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Book reviews

Varner, J. E. (ed.): Self-Assembling Architecture. *46th Symposium of the Society for Developmental Biology*. New York: Alan R. Liss 1988. XII/276 pp., several figs. and tabs. Hard bound $ 65.00.

Self-Assembling Architecture is the report of the 46th Symposium of the Society for Developmental Biology, held in St. Paul, Minnesota, USA, in June 1987. It deals with what is probably the most remarkable property of many molecules in living cells: their capacity to spontaneously form high-order structures. The report is divided into 16 chapters, which treat such different subjects as: the extra-cellular matrix of mammalian cells (chapters 1, 3, 8, 9), the organization of non-animal cell walls (chapters 2, 4–7), membrane or membrane-associated proteins (chapters 10, 11, 15), the cytoskeletal protein actin, the endoskeletal spicules of sea urchin embryo's, and moth chorion morphogenesis (chapters 12–14) and finishes with a chapter (16) on DNA topoisomerase.

The various authors treat their subjects in rather different ways: most are descriptive; some deal with the biochemistry or molecular biology of their subject. Most contributions are written as short reviews. Albeit, with the exception of a few specialized topics, recently excellent reviews on most topics, for example, the cytoskeleton, clathrins and endo-exocytosis, have been published. Detailed remarks on the various chapters can not be made in this context. However, chapter 6, "gel properties of the cell wall", does not deal with self-assembly at all, but speculates on the function of proteins in the cell wall. The same topic is more solidly discussed in chapter 4, "tying the knots in the extensin network". Absent are the remarkable high-order patterns of cellulose microfibrils in plant cell walls, where self-assembly is expected, to occur also. Chapter 12, "self-assembly of actin filaments", is rather superficial, the idea of dynamic instability is prominently absent, and no comparison with other cytoskeletal elements is made.

If the intent was to collect a number of highly diverse systems, the editor has succeeded quite well: even for a symposium proceedings the heterogenity is enormous. If, however, the intent was to compare various mechanisms and/or subjects, the failure is complete. Any attempt to structure the book and to evaluate or compare the different systems and mechanisms is absent. This may be acceptable for any symposium proceedings, but it is not acceptable if the proceedings are to be widely distributed. As it stands, it is a missed chance. None the less, even the present collection shows that cell logistics deals with self-organizing systems that need modification, not excessive and detailed control. In this sense this book may have reached its goal. Self-assembly is an intriguing phenomenon, and its significance is often underestimated.

J. W. M. Derksen, Nijmegen

Watson, J. D.; Hopkins, M. H.; Roberts, J. W.; Steitz, J. A.; Weiner, A. M. (eds.): Molecular Biology of the Gene, 4th edn. Menlo Park: The Benjamin Cummings Publishing Co 1988. 850 figs., 82 tabs. Hard bound $ 90.–.

Because of the breathtaking advances that are being made almost every day in research on the gene, no one person can hope to speak for our understanding of the gene. This fourth and latest edition of *Molecular Biology of the Gene* therefore has no less than five authors. When the first edition came out in 1965 it was much easier as the last few codons of the genetic code were just being worked out. The second edition in 1970 saw the isolation of the first repressors that bind to DNA, while the third edition in 1976 came out as recombinant DNA technology was in its infancy, and it was thought then that DNA sequencing was just around the corner.

This fourth edition builds on all of these things and above all demonstrates just what a boon has been the recombinant DNA revolution combined with the ability to sequence DNA. At first, this edition appeared as two volumes, the first covering the general principles of the structure and function of both prokaryotic and eucaryotic organisms, while the second, first published December, 1987, dealt with the molecular biology of multicellular organisms and evolution. Finally, the two volumes have been combined as one, in response to popular demand.

As might be expected, most of the first volume (called Book I in this combined version) deals with the molecular biology of bacteria, starting from simple genetics, through chemical structure of proteins and nucleic acids to replication and protein synthesis to gene regulation. The yeast genome is then considered by way of introducing the complexities of eukaryotes and contained chromosomes. Book II deals with the molecular biology of development, with immunology, with eukaryotic viruses, and cell proliferation, cancer and the origin of life itself.

An extraordinarily broad coverage of the subject is to be found in this single volume, all that one would expect from James Watson and his team of five authors. Starting from his discovery of the DNA double helix, this scientist has lead the way, and this edition of *Molecular Biology of the Gene* carries on in this tradition. In between the same two covers we have a book that is a suitable text for teaching at the undergraduate level as well as providing all molecular biologists with an easy reference to basic knowledge of the gene. It is extremely well illustrated with a very useful index. A must for all those in molecular biology.

John Jackson, Glen Osmond

Maluszynski, M. (ed.): Current Options for Cereal Improvement – Doubled Haploids, Mutants and Heterosis. Dordrecht: Kluwer 1989. 214 pp. Hard bound $ 53.50.

This book contains papers presented at the First FAO/IAEA research coordination meeting "Use of Induced Mutations in Connection with Haploids and Heterosis in Cereals" held in December 1986 at Guelph, Ontario, Canada. The 20 papers included in this book are described as project reports, invited papers, and short communications.

From the conference name and book title, three distinct areas (induced mutations, doubled haploids, heterosis) in cereal improvement and their interrelationships are covered in this collection of papers. The articles differ widely in their treatment of these topics. A limited number of articles are written in a general review format with an extensive literature review, an interpretation of recent research results, and recommendations

for future research directions. Most of the articles are written as project reports and, as such, contain recent or, in some cases, not so recent research results of specific programs. A small number of articles are written by scientists in commercial firms and discuss the problems, potential, and monetary costs of exploiting the various double haploid techniques in cereal cultivar improvement. The articles also differ widely in their format, typing, and general uniformity of presentation. In the foreword, the editor indicated that instructions to prepare the camera-ready manuscripts were given to each author. Apparently, the instructions were not always followed, and the time lag between the meeting (1986) and the book publication (1989) was becoming excessive. These problems are obvious in some articles by the absence of interpreting and citing the most recent literature available in this rapidly expanding field of science.

In my opinion, this book contains much valuable information. However, because of its limitations, the treatment is very uneven. As a result, this book can only be considered as a general reference and not as an exhaustive analysis of the current level of research accomplishments in cereal research.

P. L. Pfahler, Gainesville

Namkoong, G.; Kang, H. C., Brouard, J. S. (eds.): Tree Breeding: Principles and Strategies. *Monographs on Theoretical and Applied Genetics, 11.* Heidelberg Berlin New York: Springer 1988. 177 pp., 28 figs. Hard bound DM 128.00.

As the title suggests, this book is primarily concerned with the breeding and domestication of trees. Although directed at the forest tree breeder, there are many long-term population management concepts developed in the text that can be readily applied to other crops. This work presents a fresh view of many aspects of quantitative genetics as it relates to tree breeding. The development of basic statistical genetics concepts is done extremely well and should permit junior graduate students to benefit significantly. However, many of the ideas and thoughts presented are such that there is something even for the most advanced practitioner.

The book is organized into eight chapters and covers a wide range of concepts in population management. Topics covered include natural and artifical selection, definition of gene effects, concepts in recurrent selection, recurrent selection systems, selection techniques, environmental effects, present and future breeding problems, and provenance testing and conservation. Theoretical sections are developed only where they provide further insights to a problem. For those who are not mathematically inclined, these sections are developed in an easy to understand manner. I like the way the authors develop the concept of effective population size and, especially, how they carried this idea throughout the sections on breeding and selection. Because this book is about management of populations, it was interesting to see how the authors have applied both population genetics and quantitative genetics theory to this task.

I have no reservations in giving this book my highest recommendation. Technically, it is well done and presents some conceptually interesting and challenging ideas in population management. It will likely be of greatest specific use in graduate-level forest genetics courses. However, it is the type of work that many agricultural crop breeders and community-level ecologists would also find valuable.

W. M. Cheliak, Chalk River

Becker, P. E. (ed.): Zur Geschichte der Rassenhygiene. *Wege ins Dritte Reich.* Stuttgart New York: Thieme 1988. 403 pp., 7 figs., 3 tabs. Soft bound DM 80,–.

This interesting book deals with the history of eugenics in Germany. Eugenics took the name of Rassenhygiene from a book of that name published in 1895 by Ploetz. The Rassenhygiene movement became associated with the mystical concepts of race, Nordic superiority, and the fear that the human race would degenerate. Some representatives of this movement became associated with a dangerous type of sociopolitical prejudice: anti-semitism.

In this book the author illustrates the role of German human geneticists in the propaganda for the racial hygiene and Nazi philosophy by describing the life, the scientific work, thinking, and philosophy of some representatives of racial hygiene: W. Schallmayer, A. Ploetz, F. Lenz, W. Hentschel, C. F. v. Ehrenfels, and J. L. v. Liebenfels. For a better understanding the original papers are cited in this book, and the author has characterized the contemporary situation in society, politics and philosophy. As a result, this book is extremely interesting and exciting. Young scientists and physicians who are at work in the field of genetics, both human and medical genetics, should read such books on the history and scientific conditions that were the preconditions for the most macabre and sorrowful chapters in the history of man's inhumanity to man in the name of pseudo-scientific nationalism. This book helps provide answers to the question "how was this possible?"

F. H. Herrmanm, Greifswald

Gregorius, H.-R. (ed.): Characterization and Analysis of Mating Systems. Ekopan 1989. 158 pp., 7 figs., 2 tabs. DM 37,50.

Mating systems are currently an important topic of research both for animal and plant evolutionists. Their evolution is of interest, as well as their immediate population genetic consequences. The forest geneticist group from Göttingen has made important experimental findings with regard to the reproductive patterns of Scots pine, notably on the importance of sexual asymmetry and fertility selection. Simultaneously, the group has developed theoretical views on population genetics of mating systems. These theoretical aspects are summarized in this book by H.-R. Gregorius.

In a book with this title one would expect to find a broad review of previous work on this topic, especially as the back-cover states that previous approaches of fitting data to specific models have produced considerable confusion and disagreement. However, this book, despite its general title, is no review on what is known about mating systems and their analysis in general. In the preliminary remarks the author states that he has decided to "refrain to a possibly unusual extent from a representative citation". This is an unfortunate decision.

The author starts by introducing a set of terminology and definitions, mostly different from these established in earlier literature. The need for all these new concepts is not clearly eastablished. Much of the theory deals with probabilities of mating between different types (mating references). Then topics such as sexual selection, self-fertilization, evolution of sexual systems, and incompatibility are discussed. The discussion is quite technical, with heavy emphasis on algebra. The author fails to make a clear distinction between new contributions and repetition of earlier results.

It is hard to understand for whom this book is meant. Experimentalists will not gain many new research ideas or methods. Furthermore, the book contains hardly any mention of actual biological data, as evidenced by the low number of tables and figures. Beginning students in the area need a far less technical, more general introduction. Any reader would wish that the author would relate his theory to the extensive earlier work in the field. It is in fact peculiar to be reading a book on these topics without reference to the work of, e.g., Allard, Brown, B. and D. Charlesworth, Lande, Lloyd or Ritland, to mention just a few important contributors.

We still need a book that would review the field of evolution of reproductive systems.

Outi Muona, Oulu and PMA Tigerstedt, Helsinki

Bradbeck, U.; Bordier, C. (eds.). Post-translational Modification of Proteins by lipids – A laboratory Manual. Berlin Heidelberg New York: Springer 1988. I-IX, 146 pp., 17 tabs. Soft bound DM 59,00.

A laboratory manual on the anchoring to membranes of proteins by post-translational modification is a very timely publication. There has been a growing interest in this field over recent years, so that when a workshop was organized in Switzerland in September, 1987, devoted to the anchoring of membrane proteins by covalent attachment of fatty acids and glycophospholipids, participants were provided with a collection of methods currently in use. That collection in updated version, forms the basis of this book. It is designed to give researchers easy and practical access to the investigation of these proteins and modes of attachment to membranes. This manual has 22 chapters, each dealing with some practical aspect of this subject. Thus, the first few chapters deal with the nature of the "anchor" holding the protein to the membrane – fatty acid labelling seems to be the method of choice and is well described in the first chapter. Other "metabolic labels" can also be used, as demonstrated in the identification of the glycolipid anchor of alkaline phosphatase. The amine components of the anchor can be identified by reductive radiomethylation.

The use of non-ionic detergents in phase separation of glycolipid-anchored membrane proteins is described, and a particularly useful method describes how phosphatidylinositol-specific phospholipase C can be used, together with phase partitioning, to obtain the hydrophilic form of the membrane protein. The purification of phospholipase C from *Bacillus cereus* is described, and is essential for the successful application of the method. A host of other methods is described, including identification of fatty acid-acylated proteins by radiolabelling-chemical analysis of fatty acids and the application of identification and characterization methods for both hydrophillic and hydrophobic proteins in various tissues (animal, bacterial, plant, etc.) and in subcellular organelles. The complex subject of radioactive labelling isolation and characterization of oligosaccharides which are linked to both lipid and protein is well covered in an extensive chapter.

All in all, a very useful laboratory manual for those who deal with membrane-anchored proteins. Each of the chapters gives key references, while the book itself has a comprehensive index.

J. F. Jackson, Glen Osmond

van Holde, K. E. (ed.): Chromatin (Springer Series in Molecular Biology), 1st edn. Berlin Heidelberg New York: Springer 1988. XII, 497 pp., 164 figs (138 ill.), 56 tabs. Hard bound DM 228,00.

After reading Ken van Holde's extensive survey of chromatin research one has the feeling of being really informed on the composition, structure and function of the eukaryotic genetic material. *Chromatin* may be seen as one of the first comprehensive overviews on this topic, and it covers many aspects in a detailed, highly understandable way.

As stated by the author, he did not realize how gigantic his task was. He started in 1980 and expected to have it finished in two years. However, due to the broadness of the subject and the intense, revealing research going on, new developments emerged, and a revision of nearly all chapters had to be undertaken in the years thereafter. Nevertheless, the author has succeeded in composing a fairly current contribution to this field of research (based on a selective compilation of about 2,000 references) that is interesting for scientists from several disciplines.

The volume starts (Ch. 1) with a nice historical description of the first hundred years of chromatin research, which clearly defined DNA as the genetic material that was associated with a set of structural proteins.

In a journalistic fashion he describes the studies which have led to the development of the nucleosome model for chromatin structure (Ch. 2). This inside information is a valuable basis for reading the more recent and detailed information in the following chapters.

A critical survey of the information available on the chemical constituents of chromatin, DNA, histones and non-histone chromosomal proteins is given in Ch. 3–5: it is an excellent background description, necessary for an understanding of the functional structure of chromatin and its relation to transcription and replication. In Ch. 6 the nucleosome and the ubiquituous component of all nucleosomes, the core particle, are extensively discussed. Detailed information on the organization of the nucleoprotein complex, based on biochemical, physical and molecular analysis of the interaction of DNA and histones, finally makes it clear how chromatin can exist at several levels of stability. The higher order structure "How are the repeating units of chromatin arranged to form the complex entities that are chromosomes" is discussed (Ch. 7) in terms of linear organization of the nucleosomes and spatial arrangement of the chromosome fibers. The existing models are critically evaluated.

Finally, chromatin structure is related to its function in the process of transcription (Ch. 8) and replication (Ch. 9). These aspects are still being studied very extensively, and new results are still coming in. For this reason the author has made the choice to review in detail only some of the active gene structures. Much of the presented data is taken into account to support his tentative model for gene activation ("an educated guess").

The final chapter (Ch. 9) deals primarily with associated questions on the different but interrelating stages in the replication process (DNA replication, histone synthesis, nucleosome assembly and histone distribution, nucleosome segregation and maturation of nascent chromatin). Since many of the chromatin replication aspects are still largely unexplored (many contradictions and controverses exist), this section is far from complete. Nevertheless, it is a logical analysis of the eukaryotic replication process.

In summary, this volume contains a valuable compilation of the chromatin literature up to about 1986. Van Holde has critically analyzed many aspects, and at several points he is willing to speculate on the interpretation of the data and the models. For those who are working on this topic it contains a large amount of condensed, well-documented information. For those who would like to get a good background on the structure and function of chromatin and DNA-protein interactions, this volume is a "must". It should be present in every biology library.

H. W. J. van den Broek, Wageningen

Oxender, D. L. (ed.): Protein Structure, Folding, and Design 2. *UCLA Symposia on Molecular and Cellular Biology, New Series, Vol. 69.* New York: Alan R. Liss 1987. 550 pp., 139 figs., 50 tabs. Hard bound.

Two years after the first UCLA Symposium on Protein Structure Folding and Design was held at Keystone (Colorado) a second one took place, and the present volume of proceedings under review comprises 52 articles and some of the discussion summaries of the contributions presented at this meeting. Successful protein engineering has to be based on detailed structure investigation complemented by structure-function studies. The latter include structure modifications that become accessible by means of recombinant DNA and DNA transformation techniques together with the subsequent study of the structure and function of the changed polypeptides produced; for example, in their interaction with other macromolecules like proteins or DNA. One of the ultimate aims of protein engineering is a directed improvement of protein functions, like the catalytic activities of enzyme proteins, and the partial or complete design

of functionally active new proteins. These different fields of molecular protein research are reflected in the sectional subdivisions of the present volume.

One of the most intensely investigated fields in the transcriptional regulation of gene expression is the interaction of regulatory protein factors with corresponding DNA sequence stretches that are mostly situated outside the coding gene regions. Studies on prokaryotic genes and on phage genes dominate the eight different contributions of Section I which deals with 'Structure and Interactions of DNA-Binding Proteins'. The progress made in 'Protein Structural Analysis' of a variety of proteins from pro- and eukaryotes, including structure prediction and modelling, represents the topics of the eleven contributions of Section II. Four articles of Section III deal with 'Energy Considerations and the Molecular Dynamics of Proteins' whereas seven papers report on structure-function relations in 'Enzyme Catalysis' (Section IV). Section V comprises six reports on studies carried out on 'Protein Folding'. In vitro Mutagenesis (Section VI) represents one of the most powerful tools with which to study the effects of amino acid changes in domains that are known or thought to play an important role in protein functions; for example, the active center of enzymes or contact areas of regulatory proteins interacting with DNA (four contributions). Quite logically, this section on directed changes in the amino acid sequences of proteins is followed by Section VII, which deals with 'Peptide and Protein Design and Synthesis' and includes five articles and one discussion-group summary. Antigene-antibody reactions represent a special field of protein-protein interaction (three contributions in Section VIII), whereas structure-activity relationships in viruses are the subjects of three papers in the last Section (IX).

The contributions of this volume in general do not represent reviews, but are original contributions on special new experimental results which are of primary interest to researchers active in the field of molecular protein research. This volume of the proceedings from the UCLA Symposia on Molecular and Cellular Biology also keeps with the high scientific and technical standard that characterizes the whole series. K. Müntz, Halle

Helentjaris, T.; Burr, B. (eds.): Development and Application of Molecular Markers to Problems in Plant Genetics. *In: Current Communications in Molecular Biology.* Cold Spring Harbor, NY: Cold Spring Harbor Laboratory 1989. XI+165 pp. Soft bound $ 24.00.

This publication is a compilation of 28 non-refereed summaries of reports by invited participants at a November 1988 meeting held at Cold Spring Harbor. The purpose of the meeting was to promote the exchange of technical information, to evaluate molecular marker strategies applied to genetic problems, and give an up-to-date progress report of RFLP development and mapping. Although the title implies a general coverage of molecular markers and the organizers of the meeting wanted to emphasize methods other than restriction fragment length polymorphism (RFLP) markers, the reports center mainly on RFLP markers. The reports did not cover methodology of RFLP development in detail, but helpful pointers are given in solving RFLP methodology problems. The relative merits of random genomic vs. cDNA probes and the utility of using recombinant inbred and backcross inbred lines for high-resolution RFLP mapping were discussed.

Compared to RFLP markers, isozymes are limited by their restricted genetic variability, restricted number of available loci, and poor genomic coverage. Although RFLPs are more expensive and difficult to use, they are the molecular marker of choice. The status of RFLP clone sets and linkage maps was reported for maize, tomatoes, *Brassica,* wheat, barley, lettuce, soybeans, rice, and *Arabidopsis*. It was noted that genomic polymorphism varied among crop species, with tomatoes, wheat, and soybeans having little polymorphism compared to maize.

Several papers discuss the use of RFLP markers and nucleotide sequences in studying systematics, genetic diversity, and evolutionary relationships, and the contribution of those studies to our understanding of genomic structure and evolution. *Arabidopsis* having the smallest genome among angiosperms (700,000 kb) and containing little repetitive DNA was selected for physical genomic mapping using large, overlapping clones and special computer-assisted analytical methods. Over 90% of that genome has been cloned and mapped to 876 contigs. RFLP genetic mapping is also well along with 101 RFLPs mapped. The low amount of repetitive DNA contained in the *Arabidopsis* genome makes it the species of choice for cloning genes using chromosome-walking techniques from closely linked markers.

Eight papers emphasize mapping quantitative trait loci (QTL). Most of the economically important traits that concern the plant breeder are regulated in a complex quantitative manner by two or more genes. Mapping those loci is having an impact on our understanding of quantitative traits and will assist in manipulating those traits by conventional plant breeding. RFLP analyses will also assist in identifying and cloning QTL for future genetic engineering. Use of RFLPs to detect single gene traits can now readily be done in species with well developed RFLP maps. The various statistical analyses used were discussed and examples given. R. L. Smith, Gainesville

Harlow, Ed., Lane, D. (eds.): Antibodies, A laboratory Manual. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory 1988. 726 pp., 49 figs., 63 tabs. Soft bound $ 50.00.

This is one of the most comprehensive reference manuals on immunological methods that I have come across. Although the book focusses mainly on protein antigen, it is an excellent, and in my view, indispensible guide to any scientist working in the field of immunochemistry.

The book starts out by presenting basic principles on the antibody molecule, antibody-antigen interactions and immune response (Ch. 1–4). Although these chapters are, as the authors mention in the preface, rather brief, they are, in my opinion, sufficient for a non-immunologist to obtain an understanding of the fundamental principles of basic immunology. This part is particularly important for such investigators as these, as experimental procedures will only be performed accurately if one understands what is going on! An abundant list of references allows anyone interested in a specific subject discussed in these chapters to further extend his readings.

The theoretical introduction is followed by the more practical section of the book, which is dedicated, to start with, to methods for raising antibodies (Ch. 5). An essential decision one has to make when planning on raising antibodies is whether polyclonal or monoclonal antibodies are required. Often depending on the purity and the quantity of antigen available, one will choose between one or the other alternative. Subsequently, immunization can be planned. In this chapter, ways of immunizing different animal species are discussed. Advantages and disadvantages of the different immunization protocols, depending on the requirement of the antibody needed, are given. Emphasis is placed on methods for purifying antigens, especially protein antigens from bacterial overexpression systems, and for making these antigens, when necessary, more immunogenic. Other methods, like those commonly used to obtain membranes from cells one wants to raise antibodies against, are, as mentioned earlier, not discussed. This is regretful, since many antibodies raised against tumor antigens or virally induced antigens have been obtained by these procedures. Choices of adjuvants, doses of antigens and ways of injection are, on the other hand, dealt with in detail in this chapter.

The next two chapters (Ch. 6 and 7) are dedicated to the production of monoclonal antibodies. Since the publication by Köhler and Milstein in 1975, of their paper on monoclonal antibodies, the literature on the subject has extended so much that it would seem almost impossible to fit this topic within 150 pages. However, the authors have succeeded in this task. Although only the classical way of producing monospecific monoclonal antibodies is discussed, other methodologies for producing monoclonal antibodies, like, for instance, in antigen-directed fusions are also briefly referred to. The authors stress the importance of making a careful plan before starting with the fusion; that is to take into account the time needed from the immunization of the animals to the final expansion and freezing of the desired hybridomas. The early choice for an appropriate screening procedure is especially pointed out. Many screening strategies are discussed. The use of a fluorescence-activated cell sorter is, however, only poorly highlighted. Although the fluorescence-activated cell sorter is expensive, it is a powerful tool for screening hybridomas. The authors should have dedicated more space to this rapidely developing technology. Problems which one could encounter during the culture of hybridomas, like contamination of the cells, and possible ways to resolve them are also well dealt with in these chapters.

The following two chapters (Ch. 8 and 9) discuss ways to store, purify and label polyclonal- or monoclonal antibodies. Purification procedures like ammonium sulfate precipitation, ion-exchange chromatography or immunoaffinity purification of antibodies are reviewed quite clearly. Techniques for labelling antibodies with iodine, enzymes, fluorochromes, or by biosynthesis are also well explained. The use of colloidal gold particles as conjugates for anti-immunoglobulin antibodies, protein A or streptavidin is, however, only briefly referred to. More details about this labelling procedure should have been given as the technique is very important when subcellular localization of an antigen by electron microscopy is required.

Chapters 10–14 deal with different methods for characterizing antigens. The chapter on the staining of isolated cells or cells in tissue sections spoke to me most. This chapter brings together the wide range of protocols used by many laboratories to stain cells. The authors, however, ommited protocols used for electron microscopic studies, and this is a pity as these techniques are now widely used. The chapters on immunoprecipitation, immunoblotting, immunoaffinity purification of antigens and immunoassays are detailed and complete.

The book ends with a chapter on the specific reagents often used in immunochemistry, like protein A and G, and by a series of four extensive appendices on more general subjects, like protein technology or bacterial expression systems.

In conclusion, the book contains protocols for raising, purifying, and labelling antibodies, as well as chapters describing ways of using antibodies to study antigens. The book is further characterized by its many tables and figures, its comments on troubleshooting and its literature references. Except for its binding, which I think is poorly done, this book is certainly worth the investment. F. van Dissel, Utrecht

Falconer, D. S.: Introduction to Quantitative Genetics, 3rd Edn. Essex: Longman 1989. 438 pp. Soft bound£ 15.95.

The new edition of this outstanding book on the basics of quantitative genetics contains very few changes. The major topical addition is a discussion of the impact of mutation on quantitative genetic variation, selection and inbreeding. Professor Falconer has done a commendable job in explaining the theory developed mainly by W. G. Hill and colleagues at Edinburgh. The section on the sampling variance of a realized heritability has been expanded to include a more thorough explanation of the basis of error variance in selection experiments and how to plan selection experiments to realize certain objectives. The last edition was published in 1981. To illustrate the point that the present edition has truly been updated, at least 64 literature citations, which date from 1980 to 1988, have been added. A welcome addition is the inclusion of problems at the end of each chapter with solutions in the back of the book. These problems on quantitative genetics were published previously in a separate paperback edition, but were not always easily available. Students of quantitative genetics will gain considerable insight by solving each of these problems. The book is recommended highly for an advanced undergraduate or beginning graduate course in quantitative genetics. E. J. Eisen, Raleigh

Fundenberg, H. H.; Pink, J. R. L.; Wang, A.-C.; Ferrera, G. B.: Immunogénétique Fondamentale. Paris: Masson 1988. 287 pp. Soft bound. 140 FF.

The book is a French translation of one of the classical textbooks on immunogenetics. It is classical in two senses of the word: it has been used all over the world since the first edition appeared in 1972 and, as its last revision dates from 1984, it does not cover the molecular immunogenetics beyond the antigenic variation at the protein level. This, however, does not make the book less suitable for those students preparing themselves for the medical profession. In its translated form it may be more accessible to French-speaking students than the original English edition and consequently also contribute to their knowledge of this important discipline. J. A. van der Donk, Utrecht

AFRC Institute of Plant Research and John Innes Institute. Catalogue of Germ Plasm Collections 1989. 553 pp. Free of charge upon request to: Cambridge Laboratory – AFRC-IPSR, Cambridge CB2 2JB.

Genetical variation is essential for progress to be made in breeding. Consequently, there is a continuous need of seed collections of the wild relatives of crop plants as well as of the cultivars used in former times. The Institute of Plant Research (ISPR) and the John Innes Institute's (JII) joint Cambridge laboratory have produced an admirable compilation of information and listings concerning the present status of their collections: the AFRC collection of cereals (wheat, barley, oat; with 6,457, 4,400 and 2,391 accessions, respectively); the IPSR collection of wheat and related species, which contains many representatives of all wild *Triticum* and *Aegilops*, including the Watkins collection of 4× and 4× wheats; the JII *Pisum* germ plasm collection consisting of 2,391 entries, which includes not only *Pisum sativum* but also *P. fulvum, abyssinicum, elatius, humile, arvense, thebaicum* and *tibettanicum*, as well as a unique collection of 42 rabbit-eared-rogue mutants, isogenic types and lines, autotetraploids and lines carrying know translocations. The genetic status, country of origin, cultivar name, synonyms, accession number and sowing time are given for most of the specimens. The presentation of this catalogue to the breeding research community is an important service, which is carried out by institutes committed to providing this service both now and in the future. H. F. Linskens, Nijmegen