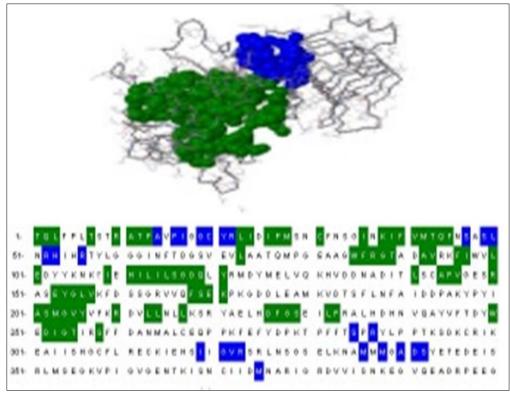
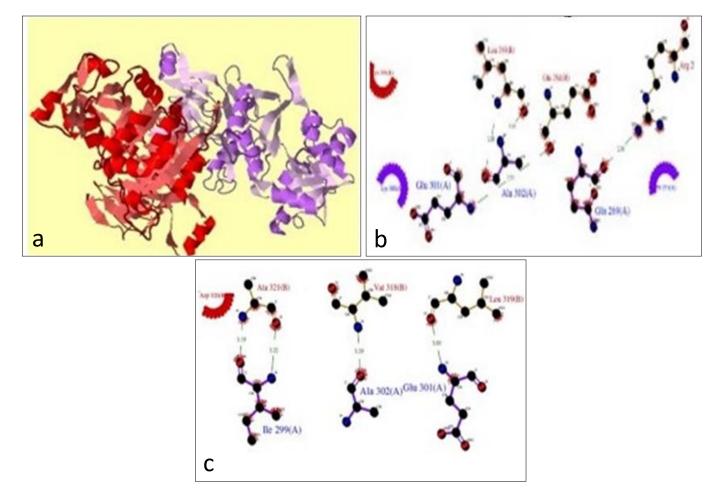
Rani S, Gupta A, D Kaushik D, Rustagi S, Malik S, Yogi R, Singh N. *In silico* structural modeling of normal and mutated subunits of ADP-glucose pyrophosphorylase from *Triticum aestivum* to study protein-protein interactions. Plant Science Today (Early Access). <u>https://doi.org/10.14719/pst.2701</u>

## **Supplementary Figures**



**Supplementary Fig. 1.**The generated model run on the CastP shows two important coupling pockets. One is area 2303.1 and volume 3755.5 (**shown in green**), the other is area 579.5 and volume 654.5 (**shown in blue**). Below is shown the composition of amino acid residues involved in each binding pocket.



Supplementary Fig. 2. a) Model of AGP-S (Magenta) and AGP-L (Red) complex interaction and hydrogen bonding pattern; b) with normal large subunit; c) with the mutated large subunit.