Figure 1

Nonsynonymous coding SNPs (nsSNPs)

- Evolutionary-based approach (Sorting Intolerant from Tolerant)
- Structure-based approach (Polymorphism Phenotyping)
- To predict the impact of these amino acid substitutions on protein activity (PupaSuite)

Based on SIFT and PolyPhen results, identified the possible mutations. Mutation analysis was performed using SWISSPDB viewer, and energy minimization for three-dimensional structures was performed using NOMAD-Ref server.

- Computing the total energy
- Root Mean Square Deviation (RMSD)

The amino acid residues in the native and mutant model protein were further analyzed for solvent accessibility (NetASA) and secondary structure (DSSP) to check the stability of the proteins.