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**Crystal Structure of Aminoimidazole Riboside Kinase from *Salmonella enterica*.** Yan Zhang<sup>1</sup>, Diana M. Downs<sup>2</sup>, Steven E. Ealick<sup>3</sup>, <sup>1</sup>Dept. of Molecular Biology & Genetics, <sup>3</sup>Dept. of Chemistry & Chemical Biology, Cornell Univ., Ithaca, NY 14853, <sup>2</sup>Dept. of Bacteriology, Univ. of Wisconsin-Madison, Madison, WI 53706, USA.

The biosynthetic pathways for purine mononucleotide and the pyrimidine moiety of thiamine in bacteria share the first five steps, but separate after the formation of 5-aminoimidazole ribotide (AIR). Aminoimidazole riboside (AIRs) kinase encoded by the gene *stm4066* in *Salmonella enterica* is able to phosphorylate AIRs to form AIR, which enters the biosynthetic pathways.

The crystal structures of *S. enterica* AIRs kinase and its complexes with the substrate AIRs and with the substrate AIRs and an ATP analog were determined at 2.6 Å, 2.9 Å, and 2.7 Å, respectively. AIRs kinase is a homodimer with one lid-covered active site per monomer. The core structure, consisting of an eight-stranded β sheet flanked by eight structurally conserved α helices, indicates that AIRs kinase is a member of the ribokinase superfamily.

A comparison of the structure of AIRs kinase with other members of the ribokinase superfamily suggests that the active site lid and the conformational changes that occur upon substrate binding may be advanced features in the evolution pathway of the ribokinase superfamily. Details on the structure and structural comparison will be presented.