02. X–1 STRUCTURE OF BACTERIORHODOPSIN.
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Two structures for bacteriorhodopsin have been determined to resolutions of 6-7 Å. One is from native (p3) purple membrane as isolated from Halobacterium halobium (Blaurock and Stoeckenius, 1971). The other is an in vitro form produced using Triton X-100 and DTAC. It is orthorhombic ($p22_12_1$) with a totally different packing of the molecules (Michel et al., 1980).

In both structures, seven rod-shaped densities stretch from one side of the membrane to the other having roughly the same length as the thickness of lipid bilayer. The rods are at angles of from 3° to 23° to the perpendicular to the membrane. Most of the polypeptide in these rods is probably α-helical.

Many other experiments on the structure have been tried to determine which part of the structure is the cytoplasmic surface, to find where the retinal is, and to try to label different parts of the structure with heavy atoms. However, the main work being pursued at the moment is to try to solve the structure at 3 Å resolution. For this model building (using standard α-helices) and molecular averaging have given some success using the 3 Å intensity data from the two crystal forms. However, the maps have not been good enough to interpret. Further progress depends on two further methods currently being tried. One is heavy atom derivatives followed by isomorphous replacement. The other is high resolution imaging. Both of these methods and where we have reached will be discussed.

References
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02. X–2 STRUCTURAL STUDIES ON A TRANSMEMBRANE CHANNEL, MATRIX PORIN FROM E.coli. By
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Matrix porin, an integral membrane protein from the outer membrane of E.coli, is being studied by high resolution X-ray crystallography. Large, single crystals of matrix porin (space group $P4_2$, a=b=154.9 Å, c =172.4 Å) have been grown from detergent-solubilized protein in the presence of polyethylene glycol and NaCl. At room temperature, a 4.0 Å native data set has been collected on film at the synchrotron facility of the EMBL Outstation in Hamburg. After processing, merging of film data yielded 9.5% on F for 33,742 reflections. A high resolution data set (~2.8 Å) has been collected at -15°C. These data are being evaluated.

From earlier X-ray results it was determined that there are two trimers in the $P4_2$ asymmetric unit. The direct diffraction data display evidence for 2-fold non-crystallographic symmetry in the hkO plane. This is supported by rotation function analyses. We have tentatively located the molecular 3-fold axes of the two trimers. The diffraction data also display interesting characteristics suggesting the existence of protein-bound, quasi-ordered detergent in the crystal. These results as well as the current status of the X-ray project will be discussed.

02. X–3 CRYSTALLIZATION OF MEMBRANE PROTEINS AND STRUCTURE OF PHOTOSYNTHETIC REACTION CENTRES. By
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Several integral membrane proteins like bacteriorhodopsin, photosynthetic reaction centres and light harvesting complexes could be crystallized from detergent containing solutions by salt precipitation. Most likely the membrane proteins are crystallized with detergents bound to their hydrophobic surface domains. The detergents used must be small, and in several cases small amphiphilic molecules like heptane-1,2,3-triol have to be added to obtain crystals . The best of the crystals are suited for high-resolution X-ray crystallography.

Crystals of the photosynthetic reaction centre from Rhodopseudomonas viridis diffract X-rays to beyond 2.5 A resolution. The reaction centres, which are a complex of four different proteins, 6 bacteriochlorophyll- and bacteriopheophytin-, and 2 quinone molecules, are still functionally active in the crystals: They perform light-driven electron transport. Three different heavy atom derivatives were obtained by conventional soaking of the crystals. The M.I.R. phases were improved by solvent flattening and phase combination. An electron density map at 3 A resolution could be calculated. This electron density map is interpreted at present. The secondary structure of the proteins is mainly helical. Atomic models for the bacteriochlorophyll- and bacteriopheophytin molecules have already been built.

02. X–4 DYNAMICS OF PROTEIN FOLDING. By
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Recent progress in the analysis of the architecture of proteins has shown that with certain exceptions the large number of different structures now known can be classified into a relatively small number of categories (alpha-helical proteins, beta-sheet proteins and mixed alpha-helical, beta-sheet proteins). This suggests that the dynamics of protein folding may not be as complicated and many faceted as implied by elementary statistical considerations based on the number of possible configurations of a polypeptide chain. A proposed mechanism for protein folding, the diffusion-collision model, takes account of the secondary structural elements and makes use of their properties to provide estimates of the kinetic parameters involved in the folding process. The diffusion-collision model is a mechanism into which it has been possible to introduce specific physical magnitudes to estimate the kinetic parameters. The diffusion-collision model is discussed and elaborated with regard to a) the nature of the elementary step of folding, and b) the combination of such steps to yield the overall folding kinetics. The model calculations for the elementary step are compared to simplified molecular dynamics simulations of a twenty-four residue polypeptide chain consisting of two eight-residue alpha-helical segments connected

by an eight-residue coil segment. The model is used to predict the folding kinetics of apomyoglobin and of the lambda-phage repressor operator-binding domain.

02. X–6 SEQUENCE DEPENDENT OLIGONUCLEOTIDE CONFORMATION FROM SINGLE CRYSTAL STUDIES. **Olga Kennard, University Chemical Laboratory, Lensfield Road Cambridge CB2 1EW, U.K.**

The double helical structure of DNA, postulated by Watson and Crick some 30 years ago, is a fundamental concept of modern molecular biology. The role of the base sequence for the transmission of genetic infomation, the now familiar triplet code, was recognised from the outset. Subsequent biochemical and genetic experiments indicated that the primary base sequence may, in addition, play a part in the control of gene expression and in DNA cleavage and repair. Enzymes involved in these events recognise and interact with specific base sequence and thus with specific, three-dimensional structures.

The availability, in the late 1970's, of synthetic deoxyoligonucleotides, opened up the possibility of examining the correlation between local DNA structure and base sequence through single crystal X-ray analysis. The paper will review the evidence so far available for such correlations in the three major structural types of DNA. The role of water in stabilising the global conformations will also be discussed.

The following references give details of the main areas covered by the review : C.R. Calladine. J. Mol. Biol., 161, 343, 1982; R.E. Dickerson. Scientific American, 249, 87, 1983; R.E. Dickerson, H.R. Drew, B.N. Conner, R.M. Wing, A.V. Fratini, M.L. Kopka. Science, 126, 475, 1982; A. Rich, G.J. Quigley, A.H.J. Wang. Biomolecular Stereodynamics Vol. 1 ed. R.H. Sarma. Adenine Press 1981; Z. Shakked, D. Rabinovich, O. Kennard, W.B.T. Cruse, S.A. Salisbury & M.A. Viswamitra, J. Mol. Biol., 161, 185, 1983; A.H.J. Wang, G.J. Quigley, F.H. Kolpak, G. van der Marel, J.H. van Boom & A. Rich, Science, 211, 171, 1981

02. X–5 BASE SEQUENCE EFFECTS IN THE STRUCTURES OF OLIGONUCLEOTIDES By Struther Arnott, R. Chandrasekaran, R. C. Millane, R.-G. He, L. C. Puigjaner, and J. K. Walker, Department of Biological Sciences, Purdue University, West Lafayette, Indiana 47907, USA.

It is of no little interest to determine whether or not the nature of the base-sequences within a nucleic acid duplex are indicated on the surface by features of the sugar-phosphate backbone. If they are, then regulatory proteins and enzymes which have to bind to specific DNA sequences might more easily recognize their host sequences. Detailed X-ray analyses of the structures of various allomorphs of poly d(A)·poly d(T), poly d(AT)·poly d(AT), poly d(IC)·poly d(IC), poly d(GC)·poly d(GC) and poly d(ACC)·poly d(GGT) in uniaxially oriented, polycrystalline fibers show that nucleotides 5'NpN 3' where 5'N is a purine and N 3' a pyrimidine have either *t, t* or *t, g-* conformations at C3'-O3', O3'-P which lead to similar orientations of phosphate groups. On the other hand, 5'PypPu 3' nucleotides commonly have *g-, t* conformations at C3'-O3', O3'-P which are associated with a markedly different orientation of the phosphate groups. It would be difficult to devise a more effective but parsimonious sequence discriminator than the way in which the two changed oxygen functions were presented on the surface of a DNA duplex.

In the case of poly d(A)·poly d(T), the chemical distinctiveness of the two antiparallel strands is amplified by the fact that the furanose rings on each strand are puckered differently -- C2'-*endo* in poly d(T) and C3'-*endo* in poly d(A). Such heteronomous duplexes have unusually pronounced directional properties.

02. X–7 THE STRUCTURE AND FUNCTION OF MEMBRANE GLYCOPROTEINS. By D. C. Wiley, Department of Biochemistry and Molecular Biology, Harvard University, Cambridge, Mass., USA.

Three membrane glycoproteins with diverse cell surface activities are being studied by high resolution protein X-ray crystallography: the influenza virus haemagglutinin, the variable surface glycoprotein from trypanosomes (sleeping sickness) and the major histocompatibility antigen from human cells (transplantation rejection).

The influenza virus haemagglutinin, HA, is the major virus membrane protein (197,000 dalton trimer) and has three biological activities: (1) the HA binds the virus to sialic acid containing cellular receptors; (2) the HA mediates a virus-cell membrane fusion event; (3) the HA undergoes antigenic variation, which is responsible for recurrent human epidemics of the disease. The crystal structure of the HA ($P4_1$, a=b= 163.2 Å, c=177.4 Å) has been solved to 3 Å resolution by single isomorphous replacement and non-crystallographic phase averaging (Wilson et al., Nature (1981), 289, 366). Biochemical results have been interpreted in terms of the crystal structure model, which allows a number of conclusions about the mechanisms of the HA's activities (Wiley et al., Nature (1981), 289, 373; Skehel et al., PNAS (1982), 79, 968; Rogers et al., Nature (1983), 304, 76).

The variable surface glycoprotein (VSG) of trypanosomes forms a protective coat which the parasite changes every few days by generating an antigenically unrelated VSG and thus escaping neutralization by the host immune system. The crystal structure ($P4_12_12$ a=b=96.3 Å, c=111.1 Å) of the N-terminal variable domain (43,000 daltons has been solved to 5.5 Å resolution by an