

**DATA STRUCTURE PROJECT PROPOSAL**

**Bio-Informatics**

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**Section: C**

**PROJECT NAME: PROTIEN STRUCTURE PREDICTION**

***MOTIVATION***: Protein structure prediction is one of the most important goals pursued by bioinformatics and theoretical chemistry; it is highly important in medicine (for example, in drug design) and biotechnology (for example, in the design of novel enzymes).

***ABSTRACT:Protein structure prediction*** is the inference of the three-dimensional structure of a protein from its amino acid sequence that is, the prediction of its folding and its secondary and tertiary structure from its primary structure. In early stage of our project we will predict secondary structure of protein.

**ALGORITHM USED: *Chou-Fasman*** is an empirical algorithm (Chou and Fasman, 1978) for the prediction ofprotein secondary structure originally developedby Robert S. Chao and Gerald D. Fasman in1978. The method is based on analyses of therelative frequencies of each amino acid inalpha helices, beta sheets, and turns based on known protein structures. From these frequencies a set of probability parameters were derived for the appearance of each amino acid in each secondary structure type, and these parameters are used to predict the probability that. A given sequence of amino acids would form a helix, a beta strand, or a turn in a protein.