

## **Homology modeling of putative thioredoxin from *Helicobacter pylori***

### **Abstract**

The tertiary structure of putative thioredoxin (trx) of *Helicobacter pylori* was generated based on structural homology of the X-ray crystallographic structure of thioredoxin from *Escherichia coli*. Inspection of theoretically predicted structure indicates that the thioredoxin of *H. pylori* is similar to that of *E. coli*. Analysis of the structure revealed that thioredoxins have a common fold, characterized by a core of twisted  $\beta$ -pleated sheet flanked either side by helices. The amino terminal end of the molecule is occupied by  $\beta$ - $\alpha$ - $\beta$  motif and carboxy terminal end by  $\beta$ - $\beta$ - $\alpha$  motif. This molecule is characterized by five strands and four helices. Among the four helices,  $\alpha$ 2 is the longest helix which was disrupted near proline. Proline72 is identified as cis-proline. This structure retained overall trx-fold with the conservation of global shape and the secondary structures. This work determines the structure of thioredoxin and is found to be unique for further insight into molecular characterization.