most intriguing problems in Developmental Biology. The *Drosophila* oocyte is arguably the most complex cell in the organism and is the only cell with the capacity to build all the cell types of the larva and fly.

The detailed morphology of oogenesis has been well documented. A germ-line derived stem cell divides to generate a cluster of 16 cells, one of which will become the oocyte and 15 which will become nurse cells. The cluster is surrounded by somatically derived follicle cells. This egg chamber functions as a unit. The nurse cells produce many of the components needed to build the oocyte and subsequently the embryo. The follicle cells produce some components of the egg, such as yolk and the external covering. However, the commune of cells does not just provide the building blocks for an embryo, such as yolk, ribosomes and materials for permitting rapid mitosis after cell division, it also sets up a complex organizational system such that very early in oogenesis the oocyte has obvious axes. The anterior/posterior and dorso-ventral axes are apparent early in the assembly of the oocyte and these same axes are determined in the developing embryo.

The study of mutants which disrupt oogenesis and embryogenesis in *Drosophila*, along with the tremendous advances in molecular biology, has provided the basis for a leap forward in our understanding of how the axes and segmentation of the embryo is assembled. It led to the molecular evidence that morphogenetic gradients, so long assumed to be present from experimental interference with development, were real.

The anterior/posterior axis is defined by localized mRNAs being translated after fertilization into proteins which establish gradients, for example, the products of the *bicoid* gene at the anterior and of *nanos* at the posterior. Many other gene products are required for the correct localization of the transcripts which are produced in the nurse cells and transported into the oocyte. The function of *bicoid* and *nanos* proteins is to turn on the appropriate zygotic genes in the correct regions of the embryo to build the head, thorax and abdomen.

The establishment of the extreme anterior and posterior regions of the embryo involves signalling from specific follicle cells lying at the anterior and posterior of the oocyte. Activation of the responding zygotic genes requires the local activation of an oocyte surface ligand followed by a signal transduction cascade. For dorso-ventral polarity a receptor is present throughout the oocyte membrane; localized proteins made in the ventral follicle cells secreted into the space between the oocyte and vitelline membrane lead to the local activation of the receptor. This in turn leads to a cascade of events in the oocyte that causes a transcription factor to enter the nuclei on the ventral side and establish the correct gene expression for products required in dorsal and ventral cells.

These pathways that establish the axes of the embryo are well understood and now the questions become: 'What has been happening earlier in development to determine the sex of the germ-line and ensure that an oocyte develops; how is regionalized follicle cell gene expression achieved; how does one cell become the oocyte and others develop into nurse cells; how is the position in the egg chamber of the presumptive oocyte selected; what drives the complex morphogenetic movement of the follicle cells; how are materials transferred to the oocyte at specific stages in oogenesis from the nurse cells and how exactly are specific transcripts localized?' These problems are now being tackled and we are beginning to discover that the oocyte is an active participant in, for example, signalling to the overlying follicle cells the position of the nucleus, which is always anterior and dorsal, thus setting up a signal transduction cascade that affects cell behaviour and transcriptional activities of follicle cells.

It is these fascinating problems and others concerned with what we know about the establishment of the germ-line (which is integrally linked to the establishment of the posterior of the embryo) and about the products needed for early mitosis in the