surface identified by NMR was flat and included a strip of three solvent-exposed Trp residues flanked by acidic residues. The overall structure of the AD2 was a TIM-barrel fold, which is a common fold in family 18 chitinases. The active site of the AD2 was in the groove-like cleft and was open to the solvent due to the lack of an additional small domain, which is observed in other family 18 chitinases.

Keywords: catalysts, enzyme structure, domains

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**Successful expression of archaecal STT3/AglB membrane protein in *E. coli* cells**  
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Oligosaccharyltransferase (OST) is an enzyme that catalyzes the transfer of the oligosaccharide from a lipid donor to the side chain of an Asn residue within a consensus sequence of Asn-X-Thr/Ser, where X can be any amino acid residue except for Pro. Asn-the OST of archaea and PglB for bacteria. All STT3/AglB/PglB proteins are characterized by 11-13 transmembrane helices in the N-terminal half of the amino acid sequence and a globular domain in the C-terminal half on the luminal/out side of the membranes. We reported that the OST of *Pyrococcus furiosus*, a thermostable archaeon, is composed of the STT3 protein alone, and catalyzes the transfer of a heptasaccharide onto peptides in an Asn-X-Thr/Ser-motif-dependent manner. We determined the crystal structure of the C-terminal soluble domain of *P. furiosus* STT3 (PfSTT3) 1,2. Here, we expressed the full-length PfSTT3 in *E. coli*, and found that the membrane fraction of *E. coli* cells had the OST activity. We then optimized *E. coli* strains and culture conditions to minimize the degradation of the full-length PfSTT3, and succeeded to obtain homogenous PfSTT3 after several purification steps, including heat treatment and His-tag affinity chromatography. The PfSTT3 is estimated to be monomeric from the elution volume of gel filtration in the presence of various detergents.

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Keywords: membrane proteins, purification, quaternary association of proteins

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**Crystal structure of Helicobacter pylori spermidine synthase suggests a distinct active site**  
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Spermidine synthase (putrescine aminopropyltransferase, PAPT) catalyzes the transfer of the aminopropyl group from decarboxylated S-adenosylmethionine to putrescine during spermidine biosynthesis. *Helicobacter pylori* PAPT (HpPAPT) has a low sequence identity with other PAPTs and lacks the signature sequence found in other PAPTs. The crystal structure of HpPAPT, determined by multwavelength anomalous dispersion, revealed an N-terminal β-stranded domain and a C-terminal Rossmann-like domain. Structural comparison with other PAPTs showed that HpPAPT has a unique binding pocket between two domains, numerous non-conserved residues, a less acidic electrostatic surface potential, and a large buried space within the structure. HpPAPT lacks the gatekeeping loop which facilitates substrate binding in other PAPTs. PAPTs are essential for bacterial cell viability; thus, HpPAPT may be a potential antimicrobial drug target for *H. pylori* due to its characteristic PAPT sequence and distinct conformation.

Keywords: *Helicobacter pylori*, spermidine synthase,