and in E.coli. (Figure 18). It thus appears that this region may be important for the small subunit to have particular structure for the biological function of the enzyme. Therefore one amino acid residue substitution in this conserved region may result in failure of the enzyme to form certain conformation and lead to loss of the biological function of the enzyme.

The amino acid position #141 is involved in substrate binding site of E.coli [Kumer et al., 1988]. The tyrosine residue at position #141 of E.coli was replaced by phenylalanine in all the plant small and large subunits of ADPglucose pyrophosphorylase sequences. It is presently unknown whether the replaced phenylalanine residue can serve as the substrate binding site. Olive et al., [1989] suggested that the role of phenylalanine residue might be the same as that of tyrosine residue in coordinating the adenine rings of ATP and ADP-glucose via hydrophobic stacking interactions. However in site-directed mutagenesis studies, the changed phenylalanine showed low affinities for substrates of E.coli [Kumer et al., 1988]. If phenylalanine residue #141 of Bt2 sequence could serve as the catalytic site of the maize enzyme, the amino acid substitution at position #147 might affect the ability or stability of catalytic conformation. According to the Chou and Fasman [1974] secondary structure predictions, the alanine residue #147 of Bt2 is a strong alpha helix former. On the other hand, the valine residue #147 of