The crystal structure of photolyase (DNA photoreactivating enzyme) from the cyanobacterium, *Anacystis nidulans*, has been solved by the multiple isomorphous replacement method. The refinement of the structure is still in progress and the current R value is 0.24 at 2.5 Å resolution.

Photolyase has activities of DNA damage recognition and binding, photon absorption, energy transfer from chromophore to DNA, resulting in photoconversion of UV-induced pyrimidine dimer to mono­mer. Photolyases are single chain proteins of 50 to 70 kDa molecular weight, containing two different chromophores in equimolar amount. Deduced FAD was found to be an essential chromophore for the binding and catalysis. The human GRO (growth related protein) MGSA (melanoma growth stimulatory activity) protein with 73 amino acid (1) is a member of a super-family of chemotactic cytokines like interleukin-8, platelet factor-4 (PF-4) monocyte chemotactic and macrophage inflammatory protein-2. The human GRO gene was chemically synthesized and the secreted recombinant GRO protein expressed in E.coli was purified by chromatography, and used for crystallization by vapor diffusion. After trials with several different precipitants, the crystals grew as regular bipyramids with cubic cell dimensions *a*=120.44 Å and space group *P4_2_2_2_1*, *Z*=4 (dimeric GRO molecule per asymmetric unit). Intensity data up to 2 Å resolution were collected by RIGAKU R-Axis imaging plate detector. The structure was solved by the molecular replacement method using the atomic coordinates for the dimer of PF-4(2) (from Protein Data Bank), and was then refined with 2.2 Å X-ray data, using CCP4 and X-PLOR programs. The current overall basic structure found in GRO crystals is similar to the dimeric solution model by NMR spectroscopy (3), but the less restrained regions, the NH- and CO-terminus regions are different from that of the PF-4 crystal structure and also of GRO NMR structure.

**References:**
accessible faces and the three four-stranded β-sheets. One therefore might characterize this fold as an inside-out cαβ domain. The present structure reflects the open conformation of the enzyme. We assume that large conformational changes upon catalysis are mediated mainly through two residues, a lysin and an arginin, which are located in the cleft between the two domains. These residues assure the open conformation of the native enzyme by the repulsive force between the positive charges of two amino groups. The binding of one of the two substrates probably results in neutralizing the repulsion between the two domains thereby allowing the movement of a catalytically active cαytin toward the cleft.

PS04.07.20 PROGRESS IN DETERMINING THE STRUCTURE OF FRAGMENT D FROM HUMAN FIBRINOGEN. G. Spraggan, S. J. Everse, R. F. Doolittle, Center for Molecular Genetics, Univ. Calif. San Diego, La Jolla, CA, USA 92093-0634

Fragment D is a complex, large molecular weight (86,000 Da) fragment derived from vertebrate fibrinogen by limited proteolysis with plasmin or trypsin. Its three constituent polypeptide chains have long been supposed to form a coiled-coil at their amino-terminal ends and to be cemented by a ring-shaped triple set of disulfide bonds. The carboxyl-terminal portions of two of the chains make up two homologous globular domains. Recently we reported the crystallization of fragment D from human fibrinogen and some preliminary characterization (Everse et al. Prot. Sci., 4:101316, 1995). The space group is P2₁, unit cell dimensions a=107.7, b=48.0, c=167.6, beta=105.7. In the interim, we have identified several isomorphous derivatives and have been able to calculate preliminary low resolution phases. The molecular envelope determined by solvent flattening of an initial fourier map has revealed a silhouette in which the boundaries of the distal domains and coiled coil are reasonably delineated. It also reveals, in contrast to our initial finding, that there is only one molecule per asymmetric unit. The solvent flattened map itself contains several features which can be attributed to secondary structure, including portions of the coiled-coil. Efforts to improve the phasing are under way.

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PS04.07.21 CRYSTALLOGRAPHIC STUDIES OF THE HUMAN PENTAXINS, SERUM AMYLOID P COMPONENT AND C-REACTIVE PROTEIN. D. Thompson, I. J. Tickle, T. L. Blundell, M. B. Pepsy & S. P. Wood. Department of Crystallography, Birkbeck College, Malet Street, London, 1Immunological Medicine unit, Hammersmith Hospital, London, 2Department of Biochemistry, University of Southampton, Southampton

The crystal structure of the two major human pentaxins have been determined to medium resolution. The pentaxins are a protein family which exhibit five fold symmetry of subunits and are capable of calcium dependent binding. The two major human pentaxins are Human Serum Amyloid P Component (SAP), which is found bound to amyloid deposits in amyloidosis and Alzheimer’s disease, and C-reactive protein (CRP), which is believed to have a role during the immune response. SAP and CRP share 52% sequence identity. SAP exists in the plasma as a dimer, two pentameric rings interacting face to face, each subunit consisting of 204 amino acids, whereas CRP exists as a single pentameric ring made up of subunits consisting of 206 amino acids.

Two CRP crystal forms have been grown. Both are tetragonal. One has a unit cell of a=375.81 and c=94.21, and contains 2 pentamers per asymmetric unit and the other is of unit cell a=190.31 and c=132.12, space group P42₁2₁2₁, and contains 2 pentamers per asymmetric unit. A complete data set has been collected on this crystal form to a resolution of 3.0Å. Crystals have also been grown of decameric SAP. These are of spacegroup P2₁ and unit cell a=105.37 b=127.711 c=121.499 and β=91.87 and contains 1 decamer per asymmetric unit. A complete data set has been collected on this crystal form to 2.5Å.

Both structures have been solved by molecular replacement using the pentameric structure of SAP (Emsley, J. et al. (1994) Nature vol. 367, p358-345) as a model.

PS04.07.22 CRYSTALS OF THE AUGMENTOR OF LIVER REGENERATION. C.-K. Wu, J. P. Rose, A. Francavilla, J. G. Prelich, A. Iacobellis, M. Hayakawa, A. Rao, T. Sahr, and B.C. Wang, 1Dept. of Biochemistry and Molecular Biology, Univ. of Georgia, Athens GA 30602, USA, 2Dept. of Crystallography, Univ. of Pittsburgh, Pittsburgh, PA 15260, USA, 3Pittsburgh Transplant Inst., Univ. of Pittsburgh School of Medicine, Pittsburgh, PA 15260; and 4Pharmaceuticals Res. Ctr., Toyobo Co. Ltd., Osaka, Shiga 520-02, Japan

Almost every school child knows that chameleons can regenerate a lost tail. This interesting phenomenon of regrowth of lost body parts common in lower animals is generally rare in mammals. The liver however, is an unique organ in that it is capable of regeneration.

A new cellular growth factor termed augmentor of liver regeneration (ALR) shown to have a proliferative effect on liver cells while at the same time producing an immunosuppressive effect on liver-resident natural killer cells and liver-resident mononuclear leukocytes has been crystallized. The crystals diffract to beyond 2 Å resolution and belong to space group P2₁2₁2₁ with a=35.5Å, b=108.1Å and c=125.1Å. Based on 4 molecules per asymmetric unit, the Matthews coefficient is calculated to be 2.16 Å³/Da which corresponds to a solvent content of 43%.

ALR has two related forms, "short" ALR which has 125 amino acid residues and "long" ALR (ALR198), which contains 73 additional residues in the N-terminal segment of ALR. The long ALR is the result of an additional intramembrane ATG initiation site which is 5' to the initiation site used to code the 125 residue protein. The ALR cDNA sequence shows 50% homology with the sequence of the dual-function gene ERV1. (Essential for Respiration and Viability) of "baker's yeast", Saccharomyces cerevisiae. The ERV1 gene products are part of the mitochondrial respiratory chain, are essential for oxidative phosphorylation and vegetative growth and also play a critical role in cell growth and regulation. Deletion of this gene has been shown to cause a severe growth defect and irreversible cessation of cell division after 3-4 days. The ALR gene could represent the mammalian equivalent of the ERV1 gene.

Details of the structure analysis will be presented.

PS04.07.23 CRYSTAL STRUCTURE ANALYSIS OF BOVINE HEART CYTOCHROME C OXIDASE. H. Yamaguchi, T. Tsukihara, H. Aoyama, E. Yamashita, T. Tomizaki, K. Shinzawa-Itoh, R. Nakashima, R. Yano and S. Yoshikawa, Institute for Protein Research, Osaka University, Suita, Osaka 565, Japan; and 2Faculty of Science, Hirogawa Institute of Technology, Kamigohori, Ako-gun, Hyogo 678-12, Japan

Bovine cytochrome c oxidase is a large membrane protein complex with molecular size of 530KDa comprising 13 different subunits and six metal centers, heme a, heme a₂, Cu₃, Cu₉, Mg and Zn. As the terminal enzyme of biological oxidation, the enzyme catalyzes O₂ reduction to H₂O at an active site with the four redox active transition metals coupling to a proton pumping process across the mitochondrial inner membrane.

The structure of the enzyme has been determined at 2.8Å resolution. Electron transfer pathway has been elucidated by the structural study. A clear electron density map at 2.8Å resolution was obtained by multi-method followed by a density modification method. Out of 3606 amino acid residues in an asymmetric unit composed of a dimer, structural models of 3560 residues as well as those of metal centers were successfully built.

The electron density map indicates a dinuclear copper center of Cu₉ with an unexpected structure of [2Cu₂-2S]²⁺ similar to a [2Fe-2S]²⁻ center. Zinc site is located at a nucleic encodes subunit on the matrix side.