catalytic site and 39Å from the allosteric site. Oligosaccharides bind in the preferred conformation for α(1-4) linked glycopyranosyl polymers in which there is an internal hydrogen bond between the O2 and O3 hydroxyls of adjacent sugars. The major interaction is with 4 turns of the long α-helix (residues 396-416) and illustrates an interesting complementarity between the secondary structures of these two different polymers. (iv) The nucleotide/nucleoside inhibitor site: This is some 12Å from the catalytic site and provides a second binding site for adenine nucleotides, nucleosides and caffeine.

Crystallographic evidence suggests all these sites interact with one another. For example binding of oligosaccharide tightens the binding of nucleotide at the allosteric site but, in the crystal, weakens the binding of G1P at the catalytic site.

Proposals for the essential features of a catalytic mechanism have been put forward from observations on the proximity of the 5'-phosphate group of pyridoxal phosphate to substrate, G1P, combined with model building studies (Johnson et al., J. Mol. Biol. 140, 565-580). In order to reconcile the X-ray evidence with known biochemistry and stereochemistry it was proposed that the substrate binding to the T state of the enzyme represents a non-productive binding mode and that when the enzyme converts to the high affinity R state in the presence of AMP and glycogen an alternative binding mode is adopted. In the proposed mechanism the 5'-phosphate group of the pyridoxal phosphate functions as a nucleophile to stabilize a carbonium-oxonium ion intermediate and a histidine, His 376, functions as a general acid to donate a proton to the glycosidic oxygen. The results obtained with glucose-1,2-cyclic phosphate (Jenkins et al., Proc. Roy. Soc. B (1981) in Press) are compatible with these proposals but further studies are required in order to test the hypothesis.

02.1-38 THE STRUCTURE OF GLUCOSE-6-PHOSPHATE ISOMERASE AT 2.6 Å RESOLUTION. A. Achari, S.E. Marshall, H. Muirhead and P.J. Shaw*. Dept. of Biochemistry, University of Bristol, Bristol, BS8 1TD., U.K.

Glucose-6-phosphate isomerase (E.C.5.3.1.9) is the glycolytic enzyme responsible for the interconversion of D-glucose-6-phosphate and D-fructose-6-phosphate. The enzyme from porcine skeletal muscle crystallizes from ammonium sulphate solution in space group $P4_32_12$, with a = 95.2 Å, c = 138.3 Å. The data for 2.6Å resolution were collected on a rotation-oscillation camera. An electron density map at a nominal resolution of 2.6 Å has been calculated using phases obtained from isomorphous and anomalous data. Phases between 3.5 Å and 2.6 Å resolution were calculated with data from a mercury derivative. The enzyme contains two identical subunits related by a diad axis. Two distinct domains in each subunit have the α/β type structure (Shaw, P.J. and Muirhead, H., J. Mol. Biol. 109, 475-485, 1977).

Sequence information is available for about one third of the molecule from five cyanogen bromide peptides (E.A. Noltmann, University of California, Riverside, U.S.A., private communication). A tentative fit of two of these peptides has been made. One of these peptides has a reactive cysteine which has been labelled chemically as a carboxymethyl residue and crystallographically as a mercurial derivative.

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02.1-39 RIBONUCLEASE-A : LEAST-SQUARES REFINEMENT OF THE STRUCTURE AT 1.45Å RESOLUTION. By Nivedita Borkakoti, David S. Moss and Rex A. Palmer, Department of Crystallography, Birkbeck College, Malet Street, London, UK.

The crystal structure of bovine pancreatic ribonuclease-A has been refined by restrained least squares analysis employing X-ray diffractometer data to 1.45Å resolution. The current R-factor for 19,238 reflections is 0.26. The rms deviation from ideality of bond lengths is 0.01Å. Minor corrections to previously reported features of secondary structure are presented and a quantitative analysis of intra molecular hydrogen bonds is given. A total of 79 water or ethanol solvent molecules in the first coordination sphere around the enzyme molecule have been clearly identified and included in the least-squares analysis. A sulphate anion, characterized chemically by laser Raman spectroscopy, and prominently displayed in the 1.45Å electron density has also been refined as part of the structure. Further new features of the structure to emerge are alternative positions for the active site H1S-119 side group which have been refined independently with individual occupation factors, a solvent molecule hydrogen bonded to the N-terminal amino group, and disorder of the side chains in the regions of residues 17 to 24 and 35 to 39 neither of which have any structural or biochemical significance for the molecule. Extensive model building by computer graphics has facilitated the production of a sound, accurate model of the ribonuclease-A structure which will now enable detailed and precise analysis of the catalytic mechanism to be undertaken.

02.1-40 THE STRUCTURES OF APO AND HOLO CYTOPLASMIC MALATE DEHYDROGENASE AT HIGH RESOLUTION. By J.J. Birktoft L.J. Banaszak and T. Meininger. Department of Biological Chemistry, Washington University School of Medicine St. Louis, Missouri 63110, U.S.A.

Cytoplasmic malate dehydrogenase (sMDH) crystallizes in one of two nearly isomorphous forms. The appearance of the different unit cells is determined by the presence of the coenzyme NAD and they are thought to contain sMDH in the apo and holo conformational states. A structural comparison at low resolution (5.0 Å) showed that although the overall folding of apo and holo sMDH are rather similar, substantial conformational differences do exist. (Weininger, Birktoft and Banaszak (1977) in "Pyridine Nucleotide-Dependent Dehydrogenases", ed. H. Sund, Walter de Gruyter & Co., p. 87).

In order to further understand these conformational differences as well as to obtain more accurate models, additional diffraction data extending to high resolution have been collected, and constrained crystallographic refinement initiated. Data for holo sMDH at two levels of NAD saturation (∿ 60% and 100%) were collected previously by diffractometry, as were the low resolution apo sMDH data. High resolution data, extending to 2.5 Å resolution, for apo sMDH were collected by oscillation photography. A Supper oscillation camera controlled by a microprocessor built and programmed by Drs. R.W. Wrenn and P.H. Bethge were used. The "SCAN12" program package as modified by Dr. R.M. Sweet and ourselves for the PDP 11/34-Optronics P-1000 system were used for the processing of the film data.

The two sets of holo sMDH data (60% holo sMDH and 100% holo sMDH) are to be refined using the Hendrickson-Konnert constrained refinement method. In the absence of a chemically determined amino acid sequence for sMDH, a