

23.X-1 THE LATTICE HYPOTHESIS.
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The story of the lattice hypothesis is an important chapter in the history of the changing concept of the structure of matter. It illustrates the fortunes of atomism, and the gradual classification of material objects into animals, minerals, and vegetables. Only at the end of the 18th century, with the work of Romé de l'Isle, did it become clear that crystal form must be an expression of intrinsic properties. The debate over what these properties might be led from Haüy's constructions to Bravais' enumeration of the fourteen space lattices in 1850. Contemporary scientific and mathematical developments prompted a more general study of regular patterns, which resulted in the enumeration of the two hundred and thirty space groups by Fedorov and Schoenflies about forty years later. But the story was still not over. As late as 1907 Friedel could remark: "I know quite well that today all scientists consulted on this matter would answer, without hesitation, that such an assumption (the existence of crystal lattices) is actually useless and wanders from the domain of science." Thus von Laue's discovery of the diffraction of x-rays by crystals in 1912 marked not only the beginning of modern crystallography but also the triumphant conclusion of a long and difficult struggle to establish the hypothesis his experiment was designed to test.

23.X-2 X-RAY CRYSTALLOGRAPHY IN THE 1930'S: A TRIBUTE TO A. L. PATTERSON ON THE FIFTIETH ANNIVERSARY OF THE PATTERSON FUNCTION. By Jenny P. Glusker, The Institute for Cancer Research, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, Pennsylvania 19111, U.S.A.

The first X-ray diffraction experiment was done in 1912 and the structures of several simple compounds were determined, often with much insight into methods of structure solution. But by the early 1930's, while it was demonstrated that even crystalline proteins could give excellent diffraction patterns, it was still not possible to obtain structural information from diffraction patterns of even very simple compounds. One breakthrough came with the use of isomorphous replacement methods to the structures of alums by Cork in 1927, work that was later clarified by Lipson and Beevers in 1935. But the major advance came from A. L. Patterson in 1934; he showed that the Fourier series with the squares of the structure amplitudes as coefficients and all phases zero gave a map that represented all possible interatomic vectors in the structure. This step will be described in historical detail together with a biographical sketch of Lindo Patterson. His contribution will be honored at this Symposium, held 50 years after the publication of the paper on the Patterson function in 1934; from that time on structure solution was greatly simplified. While small structures are now generally solved by "direct methods," the macromolecular crystallographer still relies on the Patterson function and the method of isomorphous replacement to determine crystal structures.

23.X-3 THE GROWTH PERIOD OF THE 1950s. By D. Sayre, IBM Research Center, Yorktown Heights, NY 10598, USA.

The development of crystallography is a continuous process, but there are periods of exceptional growth as well. Three in particular occurred in the early 1910s, 1930s, and 1950s, and another may be occurring now. This talk will touch briefly on each of these, but will be devoted principally to the 1950s.

23.X-4 THE CRYSTALLOGRAPHY OF THE PROTEINS
HISTORICAL ASPECTS OF PROTEIN STRUCTURE
By Robert Olby, Reader in History of Science,
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It was in the 1950s that protein structure became a major field of interdisciplinary research. This followed the overthrow of the old crystalline-amorphous distinction and the critique of the conception of pseudo-high-molecular aggregates. As a result fibrous, as well as globular proteins could be studied as macromolecules by the techniques of structural crystallography. Attempts to achieve a unified structural picture of globular and fibrous proteins also date from this period. It is argued that this "1950s synthesis" sought not only to accommodate the data on the physiology and chemistry of proteins, but also to establish amino acid sequences in support of the conception of proteins as discrete macromolecular species rather than as collections of variable chain length molecules with only mean molecular weights.

The features of this 1950s synthesis are analyzed in terms of the application to the proteins of crystallographic conceptions deriving from the study of small molecules. The extent to which these features have been incorporated in or rejected from our modern view of protein structure is discussed. Some conclusions are drawn for the cumulative model of scientific progress.