

## **COMPARATIVE ANALYSIS OF COMPUTATIONALLY PREDICTED SECONDARY STRUCTURE OF AMYLASE ENZYME**

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**ABSTRACT :** The prediction accuracy can be expected to reach 80-85% with a large 10-fold increase in present sequence knowledge. This can be shown by applying a prediction technique to a standard set of query sequences, which can be obtained from sequence databases like NCBI. The percentage of alpha helix, beta turns, extended strand and random coils shows a probable pattern for various sequences. SOPMA is used for prediction of secondary structure of proteins and it can correctly predict 69.5% of amino acids for a three-state description of the secondary structure in a whole database containing numerous chains of non-homologous proteins whose identity should be less than 25%.

**Key Words:** Amylase, SOPMA, Protein Data Bank, Membrane helix, Random coil.