bt2-C is a strong beta-sheet former. Therefore the single amino acid substitution at position #147 might disrupt the secondary structure of the polypeptide in this region and result in disability or instability of the catalytic conformation of the enzyme.

The arginine residue at amino acid position #376 of the Bt2 sequence is conserved in the equivalent small subunit sequences of rice endosperm, potato tuber (B22-1) and spinach leaf (SL-51kD) (Figure 19). The sequence identity of the amino acid residues surrounding the arginine residue shows 88-100% with the small subunits of ADPglucose pyrophosphorylase genes. The arginine residue is also conserved in the equivalent large subunit sequence of maize endosperm (Sh2) and in E.coli. In the sequence of large subunit wheat endosperm (WE:AGA3), the arginine residue is replaced by proline residue (Figure 19). The sequence identity of the amino acid residues surrounding the arginine residue is 25-50% with the large subunit of ADPglucose pyrophosphorylase genes. Even relatively low identity between the sequences of small subunit and large subunit ADPglucose pyrophosphorylase genes in this region, the arginine residue was conserved except in the sequence of wheat endosperm. With 25% identity between Bt2 and E.coli sequences in this region, the arginine is also conserved. Therefore, the arginine residue #376 appears to be important for the polypeptide to maintain biological function. In the sequence of bt2-C, the arginine residue #376 is