



METADATA

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Abstract

The vast majority of known protein and nucleic acid structures –images of which have flooded most biochemistry, cell and molecular biology textbooks– have been produced using the method of X-ray crystallography. Due to the rich mathematical background of the method, most textbooks avoid presenting details of the method, or when they do (for example, in the last chapter of Branden & Tooze's book), the presentation is somewhat fragmented and superficial. As a result, students are left with a rather mystical feeling/perception which could be summarized as follows: "... and all this information about the structure and function of proteins and nucleic acids has come from something called 'crystallography' which is so confusing and difficult that we'd better leave it here". This booklet aims to present the basic principles of protein crystallography,

i.e. the physical meaning of the crystallographic experiment, while carefully avoiding mathematics that biology students may not be familiar with. The only prerequisites of the first chapters of the book are that students have some vague recollections from high school physics and almost nothing else. In the later chapters of the book, a few mathematical topics are mentioned, but this is done so carefully and slowly that a determined biology student will be able to follow through with them. This booklet is not intended to be a textbook on protein crystallography and does not attempt to cover everything from direct methods to solvent flattening and real space averaging. The sole ambition of the book is to remove the mysticism that covers the method and to show simply the essence and physical meaning of the crystallographic experiment.

