Abstract

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Protein Structure Prediction Using an Intio Approach

Protein structure prediction (PSP) is one of the most important issues in bioinformatics because it is believed that the biological function of the protein is determined by its structure. The challenge involves predicting the correct tertiary structure from a given amino acid sequence of a protein, Many approaches have been proposed for protein structure prediction such as homology, threading and ab initio. In this paper ab intio approach is used because homology and threading approaches depend on the presence of a template in the database. So both approaches fail in the absence of these templates. On the other hand, ab initio depends on chemical and physical properties of the amino acid. The methods described in this paper, predicts the best conformation that gives the tertiary structure using the physical energy function, It gives an approximate energy value with minimal CPU time compared with other well know methods.