03-Crystallography of Biological Macromolecules

The geometry of Cu-L80 could be described as trigonal bipyramidal with one vacancy. The Cu(II) ion is located in the plane between the three strongly bound protein ligands S2N. The oxygen of DMF is at 3.2 Å distance from the copper. This arrangement resembles blue copper proteins with Type I metal sites. The visible spectrum and EPR characteristics are similar although the strongly bound ligand set differs compared to azurin or plastocyanin, which is N2S, and the weakly interacting ligand is either a carboxyl oxygen or a methionine sulfur.

PS-03.05.41 THE STRUCTURE OF PHOSPHORIBOSYLMUTAMINO-IMIDAZOLESUCCINICCARBOXYLAMIDE SYNTHASE FROM THE YEAST SACHAROMYCES CEREVISIAE AT 3 Å RESOLUTION. By V.M. Levichkov, A.I. Grebenko, V.V. Byrenin, N.P. Neleik-Adamyan, Institute of Crystallography Academy of Sciences of Russia, Leninsky pr. 59, Moscow 117333, Russia.

Phosphoribosylamidotransferase (EC 5.3.1.6) from the yeast Saccharomyces cerevisiae is a monomeric enzyme catalyzing one step in the purine biosynthesis pathway. Crystals of the enzyme which diffract to at least 2.0 Å were obtained by the vapor diffusion method (Grebenko, A.I. et al. J. Mol. Biol., 1986, 224, 258-299). Crystals belong to the space group P212121, with unit cell dimensions a = 62.3 Å, b = 63.5 Å and c = 80.9 Å, one molecule in the asymmetric unit. The crystal diffraction data at 2.5 Å resolution and four derivatives data at 3.0 Å resolution from crystals soaked in 5 mM KAu[Cl4]·2.5 mM Cu(NO3)2·1.5 mM Na2Pd(NO3)4 and 2M mercaptoethanol were collected using a SYNTEX-P2 diffractometer. The initial phases to 3.0 Å resolution were derived from the multiple isomorphous replacement method with program complex BLANK (Vagin, A.A. unpublished). Several cycles of solvent flattening with negative density truncation were applied to produce a map in which 76% of the 305 residues chain could be traced. A partial model was built using FRODO. Refinement of the partial structure by Hendrickson-Konkett method is in progress. We intend to present our most current model of the phosphoribosylamidotransferase at the conference.

03.06 – Protein–Saccharide Interaction

MS-03.06.01 ATOMIC INTERACTIONS BETWEEN CARBOHYDRATES AND PROTEINS. By Florante A. Quiocio, Howard Hughes Medical Institute and Baylor College of Medicine, Houston, TX 77030.

In recent years our laboratory has been engaged in the structural studies of five proteins that bind carbohydrates — three bacterial periplasmic receptors for the active transport of and chemotaxis toward carbohydrates (mono-oligosaccharides and linear and cyclic oligosaccharides), one antibody against bacterial cell surface polysaccharide O-antigen determinant and a soluble reductase. While high resolution x-ray crystallography is our primary experimental approach in these studies, we have also utilized site-directed mutagenesis, rapid kinetics, calorimetry, low angle x-ray scattering, and theoretical techniques. Common recurring features of the atomic interactions between proteins and carbohydrates will be presented in light of the crystallographic analysis of other proteins. Time permitting, other features of protein-carbohydrate interactions obtained by way of the other techniques will also be presented.

MS-03.06.02 CONCANAVALIN A AND ITS INTERACTION WITH SACCHARIDES

S.I. Harroj1, J.H. Naisin1, C. Emmrich1, J. Habib1, S. Weigert1, A.J. Katz (Gilboa2), J. Yariv3 & J.R. Hilliswell4.

1. Department of Chemistry, University of Manchester, Manchester, M13 9PL, UK.
2. Department of Structural Biology, The Weizmann Institute of Science, Rehovot, Israel.
3. Laboratoire de Cristallographie, URA 144, CNRS, University of Bordeaux I, 33405 Talence, France.

The crystal structures of the complexes of concanavalin A with methyl α-D-mannopyranoside (space group P212121), cell dimensions a=123.1 Å, b=128.2 Å, c=67.17 Å and methyl α-D-glucopyranoside (space group I21), cell dimensions a=167 Å have been determined and refined at 2 Å resolution. A cadmium-substituted form of the saccharide-free concanavalin A (space group I21) cell dimensions a=167 Å, b=86.5 Å, c=62.5 Å have also been refined at 2 Å resolution. A cadmium-substituted form of the saccharide-free protein has been refined at 2 Å resolution and a cobalt-substituted form at 1.6 Å resolution. In the solution of the I21 crystal structure the replacement of the native metal ions by cadmium ions was critical. This work builds on the structural studies of concanavalin A initiated in the 1970's by various groups. In particular these studies described a cis peptidic peptide between Ala 207 and Arg 208. Asp 208 is required to saccharide the Ca2+ binding site. We have determined the interaction of concanavalin A with saccharides at the atomic level. The results presented are a development of our initial studies on the mannose complex at 2.9 Å resolution.

The steric requirements for sugar binding in both the mannose and glucoside cases are particularly mediated by residues Tyr 12, Tyr 100, Asp 208 and Arg 228 as well as Asn 14 and Ser 99. Saccharide is bound to the protein by direct hydrogen bonds involving OH-3, OH-4, O3 and OH-6 and by extensive van der Waals contacts. On binding of saccharide, several water molecules leave the site and Tyr 12 and Tyr 100 rotate. Binding of both saccharides is the same except for van der Waals contacts between the axial O2 of the mannose and the protein which cannot occur in the case of the equatorial O2 of the glucoside.