and the final section on specialized investigations covers amongst other subjects hypertension, lipid metabolism, nutritional assessment, toxicology and therapeutic drug monitoring.

Clinical biochemistry is but a minor subject in the curriculum of the medical student. Yet almost every medical doctor dealing with patients will use clinical biochemistry on a daily base. This brief textbook written for persons with a thorough knowledge on medicine is highly recommended for clinicians, who want to refresh their knowledge and for medical students, who want a brief repetition just prior to their final exams. Most of all, the book is likely to be a helpful source of inspiration for those teaching clinical biochemistry both on pre and postgraduate level.

Ebba Nexø

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**RNA–Protein Interactions**; Edited by K. Nagai and I.W. Mattaj, IRL Press, Oxford, New York, Tokyo, 1995. xviii + 272 pp. £ 29.50. ISBN 0-199-635048

The editors have commissioned chapters on a small number of protein–RNA systems selected for their biological interest and for the insight they yield into how proteins recognize RNA. They include the RNase P complex, aminoacyl–tRNA–synthetase complexes, the rev and tat interactions on HIV RNA, the nuclear proteins complexed with eukaryotic pre-mRNA's, spliceosome complexes, the transcription factor IIIA-5S rRNA complex, an overview of ribosomal protein-RNA interactions and concluding with an in vitro genetics approach to investigating protein-RNA interactions.

Studies of protein–RNA interactions have a long and interesting history going back to the 1960's, and extending into the 1970's, where major protein–RNA complexes including the ribosome and tobacco mosaic virus, and smaller ones including 5S rRNA–protein complexes, the aminoacyl–tRNA ternary complex and the R17 viral RNA–coat-protein interaction were confronted with abandon. These early studies spawned a plethora of methods for examining protein-RNA interactions including the gel-shift method for detecting binding, filter binding assays, immunological purification, various footprinting methods, damage selection procedures, covalent cross-linking methods, and the phylogenetic sequence comparison approach applied to RNA structure which were later avidly (and generally with little credit) adapted for studying protein–DNA complexes. The overwhelming lesson from this period, particularly for the ribosomal protein–RNA complexes, was that protein–RNA interactions were very diverse; isolated RNA binding sites varied considerably in complexity from about 20 nucleotides (the L25 site on 5S rRNA and R17 coat protein) upwards. It was generally inferred from these studies that bulged nucleotides, irregular double helices, helix–loop junctions and unknown tertiary structural features were the crucial motifs for protein recognition; later one could add pseudoknots to this list.

Reading the present book from this perspective one is impressed by the large amount of work that has been done on a variety of systems which seems to emphasize the diversity of protein–RNA interaction mechanisms with the spliceosome systems, in particular, beginning to make even the ribosome look straightforward. Moreover, there are bulged nucleotides, irregular double helices and helix–loop junctions everywhere. There has also been a general improvement in, and extension of, the RNA technology, for example the free radical footprinting methods for examining the accessibility of the RNA backbone in complexes. However, the main new methodological advances, apart from the in vitro genetics approach, have come from examining the RNA binding proteins. With the availability of many new protein gene sequences, the phylogenetic sequence comparison approach has proven particularly useful for identifying putative binding motifs. Binding studies with peptides have also been effective and suitable for NMR studies, and the recently developed (but not mentioned) protein footprinting approach has considerable potential. X-ray crystallographic results on the amino acyl synthetases, rRNA binding protein L1 (not included) and the U1A splicosome protein have also provided important additional insight into protein binding domains.

This is a timely and well presented book covering a broad field that has been previously rather neglected. It outlines a considerable success story for the biochemists and geneticists who have identified the important structural motifs for the NMR spectroscopists and X-ray crystallographers to work on. Its main limitation, the omissions, may partly reflect publication deadlines. However, the α-sarcin interaction with 23S rRNA, which uses a bulged nucleotide in a double helix as a ruler for determining the distance to its cutting site, elongation factor G's attempt to imitate a tRNA structure, and the aminoacyl–tRNA interaction with elongation factor Tu and GTP would all have enhanced the book's interest.

Roger A. Garrett

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**In Vitro Transcription and Translation Protocol. Methods in Molecular Biology, Volume 37**; Edited by Martin J. Tymms, Humana Press, Totowa, 1995. xii + 432 pp. $ 64.50. ISBN 0-896-032884.

This text is an excellent compilation of current methods in transcription and translation investigation protocols. The various chapters are contributed by experts in their field of research, and the entire text is accordingly edited by Dr. Tymms. This volume provides an extensive catalogue of methodologies of in vitro transcription in cell-free systems and translation in extracts from various cells to *Xenopus* oocytes. In addition, specific methods are presented in several chapters that enhance studies of examining DNA expression such as microinjection in mouse oocytes and embryos, in vitro reconstitution studies, and transcriptional activation analysis by CAT assays. In general and with rare exceptions, all the chapters present brief but concise background information and rationale for the methods described. For those who see a more expansive introduction to the methods, an extensive reference list is available which provides key articles to support the presented technical information. In a manner similar to everyday laboratory preparation and experimentation, this volume provides a comprehensive list of supplies along with appropriate suppliers, and detailed description of the procedures in which the experiments are performed. What I found to be most helpful are the notes that are placed appropriately in each section which describes considerations in trouble-shooting special problems that may arise or need to be anticipated. In examining the protocols presented in the chapters of this volume, what is also evident is the effort of the contributors in providing some collective experiences and nuances with performing these methodologies. This point is illustrated in the chapter on 'In Vitro Translation Using Rabbit Reiculocyet Lysate'. The detailed discussion in the notes of the use of the coupled transcription and translation method is not published elsewhere. Moreover, some chapters provide extensive rationale and explicit protocols in an apparent effort to guide investigators who have moved into a new area of research. The chapter on 'Subtraction Hybridization' is an example of this intent where an broad discussion of the protocol, rationale, and also notes on special problems are included which would clearly assist investigators not familiar with these methodologies.