

Structure prediction and nucleic acid binding studies on human YB-1 protein

Swati Singh¹, Amit Kumar Shaw², Ashutosh Mani³ *

¹Center of Bioinformatics, University of Allahabad, India-211002.

²Department of Biotechnology, National Institute of Technology Durgapur, India-713209.

³ Department of Biotechnology, Motilal Nehru National Institute of Technology Allahabad, India-211004.

Abstract:

Cold shock domain proteins are ancient and conserved proteins. These proteins are known to be involved in many significant functions inside the cell. They possess a cold shock domain that is highly studied for its nucleic acid binding capabilities. Here we have modelled the three dimensional structure of human cold shock domain protein, validated the structure and performed nucleic acid binding studies by using molecular docking.

Key words: Cold shock domain protein, nucleic acid binding, docking