immensely from a chapter on methodology by Sissom, Polis, and Watt. Cloudsley-Thompson completes the book with a scholarly discourse on the history of humanity's association with scorpions.

In all, Polis has succeeded in bringing together essentially everything that is known about scorpions in a timely, stimulating, and very readable compilation. The book will be an indispensable resource for scorpion biologists, arachnologists, and invertebrate zoologists. I also highly recommend it to young investigators seeking research topics, especially regarding behavior, population biology, ecology, and evolution.

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Data for Drug Design

Use of X-Ray Crystallography in the Design of Antiviral Agents. W. GRAEME LAVER and GILLIAN M. AIR, Eds. Academic Press, San Diego, CA, 1990. xxxiv, 360 pp., illus., + plates. $79. From a workshop, Kona, HI, Feb. 1989

Now that it has become possible for the x-ray crystallographer to determine the structures of very large macromolecules, including viruses, often to quite high resolution, the structural information available for drug design has become vastly extended. Detailed three-dimensional data on both drugs and their receptors can, at last, be included in the input to the design of new and better drugs. This book describes such structural information on viruses, their gene products, and their complexes with other molecules. It shows how information on virus structure and on the recognition of portions of this structure by other molecules can be used to design new antiviral agents.

A wide variety of virus structures are discussed. For example, foot-and-mouth disease virus and a portion of adenovirus, both studied to 2.9 Å resolution, are described. At this resolution the protein backbone is well established and the side chains can be seen. Gene products of human immunodeficiency (HIV) and Rous sarcoma (RSV) viruses, studied to even higher resolution, are also described. Crystal structures of viral proteinases, which serve as bases for inhibitor design, and several promising peptide analogs that inhibit proteinases are included. The account of the structure of tumor necrosis factor, a "non-viral jelly-roll," and its relation to rhinovirus may interest the reader. We are reminded, however, that such useful three-dimensional structural data can only be obtained if good crystals are grown—attempts with HIV reverse transcsriptase, the enzymatic target of the anti-AIDS drug AZT (3′-azidothymidine), have so far only yielded crystals that diffract to a maximum resolution of 6 Å.

The immune system provides a well-designed mechanism for inhibiting the action of certain viruses; mimicking this inhibiting action could lead the way to potent antiviral drugs. The crystal structures of components of the immune system, including a portion of one of the molecules of the major histocompatibility complex, provide evidence for the site of antigenic peptide binding. Structures of antibody-antigen complexes demonstrate the complementarity of the two interacting surfaces that occurs when water is excluded from the interface.

Targets for anti-influenza drug design are the glycoproteins hemagglutinin and neuraminidase on the viral surface. The crystal structures of both of these proteins and of a neuraminidase-antibody complex are discussed in several papers. Antiviral drugs that have so far been effective against influenza A prevent a conformational change in hemagglutinin that would normally facilitate the fusion of the virus to the host cell prior to infection.

Many viruses are able to evade the immune system. Details of the crystal structure work on human rhinovirus, the common cold virus, described here by Rossmann, give some inkling why this may be so. The site of attachment of this virus to the host cell is shown to lie in a "canyon," inaccessible to antibodies. Therefore another strategy has to be devised to prevent attachment of the virus to the host cell and thereby inactivate the virus. In an insightful chapter that stresses the importance of detailed information on virus structure, Rossmann shows how drugs have been designed to bind inside the canyon. Though drug resistance generally ensues from such treatment, the processes involved are now, as a result of the x-ray studies, beginning to be understood.

This book succeeds admirably both in cataloguing the data on hand and in showing how structural data can be used in the design of antiviral drugs. Many of the excellent diagrams are in color, although these are, unfortunately, separated from the main text without adequate notation. In an informative preface, the editors provide an overview that establishes continuity among chapters, and there are useful lists of references at the end of each chapter. It is a pleasure to read such a well-produced book that gives some insight into how the viruses act and how this action can be prevented.

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Molecular Basis of Cancer

Oncogenes and the Molecular Origins of Cancer. ROBERT A. WEINBERG, Ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. xii, 367 pp., illus. Paper, $55. Cold Spring Harbor Monograph 18.

During the past decade we have witnessed a series of discoveries of fundamental importance to understanding the molecular basis of cancer. Through insights initially gained from studies of RNA tumor viruses, the cellular homologues of their oncogenes have been found to be activated as transforming genes in a wide variety of human malignancies. Moreover, it has been possible to elucidate the basic cellular processes—growth factor mitogenic signaling—in which many of these genes are normally involved. Equally exciting and relevant to cancer are recent discoveries of important regulatory genes, whose loss of normal function also contributes to the neoplastic process. Relatively few such genes, termed anti-oncogenes or tumor suppressor genes, have been isolated to date, and understanding of their functions is at a very early stage. However, the first of these genes to be isolated, *Rb* and p53, both seem to be involved in cell cycle regulation. Thus, research efforts in diverse areas are being mobilized along a common front aimed at better understanding the biochemistry of mitogenic signaling and cell cycle control.

At this stage of the battle, a book full of information as well as perspectives concerning what has been learned so far should be most useful for providing the uninitiated with sufficient background to forge ahead. It is for this purpose that *Oncogenes and the Molecular Origin of Cancer* was designed. Robert Weinberg, who has contributed much to our present understanding, has organized and edited this book, enlisting the efforts of several leading scientists in their respective fields. Introductory and closing chapters respectively by Nobel laureates Harold Varmus and Michael Bishop provide historical background and insights into how present knowledge is leading to new approaches toward the diagnosis, prognosis, and treatment of cancer. Coverage of growth factors and receptors as well as biochemical signaling pathways includes not only the tyrosine kinases but a lucid chapter on non-*ras* G proteins, which have been less intensively studied by cancer biologists but whose links to cancer have recently been uncovered. Excellent summaries on the *ras* oncogenes, oncogene protein kinases, and nuclear oncogenes are provided by Frank McCormick, Tony Hunter, and Robert Eisenman, respectively.