Characterization of TenA from *Bacillus Subtilis*: A Thiaminase II Angela Toms, Amy Haas, Tadhg P. Begley and Steven E. Ealick. *Department of Chemistry and Chemical Biology, Ithaca, NY, 14853* USA. E-mail: at265@cornell.edu

The biosynthesis of thiamin pyrophosphate has been the focus of considerable effort over the past decade; most of the proteins involved in assembly, salvage, transport and degradation have now been identified and in many cases structurally and mechanistically characterized [1]. A conspicuous exception is TenA, which in B. subtilis is part of the thiazole biosynthetic operon. TenA is known to be strongly repressed by thiamin [2], suggesting TenA may have a role in thiamin biosynthesis or metabolism. The structure of TenA alone and in complex with 4-amino-2-methyl-5-hydroxymethylpyrimidine have been determined to 2.6 Å and 2.5 Å, respectively. It has also been demonstrated that TenA has thiaminase II activity. The TenA structure suggests that the degradation of thiamin by TenA likely proceeds via the same addition-elimination mechanism described for thiaminase I [3]. While the chemical reaction catalyzed by thiaminases is well defined, the biological function is not vet clear. The over expression of TenA in B. subtilis results in an increase in the secretion of the degradative enzymes subtilisin, neutral protease and levansucrase [4], providing evidence of a possible relationship between TenA and the Deg proteins. DegS undergoes autophosphorylation in response to an unkown signal. It is tempting to speculate that this unknown signal may in some way be due to the binding and/or degradation of thiamin by TenA.

[1] Settembre et al., Curr. Op. Struct. Biol., 2003, **13**, 739-747. [2] Lee et al., J. Bacteriol., 2001, **183**, 7371-7380. [3] Nicewonger et al., J. Org. Chem., 1996, **61**, 4172-4174. [4] Pang et al., J. Bacteriol., 1991, **173**, 46-54.

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