RESULTS ON THE APPLICATION OF DIRECT METHODS TO PROTEIN CRYSTALLGRAPHY AND ELECTRON MICROSCOPY

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Direct Phasing of OAS Data from A Small Protein

Multiple isomorphousreplacement is now dominating the structure analysis of proteins with no structural precedent. It may occur that the derivatives are not isomorphous with the native protein. In this case multi-wavelength anomalous scattering (MAS) can in principle be used, if there are some suitable heavy atoms in the native protein or its non-isomorphous derivative. However MAS technique suffers from the difficulty of collecting and scaling data at different wavelengths accurately. OAS technique does not have this difficulty but it leads to the problem of phase ambiguity. A direct method has been proposed to solve this problem [Fan et al. (1984). Acta Cryst. A40, 489-495; 495-498.]. The method has been tested with the Hg-derivative of a known protein, avian pancreatic polypeptide [Glover et al. (1985). Adv. Biophys. 20, 1-12.]. It resulted in an interpretable Fourier map. A part of which together with the true structure model is shown in Fig. 1.

Resolution Enhancement of An Electron Micrograph

The high resolution electron micrograph of chlorinated copper phthalocyanine (Fig. 2a) [Uyeda et al. (1978-1979). Chem. Scripta 14, 47.] though provides useful structural information, it is not able to resolve individual atoms. On the other hand the corresponding electron diffraction pattern offers much higher resolution but the phase problem has been proved difficult to solve by traditional direct methods. A phase extension technique with starting phases obtained from the electron micrograph at 2A resolution has been used to derive the phases for reflections between $2A^{-1}$ and $1A^{-1}$ on the diffraction pattern. This led to an image (Fig. 2b) much closer to the true structure model (Fig. 2c).

Direct Methods of Solving Crystal Stuctures
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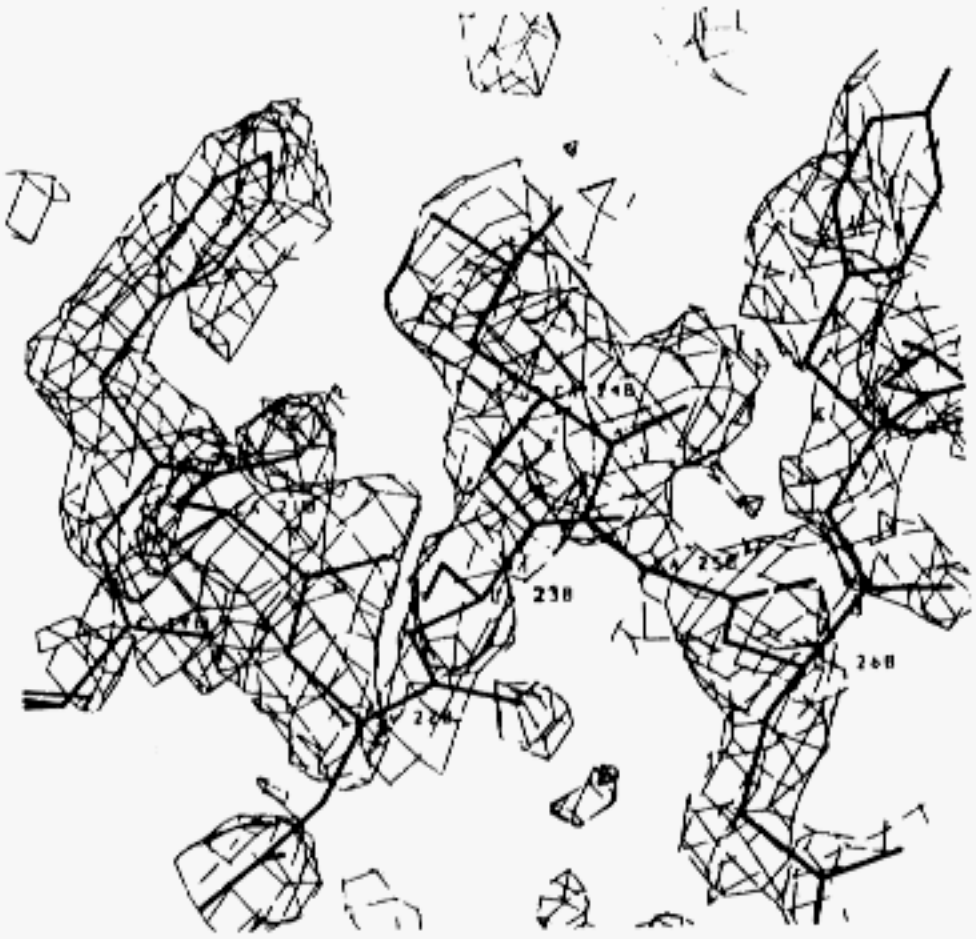

Fig. 1

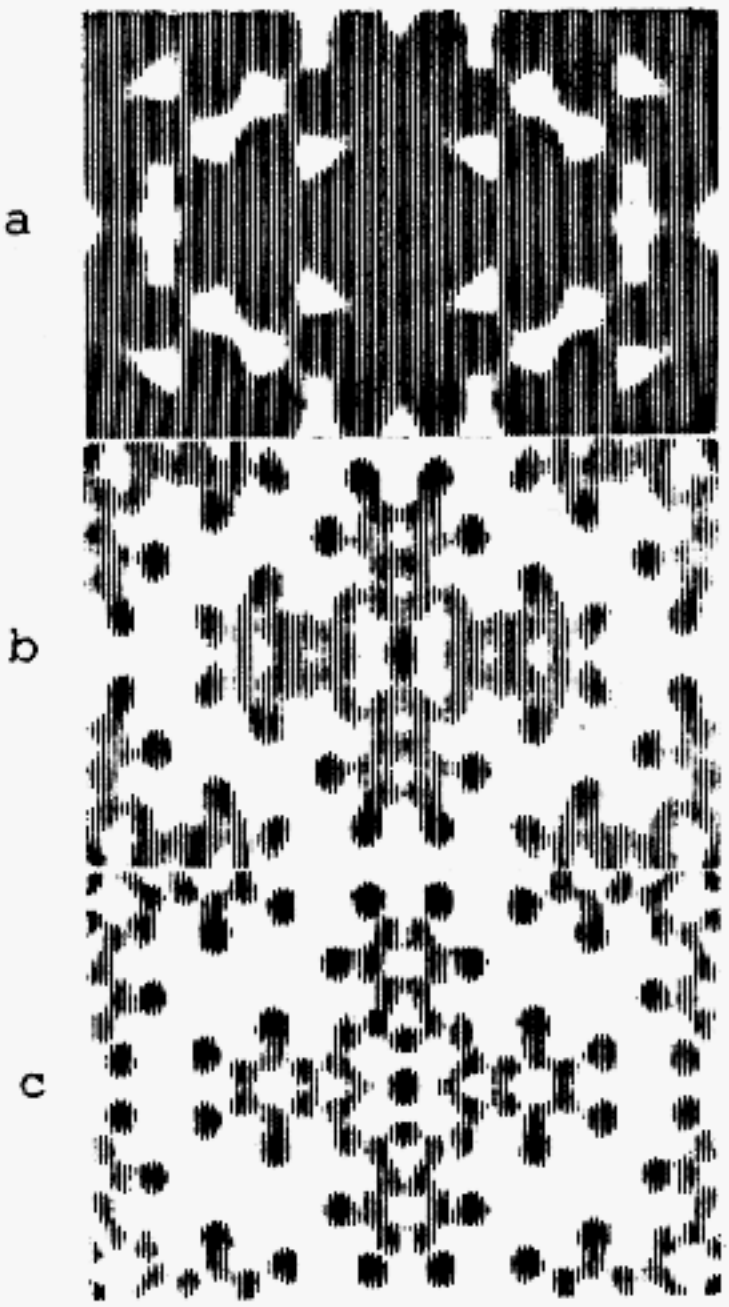

Fig. 2