Crystal Structure of Spermidine Synthase from *Helicobacter Pylori*

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Spermidine synthase (putrescine aminopropyltransferase, PAPT) catalyzes the transfer of the aminopropyl group from decarboxylated *S*-adenosylmethionine (dcAdoMet) to putrescine in the biosynthesis of spermidine. PAPT of *Helicobacter pylori* (HpPAPT) is encoded by the *speE* gene. HpPAPT has less than 20% of sequence identity with other PAPTs, even containing no signature sequence. The three-dimensional structure of HpPAPT has been determined by multiwavelength anomalous dispersion (MAD) in this study. HpPAPT consists of an N-terminal beta-stranded domain and a C-terminal Rossmann-like domain, with a binding pocket between two domains. The oligomerization of HpPAPT is mostly made by the N-terminal domain and sensitive to the pH values of buffer. Our structure illustrates that HpPAPT has a distinctive binding pocket with a bigger space, a unique electrostatic potential surface of less acidity, and numerous unconserved residues. Due to the lack of the gatekeeping loop, HpPAPT may need to perform a significant conformation change to accommodate the ligand binding.

Keywords: spermidine synthase, putrescine aminopropyl-transferase, *Helicobacter pylori*