Crystal Structures of *Bacillus Cereus* AdoP Complexed with Substrates

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Purine nucleoside phosphorylases (PNP, E.C. 2.4.2.1) catalyze the reversible phosphorolysis of purine (deoxy)nucleosides, generating the corresponding purine base and (deoxy)ribose 1-phosphate. PNPs purified from a broad range of organisms can be ascribed to two main categories on the basis of substrate specificity, molecular mass, subunit composition and amino acid sequence: low-molecular-mass homotrimers specific for 6-oxopurines, and high-molecular-mass homohexamers, accepting both 6-oxo- and 6-aminopurines [1].

Bacillus cereus adenosine phosphorylase (AdoP) belongs to the high-molecular-mass PNP class on the basis of amino acid sequence homology and molecular mass determination, but it differs from the other members of this subfamily because it exhibits a high preference for adenosine over inosine.

To investigate the structural basis of the unusual substrate specificity shown by *B. cereus* AdoP, we determined the structures of the wild type enzyme and an active site mutant, both complexed with substrates. Comparison of the different structures provides insights to the unique substrate preferences of *B. cereus* AdoP.

[1] Bzowska A. *et al*., *Pharmacol Ther*, 2000, **88**(3), 349-425.

Keywords: purine nucleoside phosphorylase, substrate specificity, structure comparison