

Structure modeling and computational prediction for locating functionally important sites in hsp27 proteins in human

A G Ingale

North Maharashtra University, India

The present study commences with prediction of 3-D structure of HSP 27 protein using comparative modeling and followed by evaluation of the predicted structure. The 3-D structure of HSP 27 protein is experimentally not known; therefore computational method was resorted to build a model through comparative modeling, allowing us to study its interactions. A 3-dimensional model (3-D) was developed for the Heat shock protein (HSP27) using homology modeling method. For the modeling, two template proteins were obtained by mGenTHERADER, namely the high-resolution X-ray crystallography structure of a FERREDOXIN (1FCA) of *Clostridium acidurici*. Three dimensional structure of protein is of great significance for the rational design of many different types of biological experiments. In current study 3-D modeling of Heat shock protein beta-(HSP27) was performed by using GenThreader followed by modeller9v7. The validation of predicted 3-D structure was done using Procheck, Anolea, Gromos96 and Swiss Pdb-viewer tools. CASTp was used further to study surface features and functional binding pockets in protein. The information thus discussed provides insight to the molecular understanding of Heat shock protein beta-(HSP27). The predicted 3-D model may be further used in characterizing the protein in wet laboratory.

Biography

A G Ingale obtained Ph.D. in Biotechnology from Sant Gadge Baba Amravati University, Amravati (India). He was the Founder Head, Department of Biotechnology, Dr. Babasaheb Ambedkar Marathwada University, Aurangabad (MS) India. Ingale is President of Society for Biotechnology and Bioinformatics, India. He is also the editor in-chief of the Journal of Biotechnology and Bioinformatics (JBB) and International Journal of Modern Biotechnology. He has received the award as a Fellow of Society of Sciences (FSSc), Dumka. His primary field is immunology with research emphasis on CD antigens and the structure-function prediction using Bioinformatics approach. He has recently entered the developing field of Lectin Biosensor and GlycoNanobiotechnology research. In Genomics research area he has been working on constructions of transgenic Okra against pest (*Lipidopteron*) and pigeon pea against bollworm. In proteomics research area he is working on proteomics of lectin and other plant and microbial proteins. Finally, his main research area is bioinformatics. In this, he has developed a database of CD markers and Toxin database is on completion. He has published several research papers in national and international, journals of repute. He has submitted protein and nucleotide sequences on NCBI and viral protein models are being submitted in PDB database. Currently, Dr. Ingale is holding major research projects as a Principal Investigator and Head of the Department of Biotechnology, North Maharashtra University, Jalgaon (MS) India.

agibitech@gmail.com