**Putative Effect of nsSNPs on Drug binding**

Drug binding analysis was also carried out to confirm the structural variation and possible dysfunction of the final product of each 40 GC genes between wild type and mutant model. We have utilized DrugBank to select the drugs against the protein receptor of 40 GC genes. DrugBank suggested that some drugs were available against the corresponding protein of 10 GC genes. Thereafter, we have performed molecular docking analysis between the suggested drugs and protein receptor of 10 GC genes. We have found the result of 8 GC genes which bound the different interacting residues with different binding affinity where the same docking area was used for docking runs. These results confirmed the structural variation and drug could not be effective against mutant model if the individuals with this polymorphism.