03-Crystallography of Biological Macromolecules

PS-03.12.06 X-RAY STRUCTURAL STUDY OF APO-HAEMOPORPHYRIN BY G. Pelaquì, J. Yavin, A. Daunat, B. Coulot, and B. Langlois d'Essonval, R. Busset, Laboratoire de Cristallographie, Université de Bordeaux I, 33405 Talence, France.

Until recently, interest in ferriin structures was subservient to ferriin function in iron storage. This changed with the report of Kadies, F.H.A., and Moore, A.J.R. (FEBS Letters, 1990, 271, 61-64) who showed that horse spleen ferriin binds haem non covalently, with a stoichiometry of about 16 haems per 24 subunits.

Horse spleen ferriin thus affords for the first time the structure of an apo-haemoferritin.

Octahedral crystals of horse spleen apo-ferriin complexed to 

protoporphyrin IX were obtained by addition of stoichiometric amount of metalloporphyrin to a solution of apo-ferriin prior to crystallization. The crystals belong to the F432 space group with a parameter of 184.0 Å. The structure was solved by molecular replacement, starting with a horse spleen apo-ferriin model.

The structure of the complex has been refined to an R value of 16% with data collected to 2.6 Å (completeness 83%).

All the 174 residues were located. In the last cycles of refinement, the haem binding site was observed and 175 water molecules were positioned.

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PS-03.12.07 STRUCTURAL STUDIES ON BOVINE PLASMA RETINOL BINDING PROTEIN (RBP). By G. Zanotti*, R. Berni*, P. Bradon and H.L. Monaco, Biopolymer Research Center and Dept. of Organic Chemistry, University of Padova, "Institute of Biochemical Sciences, University of Parma and Dept. of Genetics and Microbiology, University of Pavia, Italy.

Retinol transport, from its store to target cells, is performed by plasma retinol binding protein (RBP), a single domain protein of about 21 kDa (Goodman, D.S., 1984, in "The Retinoids", Academic Press, New York). RBP, synthesized in epithelial cells, is secreted in the blood, where it interacts with thyroxine binding protein (TTR). Upon delivery of retinol to cell surface receptors, the resulting apo-RBP possesses low affinity for TTR and can be selectively filtered through kidney glomeruli.

The three-dimensional structures of human and bovine RBP, in the complexed and uncomplexed forms with retinol, were determined (Cowan, S.W., Newcomer, R.E. and Jones, T.A., 1992. Proteins: struct. Funct. Genet. B, 44-61; Zanotti, G., Ottolino, S., Berni, R. and Monaco, H.L., 1993, J. Mol. Biol., in press; Zanotti, G., Berni, R. and Monaco, H.L., 1993, J. Biol. Chem., in press). It was shown that a limited conformational change is present in the unliganded protein prepared in vitro by extracting retinol during the protein purification or with ethyl ether. The crystal structure of TTR has also been determined.