

# The third dimension for biologists

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**Foundations of Structural Biology** by Leonard J Banaszak. Academic Press, 1999 \$59.95 (ISBN: 0-12-077700-2).

Leonard J Banaszak belongs to the early generation of protein X-ray crystallographers. One would therefore have expected him to write an X-ray crystallography textbook. He wrote a completely different book, however, because he worried about the access that biologists have (or fail to have) to protein structures deposited in the Protein Data Bank (PDB; <http://www.rcsb.org>). It is indeed true that some biologists become confused when confronted with the wealth of detail in a protein molecular model. As a consequence they miss not only the beauty of the structure but also the link between structure and function. In my opinion, this handicap is less serious with the younger biologists who easily surf through the internet and, when familiar with Lubert Stryer's famous book, do appreciate three-dimensional structures.

The main emphasis of the book is on the principles of biomolecular structures and how to visualize these structures by computer graphics and stereovision. After a short introductory chapter, the techniques for the structure determination of biomacromolecules are presented in chapter 2 in a very superficial way. As for X-ray crystallography it is just enough to get a feeling for the meaning of the various terms the professionals use in their jargon. Unfortunately, there is no room for anomalous dispersion. When I showed this chapter to a biologist he confessed that he still did not understand what is meant by the phase problem; and I am afraid it was not his fault. The third chapter is the best chapter of the book, certainly for the biologist who seriously wants to study biomacromolecules in three dimensions. This chapter has been devoted to the PDB and explains how to extract and study the entries. The main focus is on the PDB website and detailed instructions are given on how to use this structural database. One should keep in mind that this website is steadily being modified and improved to make it ever more user friendly.

Occasionally, but very seldomly, I come across somebody with glittering eyes who tells me, a crystallographer, that a difference has been found between an X-ray and a nuclear magnetic resonance (NMR) structure of the same protein. In the end this always turns out not to be true. I can recommend these people to read chapter 4, in which the reader is told in great detail that he/she should once-and-for-all forget about this misconception of a difference between the protein structure in the crystal and in solution. Chapters 5–8 on secondary and higher level structures give the same information as many biochemistry textbooks but with more emphasis on the third dimension. Water is an essential part of a crystalline protein structure and this is discussed in chapter 9. In the final chapters 10, 11 and 12, protein and nucleic acid complexes, metal-containing proteins and lipid–protein interactions are described. Again, the reader is encouraged to practice computer graphics and stereovision.

The design of the book is functional with its plastic ring binder. Readers who are used to the colorful pictures of protein molecular models, as published in journals, will be somewhat disappointed in the black and white figures in the book. This does certainly not mean that the figures are less informative. It also helps to keep the price reasonable. Each chapter ends with references to literature for further study as well as with problems to be solved by the reader.

In conclusion, this is neither a book for learning how to determine biomolecular structures nor does it give better biostructural information than the standard biochemistry books. However, it is a solid text for biology students as well as scientists who are seriously interested in observing and studying the three-dimensional structure of biomacromolecules.