Protein structure prediction in recent years has become very important due to the fact that there are numerous genome sequencing projects going on or completed. However, the number of known protein structures corresponding to the number of discovered genes is less. So it becomes necessary to predict the structure from the amino acid sequence, while the actual experimental structure may take much longer to solve. There are different approaches that are used in structural bioinformatics to predict a protein structure. These include homology modeling, threading and \textit{ab initio} modeling.

The aim of this thesis is to predict the protein structure of the polyhydroxyalkanoate depolymerase (PhaZ7) an enzyme from the bacterium \textit{Paucimonas Lemoignei}. The thesis examines the various methods, servers and tools commonly used in the field of structural bioinformatics to predict the secondary as well as the tertiary structure of the enzyme based on its amino acid sequence, and also introduce the reader to the background of PhaZ7.

The important task from the structural bioinformatics point of view was to predict a structure that could prove useful for structure based studies of PhaZ7 and use the structure for various aspects of structural studies like secondary elements, structural similarities between the model and homologues, functional domain and use it for sequence to structure and structure to function studies until the experimentally solved structure was available.

Homology modeling proved to be very helpful to obtain a useful structure amongst all the prediction techniques used. This study was successful, because it helped in the visualization of important features in the structure. A comparison between the models generated and the experimentally solved structure is presented at the end of the thesis to understand the proximity of the two. This master's thesis was done in the protein crystallography group in BTK.

Keywords: \textit{Paucimonas Lemoignei}, PhaZ7, structural bioinformatics, protein structure prediction, homology modeling, threading