Stucture of *S. typhimurium* Formylglycinamide Ribonucleotide amidotransferase

Ruchi Anand[a], Aaron A. Hoskins[b], JoAnne Stubbe[b], Steven E. Ealick[a], [a]*Dept. of Chemistry and Chemical Biology, Cornell Univ., Ithaca, NY 14853.* [b]*Dept. of Chemistry and Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA*. E-mail: ra62@cornell.edu

Formylglycinamide ribonucleotide amidotransferase (FGAR-AT) catalyzes the ATP-dependent conversion of formylglycinamide ribonucleotide, and glutamine to formylglycinamidine ribonucleotide (FGAM) and glutamate in the purine biosynthetic pathway. In eukaryotes and Gram negative bacteria, FGAR-AT is encoded by the purL gene as a multidomain protein. In Gram positive bacteria and archaebacteria FGAR-AT is a complex of three proteins: PurS, PurL and PurQ. We have determined the structure of FGAR-AT from *Salmonella. typhimurium* at 1.9 Å resolution. The structure reveals four domains: an N-terminal domain structurally homologous to a PurS dimer, a linker region, an FGAM synthetase domain homologous to an aminoimidazole ribonucleotide synthetase dimer, and a triad glutaminase domain. A structural ADP molecule was found bound. A glutamylthioester intermediate was found in the glutaminase domain at C1135. The N-terminal domain is hypothesized to form the channel through which ammonia passes from the glutaminase domain to the FGAM synthetase domain.

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