

is cleaved for up to 75 residues during crystallization automatically. The final core structure reveals a novel hybrid comprising a tudor-like (Sm-like) domain interdigitated with a Immunoglobulin-like (Ig) or fibronectin type (Fn) III domain. In the crystal, the monomers form an annular pentamer of dimers of pseudo five-fold symmetry, due to different dimer-dimer interactions employed. The resulting asymmetrical star-like complex has a outer dimensions of approximately $110 \text{ \AA} \times 90 \text{ \AA} \times 65 \text{ \AA}$, and a shortest diameter of approximately 20 \AA ; in the center. The outer dimensions of the atomic Xanthomonas hook-capping FlgD complex turn out to be very similar to those of the Salmonella filament cap complex observed by electron microscopy. This atomic hook cap structure may help understand hook protein-cap protein interactions, hook protein insertion, and hook length control, the three features that are crucial for understanding the bacterial flagellar biogenesis.

Keywords: FlgD, hook capping, flagellar biogenesis

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Structure of DFA0005 complexed with α -ketoglutarate: A novel member of the ICL/PEPM superfamily

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The pale-pink alkali-tolerant *Deinococcus ficus* (DF strain CC-FR2-10T) is a novel bacterium isolated from the rhizosphere of the sacred tree *Ficus religiosa* L. It is found to possess high degrading power for food and organic waste at pH 10 and is being applied to industrial usage. It contains one chromosome of 2801970 bp, and three mega-plasmids of 642681, 395118, 311736 bp, respectively. The total genome sequence has been recently completed (Lin et al, manuscript in preparation), and a structural genomics project is followed to study the structures of proteins encoded in this genome and to study the alkali adaptation mechanism exhibited by this alkali-tolerant bacterium compared with their non-alkaline counterparts. The crystal structure of the DFA0005 protein complexed with α -ketoglutarate (AKG) from an alkali-tolerant bacterium *Deinococcus ficus* has been determined to a resolution of 1.62 \AA . The monomer forms an incomplete $\alpha 7 / \beta 8$ barrel, with a protruding $\alpha 8$ helix that interacts extensively with another subunit to form a stable dimer of two complete $\alpha 8 / \beta 8$ barrels. The dimer is further stabilized by four glycerol molecules situated at the interface. One unique AKG ligand binding pocket per subunit is detected. Fold match using the DALI and SSE servers identifies DFA0005 as belonging to the isocitrate lyase / phosphoenolpyruvate mutase (ICL/PEPM) superfamily. However, further detailed structural and sequence comparison with other members in this superfamily and with other families containing AKG ligand indicate that DFA0005 protein exhibits considerable distinguishing features of its own and can be considered a novel member in this ICL/PEPM superfamily.

Keywords: *Deinococcus ficus*, ICL/PEPM superfamily, alpha-ketoglutarate ligand

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RecX adopts a tandem repeats of three-helix bundle: Insights into RecX inhibition of RecA activities

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The bacterial RecA protein plays a key role in recombinational DNA repair in bacteria. It is a DNA-dependent ATPase that promotes DNA strand exchange reactions, and induces SOS response. However, the activities of RecA protein must be regulated in the cell to avoid aberrant DNA recombination. Currently, many additional proteins are known to regulate RecA function such as RecF, RecO, and RecR and DinI proteins. RecX protein is an inhibitor of RecA function both in vivo and in vitro. However, RecX protein is among the least understood of these RecA modulator proteins. But it has been found that RecX protein inhibits RecA protein ATPase, coprotease, and recombinase activity. Direct interaction between RecA and RecX has also been well demonstrated. Reconstituted RecA/RecX nucleoprotein filament from EM and RecA crystal structure show that RecX protein binds to the helical groove of RecA filament, spanning the monomer-monomer interface from the C-terminal domain of one RecA monomer to the core domain of the second. However, detailed RecX crystal structure is still unavailable until to date. We have solved the first RecX crystal structure from *Xanthomonas campestris* to a resolution of 1.6 \AA ; crystallography. The tertiary structure of RecX indicates it adopts a novel three tandem repeats of three helix bundle. Enzyme assays indicate that RecX can efficiently inhibit the ATPase, coprotease, and recombinase activity of the RecA protein. A docking study of RecA dimer and RecX monomer reveals the tight interactions between these two proteins. Model study shows that RecX proteins can fit well into the major helical groove, with its C-terminus fitted into the notch between two adjacent RecA monomers in the RecA nucleofilament, as revealed by the cryoEM study.

Keywords: RecA, RecX, recombination

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Structure of Xcc UMPK/GTP complex reveals a novel GTP-binding site and allosteric mechanism

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Uridylate kinase (UMPK) is a key enzyme in pyrimidine biosynthesis. Due to its importance in nucleic acid biosynthesis, UMPK is ubiquitous in every living organism, including bacteria, archaea, and eukarya. However, UMPKs of bacterial origin are very different from the UMPKs of eukaryotic origin. In general, the eukaryotic enzymes have a broader substrate preference, exhibiting