residue is replaced by another aromatic, hydrophobic residue, phenylalanine in \textit{Sh2} and \textit{Bt2} (Figure 8), the amino acids surrounding it show relatively high level of identity, 79\% in the residues 176-186.

It thus appears that despite the low similarity between two subunits of maize ADPglucose pyrophosphorylase, there is sequence similarity in regions corresponding to the functional domains except the activator-binding site of E.coli where only the small subunit contains the similarity with E.coli. However the presence of two subunits for maize ADPglucose pyrophosphorylase may not be explained by this differential conservation at the activator binding site between \textit{Sh2} and \textit{Bt2} since there is another activator binding site at the carboxyl terminus of both subunits.

4.5 \textit{DNA Sequence Comparison between the Rice cDNA Clone and Bt2}

The strategy adopted for isolating a cDNA clone of the \textit{Bt2} locus was based on the DNA sequence conservation between rice and maize ADPglucose pyrophosphorylase gene. The nucleotide sequences of \textit{Bt2} and rice and the amino acid sequences of \textit{Bt2} and rice are compared in Figure 9. The sequence data showed a great extent of similarity at the nucleotide level as well as amino acid level; 81\% similarity at the nucleotide level and 86\% similarity at the amino acid level in the protein coding region. About 50\% of dissimilarity came from the 5’ end of protein coding region.