It is of major importance to note that Sh2 and Bt2 loci, known through genetic tests to encode complementary rather than duplicate functions, share much sequence similarity at the protein level. Both genes are approximately equal in terms of the percentage of amino acids found in common with the E.coli enzyme. Thus, it would appear that Sh2 and Bt2 arose via a gene duplication followed by sequence divergence. The genes are related but have evolved to the point where the function of each gene is necessary for ADPglucose pyrophosphorylase function.

Since the ADPglucose pyrophosphorylase is allosterically regulated by 3-phosphoglycerate and Pi in plants [Preiss, 1982] the enzyme contains several functional sites, of which one is involved in catalysis and probably two different sites are involved in allosteric activation and inhibition [Haugen et al., 1976].

The lysine residue #98 (Figure 8) at the N-terminal and the sequence surrounding it are important for allosteric activation of the E.coli ADPglucose pyrophosphorylase [Parson and Preiss, 1978a; 1978b]. The amino acid sequence at the position #98 of Bt2 which encodes small subunit of maize endosperm ADPglucose pyrophosphorylase was conserved and the similarity of the sequence surrounding it is 90% (residue #95-104) identical to the sequence of E.coli. However in the Sh2 which encodes large subunit of maize endosperm ADPglucose pyrophosphorylase, the amino acid at the position #98 is