PS04.10.14 YEAST CYTOSOLIC CYCLOPHILIN A AS ANALOGY OF HUMAN ISOFORM. Michiko Konno, Sawako Fujioka, Akiko Kashima, Ochanomizu University, Department of Chemistry, Faculty of Science, Otsuka, bunkyo-ku, Tokyo 112 Japan

Prokaryotes to eukaryotes have ubiquitously and abundantly cyclophilin (CyP) soluble in the cytoplasm; CyPA and membrane-bound CyP; CyPB. While CyPB is seen to be homolog to ninaA, biological role of CyPA is still poorly understood. Even though yeast strains lacking either or both CyPs have been reported to grow normally, CyPA should be involved in some important machinery for life cycle of alive cell. Close comparison of structrural natures between yeast CyPA here determined and human CyPA (hCyPA) previously reported (1) is made to confirm functional identity of these two.

Crystals belong to *triclinic*, space group *P1* with lattice constants of a=44.45(2), b=53.11(2), c=32.018(6) Å, α=84.92(2), β=95.22(4), γ=108.56(4)°, Z=2, Dobs=1.21gcm^{-3}, Vm=2.07Å^{3}Da^{-1}, Vsol=40.6%. Intensity data were collected using Sakabe camera at BL6A2 of Photon Factory in Tsukuba. The structure of yCyPA was solved by molecular replacement method using hCyPA as a search model (XPLOR program). Refined model of two CyPA molecules and 126 water molecules gave Rfactor of 18.5% for 17931 reflections ($F>2\sigma$) in the region of 5.0 to 1.9 Å resolution. All Cα atoms of two CyPAs are well superimposed with a r.m.s. deviation of 0.23 Å.

yCyPA also has β-barrel structure composed of two orthogonal four stranded antiparallel β-sheets flanking two α-helixes at the top and bottom as in hCyPA and E. *coli* CyPA (2). The predicted peptide binding site is identified to be located in the cleft on the upper β-sheet. In yCyPA the same residues take the same arrangement as those essential to recognition and binding of peptide-substrates in hCyPA. The hydrophobic pocket, by which peptide-substrates are recognized, is formed by side chains of five non-polar residues; Phe58, Met59, Trp119, Leu120 and His124 with Phe111 at bottom; and Arg53 and Asn100 are positioned on the opposite side of the pocket such that the backbone of the peptide containing a proline can be hydrogen bonded by these two residues to make the proline *cis*-form.

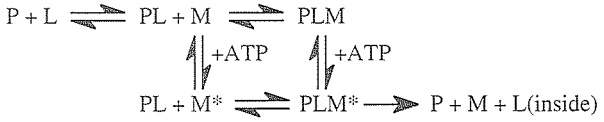
(1) H. Ke, *J. Mol.Biol.* (1992) **228**, 539-550.
(2) M. Konno *et al.*, *J. Mol.Biol.* (1996) **256**, 897-908.

PS04.10.15 CRYSTAL STRUCTURE OF A PHOSPHATASE RESISTANT MUTANT OF SPORULATION RESPONSE REGULATOR SPO0F FROM BACILLUS SUBTILIS. Madhusudan, John M. Whiteley, James A. Hoch, James Zapf, Nguyen H. Xuong* and Kottayil I. Varughese*, The Scripps Research Institute, La Jolla, CA 92037 and *University of California at San Diego, La Jolla, CA 920930359

Spo0F is an aspartyl pocket containing phosphotransferase in the signaling pathway controlling sporulation in *Bacillus subtilis*. It belongs to the superfamily of bacterial response regulatory proteins, which are activated upon phosphorylation of an invariant aspartate residue in a divalent cation dependent reaction by cognate histidine kineses. We have determined the crystal structure of a Rap phosphatase resistant mutant, Spo0F Y13S, at 1.9 Å. The structure was solved by single isomorphous replacement and anomalous I scattering techniques. The overall structural fold is $(\beta/\alpha)5$ and contains a central β-sheet. The active-site of the molecule is formed by three aspartates and a lysine at the carboxyl end of the β-sheet and it accommodates a calcium ion. The structural analysis reveals that the overall topology and metal binding coordination at the active-site were similar to the chemotaxis response regulator CheY. Structural differences between Spo0F and CheY in the vicinity of the active-site provide insight into how similar molecular scaffolds can be adapted to perform different biological roles by alteration of a few amino acid residues. These differences may contribute to the observed stability of the phosphorylated species of Spo0F, a feature demanded by its role as a secondary messenger in the phosphorelay controlling sporulation.

PS04.10.16 A DOMINANT-NEGATIVE MUTANT OF *E. COLI* MALTOSE-BINDING PROTEIN: X-RAY STRUCTURES AND GENERAL LESSONS. Sherry L. Mowbray and Brian H. Shilton, Department of Molecular Biology, Swedish Agricultural University, S-751 24 Uppsala, Sweden

Studies of a dominant-negative mutant of *E. coli* maltose-binding protein shed new light on the mechanism of binding protein-dependent transport systems. X-ray structures and small-angle X-ray scattering studies of open, ligand-free forms of the mutant show that the unliganded protein is essentially identical with the wild type protein, while only a small region of the protein located between the two structural domains is altered in the closed, ligand-bound form. The physiological effects of the mutant can be explained by the kinetic scheme:



where P, L and M are binding protein, ligand, and membrane permease complex, with M* representing the activated form necessary to transport. It is proposed that wild type binding protein promotes the M to M* transition through binding more tightly to M*, in the same way that enzymes function by binding more tightly to transition states. In the mutant, the binding to M* is weaker, and though binding to M can occur, the transition to M* is in that case not favored. This proposal explains the basic function of the transport system, as well as a number of previously puzzling results. The structures of both binding protein and membrane permease are likely to be more open in the activated complex, a suggestion supported by the observation that multiple forms are possible within the primarily "closed" and "open populations in solution.

PS04.10.17 CELL CYCLE PROTEINS. M.E. Noble*, J.A. Endicott*, N.R. Brown*, E. Garman*, R. Dzivenu*, A. Lawrie*, L.N. Johnson*, P. Nurse, and R.T. Hunt+.*Laboratory of Molecular biophysics, South Parks Road, Oxford, U.K., +ICRF, Clare Hall Labs., South Mimms, Herts, U.K., = ICRF, Lincoln's Inn Fields, London, U.K

Progress through the cell cycle is regulated by the "Cyclin Dependent Kinases" (CDKs). Different CDKs are activated at appropriate times by association with cognate "cyclins", and by phosphorylation of a conserved threonine. CDKs may also be found in complex with other proteins, such as p13^{suc1} and the CDK inhibitors. Our aim is to study proteins of the cell cycle, and to understand the structural principles behind their actions and interactions. This study has produced the crystal structures of p13^{suc1}, and of an active 260 residue fragment of cyclin A (cyclin A3)[2].

Although p13^{suc1} is essential for successful passage through the cell cycle, its mode of action is not known. Our structure of p13^{suc1} reveals a compact, principally beta-sheet fold. It differs from the structure of a human homologue of p13^{suc1}, and from another structure of p13^{suc1} itself [3], where details of the protein purification and crystallisation were different. These proteins formed dimers, in which beta strands from distinct monomers interlace to form a beta-sheet like that observed in our structure.

We are currently producing mutants to probe the function of $p13^{suc1}$.

Cyclin A is first observed late in the G1 phase of the cell cycle, and its abundance increases throughout S and G2. It forms complexes with either CDK2 or CDC2. Our structure of a genetically truncated form of cyclin A (residues 171-432) consists of two strikingly similar helical domains, despite low sequence homology. Comparison with the structure of a complex between a fragment of cyclin A and CDK2 [4] showed that in contrast to the major structural changes of CDK2, cyclin remains essentially unaltered when complexed. Thus, cyclin acts as a template, complimentary to the basally active conformation of CDK2 in the complexed structure.

Our poster will describe details of the results mentioned above, as well as the results of on-going work to further characterise these proteins.

[1] Endicott et al., EMBO J. **14**, 1004. [2] Brown et al., Structure **3**, 1235 [3] Bourne et al., PNAS **92**, 10232. [4] Jeffrey et al., Nature **376**, 313.

PS04.10.18 CRYSTALLOGRAPHIC AND BIOCHEMICAL ANALYSIS OF AN INHIBITOR OF APOPTOSIS, BCL-2. Jason W. O'Neill and Kam Zhang, Division of Basic Sciences, Fred Hutchingson Cancer Research Center, Seattle, WA

Programmed cell death (apoptosis) plays an important role in animal development and homeostasis of cell numbers. The primary regulator of human apoptosis is Bcl-2, a novel cellular gene which can function to block most modes of apoptosis. Elevated levels of Bcl-2 protein are strongly correlated with tumorgenesis and is found deregulated in a variety of cancers, including; colorectal (90%), breast (70%), and lymphoma (65%). Bcl-2 may function to inhibit apoptosis through effects on antioxidant protection pathways or by modulating the apoptotic effects of Ca^{2+} release from ER. The regulation of Bcl-2 is thought to occur through phosphorylation and/or heterodimer formation with related promoters of apoptosis, such as Bax. To pursue Bcl-2's function and regulational control: *a)* We have expressed human Bcl-2 in *E. coli* using a pET-His-tag expression vector. Bcl-2 has been successfully purified to high concentrations and is found as a homodimer as measured by dynamic light scattering. Currently we are undergoing crystallization trials. *b)* We also look at the effects of phosphorylation to Bcl-2's function, and how the addition of Bax influences Bcl-2's function using an *in vitro* apoptotic assay. Combining the 3D-structure with the biochemical data will be critical in unraveling Bcl-2's biological mechanism and for its regulation during apoptosis. Furthermore, this knowledge will be extremely useful in structure based design of inhibitors of Bcl-2, which could lead to potent therapeutics for cancers and a broad range of other malignancies.

PS04.10.19 THE STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE-lB COMPLEXED TO A HIGH AFFINITY INHIBITOR. Andrew D. B. Pannifer*, Terrence R. Burke Jr.†, David Barford*, *Laboratory of Molecular Biophysics, Rex Richards Building, South Parks Road, Oxford, OX1 3QU, UK, †Laboratory of Medicinal Chemistry, Bethesda, MD, USA

The 2.4 Å resolution structure of protein tyrosine phosphatase-lB complexed to the high affinity, non-hydrolyzable inhibitor hydroxy-naphthalene difluorophosphonate is presented. The inhibitor is competitive, binding at the active site with a sub-micromolar K_i and acts as a phosphotyrosine analogue. The labile phosphorus-oxygen bond of phosphotyrosine is replaced by a phosphorus-carbon bond in the inhibitor, thereby rendering the phosphate moiety non-hydrolyzable.

The naphthalene group of the inhibitor mimics the phenyl ring of phosphotyrosine, occupying a hydrophobic cleft formed by tyrosine 46 and phenylalanine 182. The phosphate group occupies the established phosphate binding pocket. Specific interactions between the phenolic oxygen of the inhibitor and residues at the active site of the enzyme have also been identified and these are likely to account for the low K_i.

PS04.10.20 CRYSTALLOGRAPHIC ANALYSIS OF A FRAGMENT FROM CHICKEN TENASCIN CONTAINING TWO FIBRONECTIN-TYPE III DOMAINS Klaus Piontek, Daniel Bisig, Peter Weber, Lloyd Vaughan, Kaspar Winterhalter, Laboratory of Biochemistry, Swiss Federal Institute of Technology (ETH), CH-8092 Zürich, Switzerland.

Tenascin-C is an extracellular glycoprotein composed of six identical polypeptide chains which are linked together at their N-terminal ends to form a hexabrachion structure. Each polypeptide comprises a serie of 13.5 tandem repeats homologous to epidermal growth factor followed by 8-13 fibronectin type III (TNfn)-like domains and finally one fibrinogen-like domain at the C-terminus. Alternative splicing of TNfn domains between the domains 5 and 6 leads to the three major isoforms found in chicken. In the smallest isoform (190 kDa) these two domains are adjacent to each other. Tenascin-C isoforms are differently expressed in development and in response to malignancy, leading to the expectation of isoform-specific functions. TNfn5 binds heparin and other iduronic acid-containing glycosaminoglycans, presumably *via* a conserved heparin binding motif. Furthermore, TNfn56 binds to the neural cell adhesion molecule contactin/F11, an interaction which is inhibitable by heparin. To explore these interactions in greater detail we have prepared a fusion protein containing domains 5 and 6 and attempt now the crystal structure determination of this 20 kDa protein.

TNfn56 crystallizes from 27% PEG2000, 100mM Na-acetate, pH 4.5 at RT in a monoclinic ($P2_1$, a=47.7Å, b=54.9Å, c=97.0Å, ß=104.4°, V_m=3.08 $Å^3$/Da, 2 mol/a.u.) and an orthorhombic ($P222_1$, a=45.3Å, b=71.9Å, c=58.0Å, V_m=2.36 $Å^3$/Da, 1mol/a.u.) form. Both crystal forms diffract to about 2.6 Å resolution. The majority of the monoclinic crystals is twinned and the diffraction limit of this form frequently lies only between 3.2 and 4.0 Å. Furthermore, the formation of the orthorhombic form can not be directed. Despite the sparse availability of suitable single crystals we have collected a data set of monoclinic crystals to 2.6 Å resolution utilizing synchrotron radiation (DESY/Germany) and a data set to 2.8 Å resolution on a conventional X-ray source. Presently we attempt the structure determination with the molecular replacement technique and, in parallel, with isomorphous replacement.

PS04.10.21 CURRENT PROGRESS ON CRYSTALLOGRAPHIC COMPLEXES OF TRANSDUCIN. Susan M. Redford, Heidi Hamm‡, Joseph Noel, Structural Biology Lab, The Salk Institute, La Jolla, CA 92037, ‡University of Illinois College of Medicine, Chicago, IL 60680

The opportunity to understand the structure and function of a G protein signal transduction cascade at the atomic level is the underlying goal of this research. The current studies employ peptides that mimic rhodopsin's functionally essential cytoplasmic face in complex with $G_{t\alpha\beta\gamma}$ to probe the structural consequences of receptor/G-protein binding. Recently the heterotrimer structure, $G_{t\alpha\beta\gamma}$ has been reported to 2.0 Å resolution. In these studies, a chimeric Gtα Gtα/iα, which has been *E. Coli* expressed, is substituted for $G_{t\alpha}$. $G_{t\alpha/i\alpha\beta\gamma}$ crystals are then grown in complex with peptides which mimic rhodopsin's cytoplasmic loops 2 and 3.

Signaling cascades provide mechanisms to receive, transmit and amplify cellular messages, and thus are critical pathways for mounting a cellular response to an extracellular stimulus. Heterotrimeric G-proteins have evolved as ubiquitous solutions for signal transduction and amplification throughout many cells, and are involved in processes such as vision, olfaction, hormone signaling, and responses to cytokines. The α subunit has been studied extensively biochemically, as it contains the GTPase function,