

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 information, 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<sub>1</sub>, 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<sub>1</sub>2<sub>1</sub>2 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