

Figure 1: Graphical representation of the thermodynamic cycle involving confinement method.

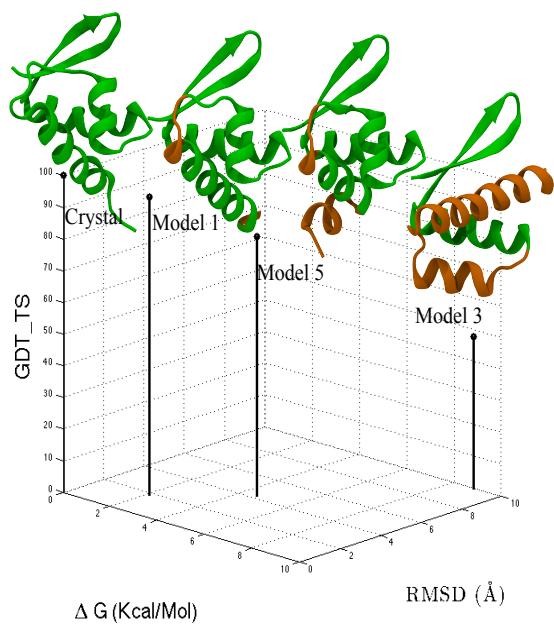


Figure 4: The native and three submitted model structure, along with their GDT_TS, RMSD and relative Free energy values of protein BVU3908 from *Bacteroides vulgatus* (PDB id: 2L01 and CASP code: T0559).

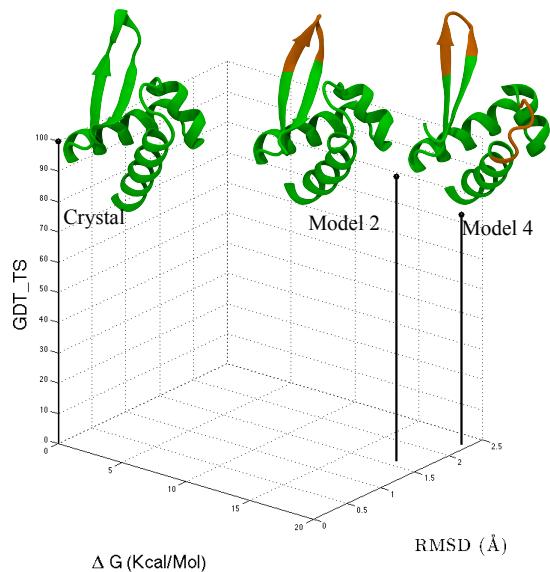


Figure 5: Native and two model structure of protein BT2368 from *Bacteroides thetaiotaomicron* (pdb id: 2L02 and CASP code: T0560). The two models were from the group "Splicer".

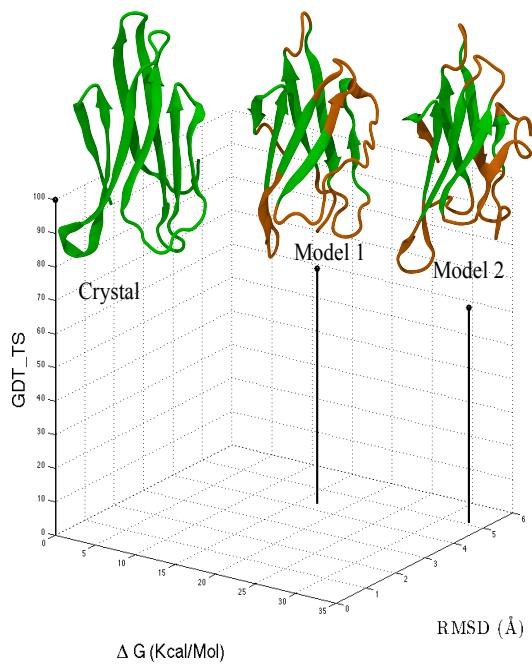


Figure 6: X-ray crystallographic structure and two submitted models of fas apoptosis inhibitory protein (pdb id: 3MX7 and CASP code: T0540). Model 1 and Model 2 in this analysis were submitted by the group LTB and MUFOLD respectively.

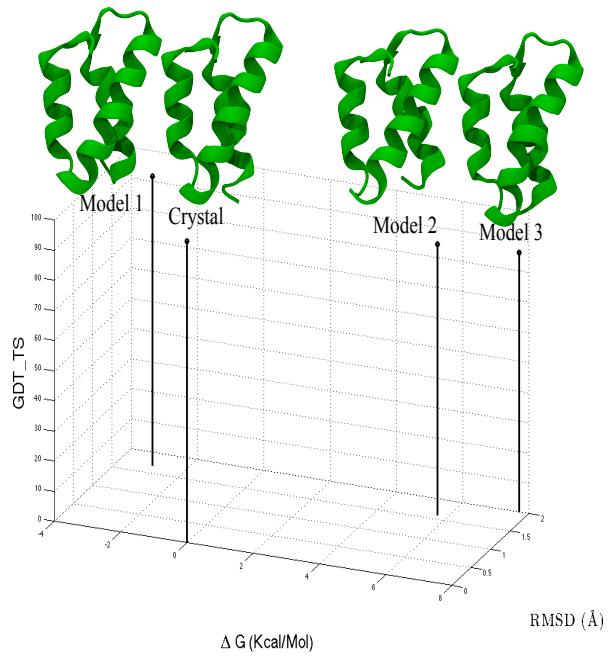


Figure 8: The native and three model structure of engineered protein from Asr4154 protein (PDB ID: 2L09 and CASP code:T0538). The model 1,2 and 3 are from the group PconsR, Shell and FOLDIT respectively.

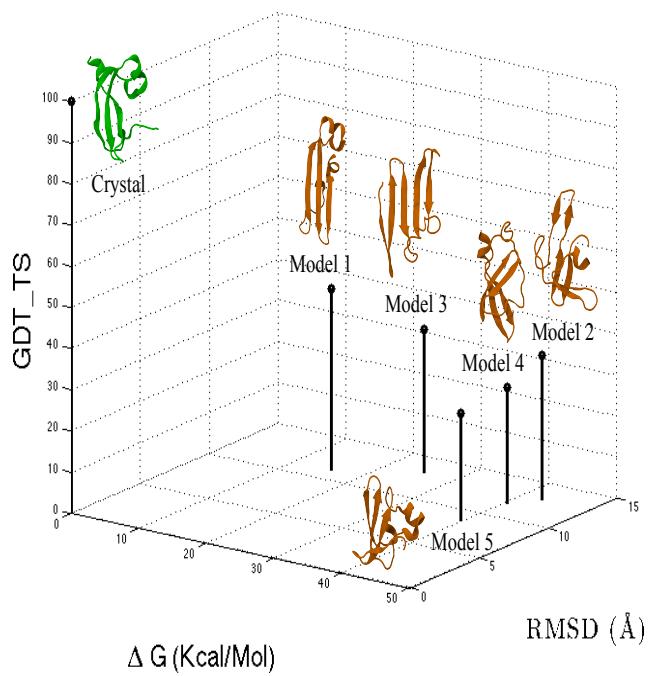


Figure 9: The native structure and 5 models of extracellular domain of the jumping translocation breakpoint protein (pdb id: 2KJX and the CASP code: T0531).