overlapping regions and do not, therefore, take into account the size of gaps between the overlaps. There is 45% similarity between amino acid sequence on \textbf{Bt2} cDNA and that of \textbf{Sh2} cDNA. In addition, \textbf{Bt2} cDNA is 35% identical to \textit{E.coli} ADPglucose pyrophosphorylase. \textbf{Sh2} cDNA was reported to be 27% identical to \textit{E.coli} ADPglucose pyrophosphorylase gene [Bhave et al., 1990] while it shows 24% identity to \textit{E.coli} ADPglucose pyrophosphorylase gene in this alignment. 23% of the amino acids are conserved in all three proteins. Despite the overall low similarity between those two maize endosperm cDNAs and \textit{E.coli} ADPglucose pyrophosphorylase gene, there are several well conserved domains, for example, amino acid residues #98-105 (88% identity), #118-125 (83% identity), #176-186 (79% identity), #262-264 (100% identity), #296-303 (100% identity), #358-364 (90% identity), #371-373 (100% identity), #399-401 (100% identity). Some of these domains are probably related to important regions of enzyme and will be discussed later.

The N-terminal and carboxyl terminus amino acid sequences of \textit{E.coli} ADPglucose pyrophosphorylase differ from those of the \textbf{Sh2} cDNA and \textbf{Bt2} cDNA. Thus these regions appear to be unique to \textit{E.coli}. \textbf{Bt2} and \textbf{Sh2} sequences share a great deal of identity at the carboxyl end of polypeptide. Such \textit{E.coli}- or maize specific regions may have some significance in the locations of the binding sites of the enzyme and will be discussed later.