**Domain Mapping of the nsSNPs**

To assess the impact on final protein product of 40 GC genes, we retrieved the amino acid sequences of final product (protein) of the corresponding genes. The SNPs in domain regions have been thought to be strong candidates that alter protein functions. Thus, we have tried to explore whether our identified nsSNPs fall within the domain regions. We have utilized ScanProsite, Pfam and InterPro tools to find out all possible domains of the 40 GC gene products. Our findings suggest that most of the selected nsSNP were located within some domains or motif regions. We have addressed the individual domain IDs, name of the domains, their functions as well as their specific positions within the protein.

**3D Modelling and Free Energy Deviation Calculation**

We performed BLAST against the Protein Database (PDB) to find out the structure of the closest related proteins. We selected the closest template for each protein sequence of corresponding 40 genes. Then we built the 3D model and checked the quality of each model. Further, we replaced the amino acid (nsSNP) from wild type protein sequence and assessed the quality of the model. YASARA view mutation tool carried out the mutations (G59S, P62S, L184S, L224P, A276V, L361P, R592H, T595M, and I673T) separately of each final product of corresponding genes and it showed the decreased free energy for all the mutant models than the wild type models. These results point toward noteworthy change in the structure of each protein that can demolish its natural function.