Crystal Structure of NH_3-dependent NAD+ Synthetase from *Helicobacter pylori*

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Nicotinamide adenine dinucleotides (NAD+ and NADP+) play a central role in all living systems. They are essential and ubiquitous coenzymes, and are involved in biochemical processes ranging from redox reactions to DNA repair, DNA recombination, and protein-ADP ribosylation.

The prokaryotic and eukaryotic forms of NAD+ synthetase differ in terms of their substrate requirements. Prokaryotic NAD+ synthetase uses ammonia as a nitrogen source, whereas eukaryotic NAD+ synthetase requires glutamine. However, eukaryotic NAD+ synthetase belongs to the amidotransferase family, and has an additional domain that enables the enzyme to use glutamine as a nitrogen source. The amidotransferases are composed of a glutamine amide transfer (GAT) domain and a synthetase domain, and can be divided into F- and G-type amidotransferase families based on their GAT domains.

The need to identify new targets for antibacterial agents is growing due to increasing drug resistance. NAD+ synthetase from bacterial pathogens like *Helicobacter pylori, Mycobacterium tuberculosis, and Peudomonas aeruginosa*, is an attractive target for the development of new antibacterial drugs. We determined the crystal structures of *H. pylori* NAD+ synthetase in apo- and complex forms with NaAD & ATP to a resolution of 2.3 and 1.7 Å, respectively.

[1] Ozment C. e*t al., J Struct Biol,* 1999, **127**, 279. [2] Devedjiev Y. *et al., Acta Crystallogr D,* 2001, **57**, 806. [3] Gil Bu K. *et al., Proteins*, 2005, **58(4)**, 985.

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