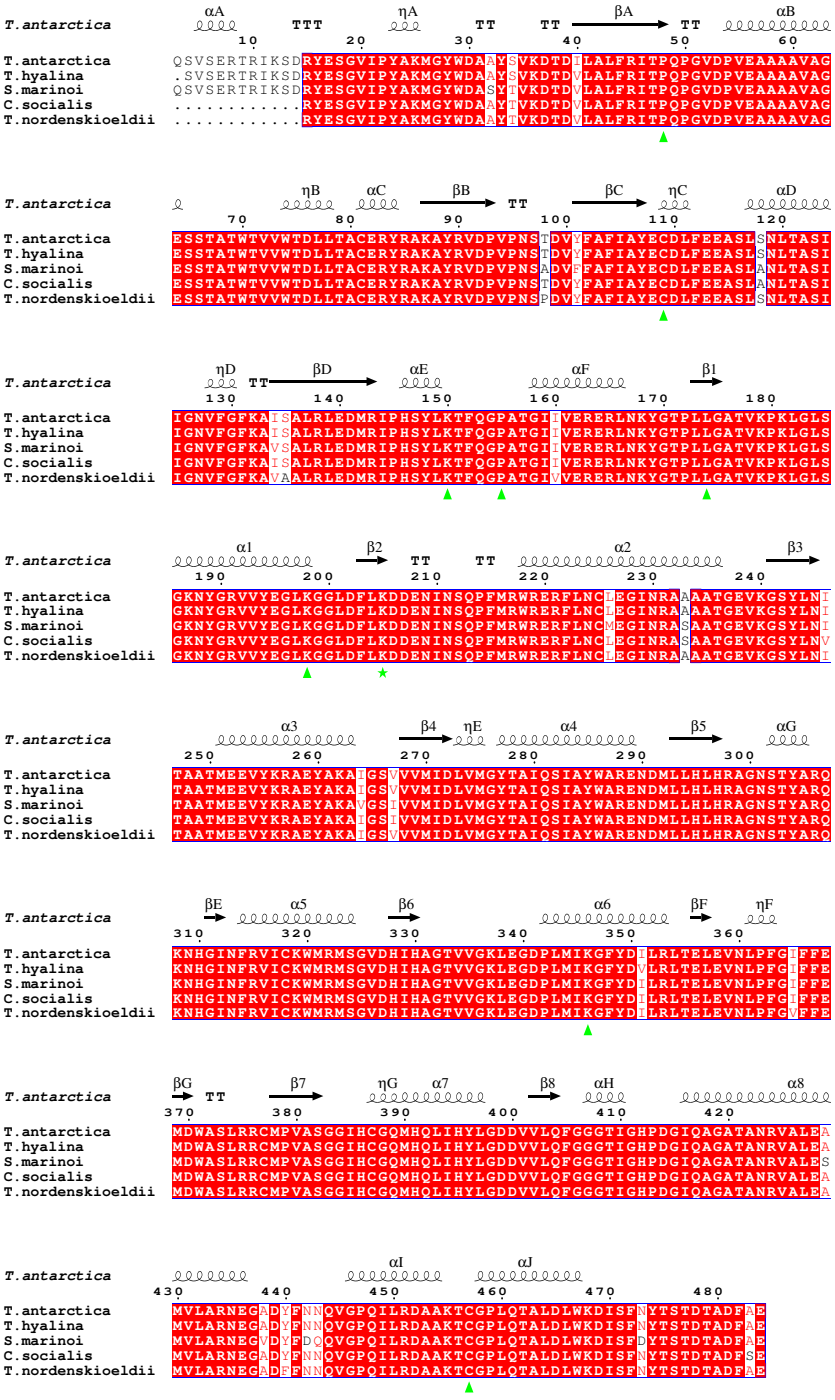
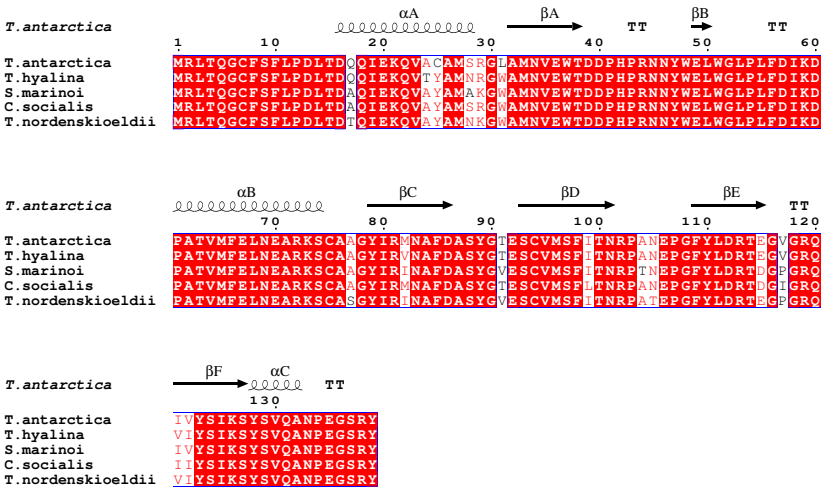
Supporting Figure 1. Amino acid sequences of *rbc*L and *rbc*S deduced from the analysis of the crystal structures of diatom Rubiscos. Conserved residues are *boxed*, strictly conserved residues have a *red background*, residues well conserved within a group are indicated by *red letters*, and the remaining residues are in *black letters*. Gaps are represented by dots. Residue numbering along the top refers to *T. antarctica*. *Symbols above* blocks of sequences correspond to the secondary structure: α, α-helix; β, β-strand; η, 3_{10}-helix. The secondary structure elements were named βA, βB..., αA, αB...etc, except for the strands and helices of the C-terminal βα barrel, which were named β1, β2..., α1, α2, etc according to Knight *et al.,* 1990. *Symbols below* blocks of sequences indicate the location of modified residues (green triangles) and the carbamylated lysine residue (green star). The sequence alignment was created using the PDB coordinates 5MZ2 (*T. antarctica*), 5N9Z (*T. hyalina*), 6FTL (*S. marinoi*) and 5OYA (*C. chaetoceros*).





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