02. STRUCTURAL MOLECULAR BIOLOGY


Current understanding of the structure of antibody combining sites is based on the three-dimensional structures of the Fab fragments of myeloma proteins and their complexes with small molecules. No crystallographic information is available for the interaction of an antibody with a macromolecular antigen, however, even though such interactions are more extensive and potentially more important for the elucidation of the physiological properties of antibodies. We have used the lysozyme fusion techniques of Köhler & Milstein to obtain hybrid cell lines secreting monoclonal anti-egghatching lysozyme antibodies (HEL). Complexes between the Fab fragments of several of these antibodies and HEL were prepared and subjected to crystallization trials. One of these complexes (Fab D13-HEL) was crystallized from PEG solutions in space group P21 with a = 55.7 b = 143.5 c = 49.1 β = 120°. Rotation photographs show reflections to at least 2.0 Å resolution using synchrotron radiation (Mariuzza et al. 1983 J. Mol. Biol. 170, 1055–1068).

Diffractometer data have been collected to 6 Å resolution for a native crystal and three derivatives. The derivatives were solved from isomorphous difference Patterson maps, and refined using the Flp method. Phs calculation gave a mean figure of merit of 0.75. The electron density map clearly shows the molecular boundaries, and the immunoglobulin domains are recognizable. There is no clear boundary between the densities corresponding to the Fab fragment and lysozyme, indicating a close intermolecular interaction.

02.5–2 STRUCTURE OF DEOXYCYTIDINE 5’-PHOSPHATE 5’-DINUCLEOTIDE, 12M.0 By J. Pandit, T.P. Sheshadri and M.A. Visweswara, Department of Physics and IOM Centre on Genetics and Cell Biology, Indian Institute of Science, Bengaluru 560 012, India.

Interactions with cations and water molecules are expected to play an important role in influencing nucleotide conformations. We report here the structure of a highly hydrated form of 5’-dCMP. A striking feature of the structure is that the two independent molecules in the crystal have identical environments but totally different nucleotide conformations. (See Figure below)

Crystal data are: P1, a = 7.306(2), b = 10.055(2), c = 16.570(2) Å α = 100.95(1), β = 93.07(1), γ = 90.89(2), Z = 2, V = 0.055. Molecular conformations are Molecule A: anti (x = 231.7°, y = 354°, gauche-trans), Molecule B: anti (x = 195.3°, c3’-exo, gauche-trans)

A pseudo-inversion symmetry is present in the crystal, which applies to all the solvent and molecular atoms except for the atoms on the furanose ring. The interactions between the nucleotide and water/sodium ions are exactly identical in the two molecules as a consequence of this symmetry. The presence of such a partial 2D plane of symmetry relationship between the two molecules suggests the interesting possibility that these molecules could serve as the monomer units for generating left and right handed RNA structures.

Another noteworthy feature of the molecular interactions is the pronounced stacking of the cytosine rings (see Figure below) a feature also present in the orthorhombic crystal form of the same nucleotide (dCMP, Na, H2O).


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MOLECULE A

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