dual specificity toward UMP or CMP, while the enzymes of bacteria origin exhibit a more dedicated UMP-specific activity, and appears to be essential for bacterial growth. Thus, bacterial UMPKs may represent potential targets for developing antibacterial drugs. Although several UMPK apo-form structures are available, the ATP-binding and UMP-binding loops are usually flexible and invisible in the apo-form structures. This phenomenon makes it difficult to inspect the induced-fit movements for these flexible loops. Also, no structure has yet been published for the UMPK/GTP complex until to date to get a more thorough understanding of the GTP regulation mechanism. In the present abstract, we have solved the UMPK structures of apo-form and GTP-bound complex form from Xanthomonas campestris using crystals grown under strong magnetic field by X-ray crystallography. We are able to clearly detect the structures of the ATP-binding and UMP-binding loop. Besides, a novel GTP-binding site located in the central hole of the monomers is also detected. Substantial shifting in these two flexible loops is found to be induced when the allosteric effector GTP is bound. Detailed conformational change of UMPK in the presence of allosteric GTP will be discussed.

Keywords: UMPK, allosteric mechanism, GTP regulation mechanism

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### Structural studies of novel proteases from the CATH family of zinc peptidases

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Proteins in the CATH family of zinc peptidases (phosphorylase/hydrolase-like fold in SCOP) have a broad phylogenetic spread across all kingdoms of life and show substantial sequence divergence. They are in 8 PFAM families and form the large peptidase_MH clan. Despite several structures in the PDB, only half of the members have reliable homology models. The JCSG aims to improve this coverage by determining novel structures. HMMs were used to identify 226 members with cDNA available in the JCSG genome pool. Of these, 161 have <30% sequence homology to a structure in PDB. After clustering at 90% sequence identity to remove close homologs, 135 targets were chosen. To date, 8 targets have been solved, with 6 others in crystallization trials. We have analyzed features that support different functions, focusing on active sites, ligands, domain architectures and oligomerization. Even with a modest increase in structural coverage, we could assign new functional roles within the clan and more clearly discern the evolutionary connections in its PFAM families. We also identified many proteins of biomedical importance. Four structures can be used to model ~130 proteins in prevalent pathogenic bacteria and may allow the design of new therapies. Two carboxypeptidases are close homologs of an enzyme that is used in prodrug and cancer therapy. An AstE/AspA-like member is related to a protein involved in a brain disease. We also obtained the first structure of an aminopeptidase with irons bound in the active site, which hints at functional novelty. A putative Xaa-His dipeptidase represents the first structure of a PepD and reveals a dimeric form. The JCSG is funded by NIGMS/PSI, U54 GM074898. SSRL is funded by DOE BES, and the SSRL SMB program by DOE BER, NIH NCRR BTP and NIH NIGMS.

Keywords: structural genomics, structural biochemistry enzymology, zinc peptidase

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### Structural and functional analysis of a universal stress protein from *Thermus thermophilus* HB8

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The universal stress protein (Usp) superfamily [Pfam PF00582] is characterized by a conserved domain consisting of 130-160 amino acids. More than 1000 Usp proteins are found in various organisms including bacteria, archaea, and eukaryotes. Escherichia coli possesses six proteins containing a Usp domain. They are induced under a large number of stress conditions; nutrient starvation, heat shock, oxidants, uncouplers, and DNA-damaging agents. However, the biochemical mechanism of Usp proteins remains unknown. The genome sequence of the extremely thermophilic bacterium Thermus thermophilus HB8 has revealed that five proteins belong to the Usp superfamily. Two are in a single domain, two are in tandem, and one is a component of the tentative potassium uptake protein TrkA. TTHA0895 is a single domain Usp protein from Thermus thermophilus HB8 and consists of 137 amino acid residues with a molecular mass of 14759 Da. In order to determine its structural properties, TTHA0895 was crystallized in the absence and presence of ATP. Form I, crystallized in the absence of ATP, belongs to tetragonal space group $P4_32_12$ with unit-cell parameters $a = b = 73.1$, $c = 57.9$ Å, and form II, crystallized in the presence of ATP, belongs to orthorhombic space group $I222$ with unit-cell parameters $a = 33.1$, $b = 75.1$, $c = 88.7$ Å. The crystals contain one monomer per asymmetric unit. X-ray data have been collected to 1.65 and 1.55 Å resolution for forms I and II, respectively. Here we report the X-ray structures of forms I and II, and the possible ATPase activity of TTHA0895. In addition, the expression of TTHA0895 from the log phase to the stationary phase of bacterial growth has been examined by means of mRNA (microarray) analysis. The presence of tetracycline had no effect on TTHA0895 regulation.

Keywords: structure and function of proteins, structures of biomolecules, structural genomics

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### Crystal structure and molecular dynamics simulation of ubiquitin-like domain of murine Parkin

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Parkin is the gene product identified as the major cause of autosomal