Fig. 3. Multiple sequence alignment using the CLUSTAL X v.1.8 program of the partial GAPDH sequences from photosynthetic eukaryotes and bacteria. Sequences obtained in this work as well as published amino acid sequences of bacterial and plant sources, as described in Materials and methods, were included. The conserved motives including the catalytic important residues Glu 264 and Cys 298 (showed in bold) are underlined. The degenerate primers used in PCR experiments are indicated by arrows.