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Structure and Assembly of a PLP Dependent Dodecameric L-aspartate β-decarboxylase. Hui-Ju Chen[a,b], Tzu-Ping Ko[a], Chia-Yin Lee[c], Nai-Chen Wang[a], Andrew H.-J. Wang[a,b]. [a]*Institute of Biological Chemistry, Academia Sinica, Taipei 115, Taiwan.* [b]*Institute of Biochemical Science , National Taiwan University, Taipei 10617, Taiwan.* [c]*Department of Agricultural Chemistry, National Taiwan University, Taipei 10617, Taiwan.*
E-mail: d89242003@ntu.edu.tw

The type-I PLP enzyme L-aspartate β-decarboxylase (ASD) converts L-aspartate to L-alanine and CO_2, which also has minor aminotransferase (AT) activity. Similar to the homodimeric AT, the protein subunit of ASD comprises a large and a small domain, of 410 and 120 residues, respectively. The crystal structure reveals a dodecamer made of six identical dimers arranged in a truncated tetrahedron whose assembly involves tetramer and hexamer as intermediates. Helical motifs I and II, which is not seen in AT, participate in the oligomer formation of ASD. Triple mutations of S67R/Y68R/M69R or S67E/Y68E/M69E in motif I produced an inactive dimer, attesting that the dodecameric structure is essential to the enzyme's function. The cofactor PLP is bound covalently to Lys315 in the active site, while its phosphate group interacts with a neighboring Tyr134. Removal of the bulky side chain of Arg37, which overhangs the PLP group, improved the substrate affinity. Mutations in flexible regions produced the more active K17A and the completely inactive R487A. Lys17 is located in a flexible N-terminal region, where conformation changes are likely to facilitate substrate entrance to the active site. The role played by Arg487 and is not entirely clear, although the structure suggests that substrate binding may trigger essential conformational changes of its associated loop for catalysis. ASD has been implemented in facilitating separation of D-aspartate, which is highly demanded in manufacturing of many antibiotics, from the D,L-mixture produced by reacting fumaric acid with ammonia. The second product L-alanine is also useful, for example, in food industry.

Chen HJ, Ko TP, Lee CY, Wang NC, Wang AHJ., **2009**, *Structure*, 17, 1-13.

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Crystal Structure of *Staphylococcus Aureus* Phosphopantetheine Adenylyltransferase in Complex with 3'-phosphoadenosine 5' -phosphosulfate (PAPS) Reveals a New Ligand Binding Mode. Hye-Jin Yoon[a], Hyung Ho Lee[a], Ji Hyeon Park[a], Se Won Suh[a]. [a]*Department of Chemistry, Seoul National University, Korea.*
E-mail: yoonhj@snu.ac.kr

Coenzyme A (CoA) is an essential cofactor in numerous biosynthetic, degradative, and energy-yielding metabolic pathways and is required in several key reactions in intermediary metabolism. It is synthesized in five steps from pantothenate (vitamin B5), cysteine, and ATP. Phosphopantetheine adenylyltransferase (PPAT), a member of the nucleotidyltransferase superfamily, catalyzes the penultimate step in this biosynthetic pathway. That is, it catalyzes reversible transfer of an adenylyl group from ATP to 4'-phosphopantetheine (Ppant), yielding dephospho-CoA (dPCoA) and pyrophosphate. Bacterial PPAT and mammalian PPAT are highly dissimilar, thus making the bacterial enzyme an attractive target for antibacterial discovery. Previous structural studies of PPAT revealed how the PPAT enzyme recognizes several ligands. ATP, ADP, Ppant, and dPCoA bind to the same binding site in highly similar manners, while the mode and site of CoA binding is somewhat different. To aid structure-based discovery of new antibacterial compounds against major human pathogens such as *S. aureus*, detailed structural information on the binding modes of different ligands to the PPAT active site is desirable. In this study, we have solved the crystal structure of *S. aureus* PPAT as a binary complex with 3'-phosphoadenosine 5'-phosphosulfate (PAPS), representing the first such complex of any PPAT with PAPS. The PAPS binding site overlaps with that of ATP but their binding modes are distinct from each other. Therefore, this study provides additional structural information for structure-based design of PPAT inhibitors as a potential antibacterial agent.

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Single-stranded DNA-binding Protein Complex from *Helicobacter Pylori.* Yuh-Ju Sun[a], Kun-Wei Chan[a]. [a]*Institute of Bioinformatics and Structural Biology, Tsing Hua University, Hsinchu 300, Taiwan.*
E-mail: yjsun@life.nthu.edu.tw

Single-stranded DNA-binding protein (SSB) plays an important role in DNA replication, recombination, and repair. SSB consists of an N-terminal single-stranded DNA-binding domain with an oligonucleotide/oligosaccharide binding fold and a flexible C-terminal tail involved in protein-protein interactions. SSB from *Helicobacter pylori* (*Hp*SSB) was isolated, and the ssDNA-binding characteristics of *Hp*SSB were analyzed by fluorescence titration and electrophoretic mobility shift assay. The crystal structure of the C-terminally truncated protein (*Hp*SSBc) in complex with 35-mer single-stranded DNA [*Hp*SSBc-$(dT)_{35}$] was determined at a resolution of 2.3 Å. The *Hp*SSBc monomer folds as an OB-fold with a Y-shaped conformation. The ssDNA wrapped around the *Hp*SSBc tetramer through a continuous binding path comprising five essential aromatic residues and a positively charged surface formed by numerous basic residues.