**Abstract**

The main objective is to predict the structure of proteins. The key to the wide variety of functions shown by individual proteins is in their three dimensional structure adopted by this sequence. The main objective is to understand protein function at the molecular level, it is important to study the structure adopted by a particular sequence. This is one of the greatest challenges in Bioinformatics. There are 4 types of structures; Primary structure, Secondary structure, Tertiary structure and Quaternary structure. Secondary structure prediction is an important intermediate step in this process because 3D structure can be determined from the local folds that are found in secondary structures by ensemble learning methodology.