Pantothenate kinase of *Helicobacter pylori*: Comparative characterization of a previously unidentified form of the first Coenzyme A biosynthetic enzyme.

Brand, L.A., **Strauss, E.**

Department of Chemistry and Polymer Science, University of Stellenbosch, Private Bag X1, Matieland, 7602, South Africa

Coenzyme A is an essential cofactor biosynthesized in five enzymatic steps from pantothenate. The first of these steps is catalyzed by pantothenate kinase, which catalyses the phosphorylation of pantothenate to phosphopantothenate. Currently, two isoforms of the enzyme have been identified, one predominantly eukaryotic, inhibited by acetyl-CoA and the other prokaryotic, inhibited by CoA itself. *Helicobacter pylori* is a gram negative bacterium that does not contain a gene homologous to either the prokaryotic or eukaryotic pantothenate kinase. However, since CoA biosynthesis is essential a protein capable performing the pantothenate kinase reaction must be encoded by the *H. pylori* genome. Since previous genetic complementation experiments in *Bacillus subtilis* have implicated an as yet unidentified protein in the phosphorylation of pantothenate, we set out to clone, express and characterise the homologous protein from *H. pylori*. Our results show that certain conserved aspartate residue(s) in the active site of the enzyme are instrumental in phosphate transfer. This suggests that this protein is a third distinct isoform of pantothenate kinase which is more closely related to other enzymes involved in transferring phosphate groups via phosphorelays, such as those in bacterial two-component systems and certain members of the HAD superfamily, than the currently described pantothenate kinase isoforms.