CHAPTER 7
CONCLUSION

The role of carbon in the hydrophobic nature of abnormal proteins was the main focus of this work. A simple sequence analysis with details to hydrophobic elements was carried out. Particularly, role of carbon along protein sequence, amino acid composition of hydrophobic regions, carbon distribution in viral, disorder, toxic proteins and mutational sites were studied. It was concluded that carbon plays an active role in abnormality of proteins.

Carbon content and distribution were different in viral proteins. The carbon distribution studies on viral proteins revealed that the viral proteins had higher amount of carbon. The atomic composition plays a role in the evolution of proteins, and the difference in carbon distribution in proteins cause disease. A difference in carbon distribution pattern was noticed in most of the H1N1 proteins and the distribution was not normal.

The analyses of mRNA sequence of Influenza A virus revealed that the adenine content was higher in all sequences. Further, thymine distribution in different frames was checked. Most important observation was that of excess thymine in frame 4 of strand 2 are responsible for production of protein with a different amino acid composition. Unusual thymine distribution in frame 3 was also observed. The thymine distribution was different in viral mRNAs compared to animals and minimizing this excess thymine may give normal proteins.

The carbon distributions in toxic proteins were described in relation to their functions. Computational analysis of carbon distribution in TSST, tetanus and diphtheria toxins depicted abnormal distribution of carbon.
A long stretch of hydrophilic/hydrophobic regions are considered as disordered regions. This disorder is due to unfolding or misfolding due to reduction of carbon or carbon rich stretch. Carbon analysis on SOD and tau identified a long disordered hydrophilic region.

The misfold due to carbon rich regions and unfold due to carbon less regions are responsible for disorders in proteins. This was confirmed by the analyses of methyl CpG binding protein and GHR protein.

The study will be helpful in disease solving at sequence level and for the identification and development of abnormal sites in proteins. It can also aid in the evolutionary understanding of proteins. These new findings in terms of carbon distribution on unusual proteins will be put forth. Thus, the carbon distribution study along the protein chain is the most significant step towards understanding the biological features, which can provide possible approaches for the design of new drugs to overcome the diseases.