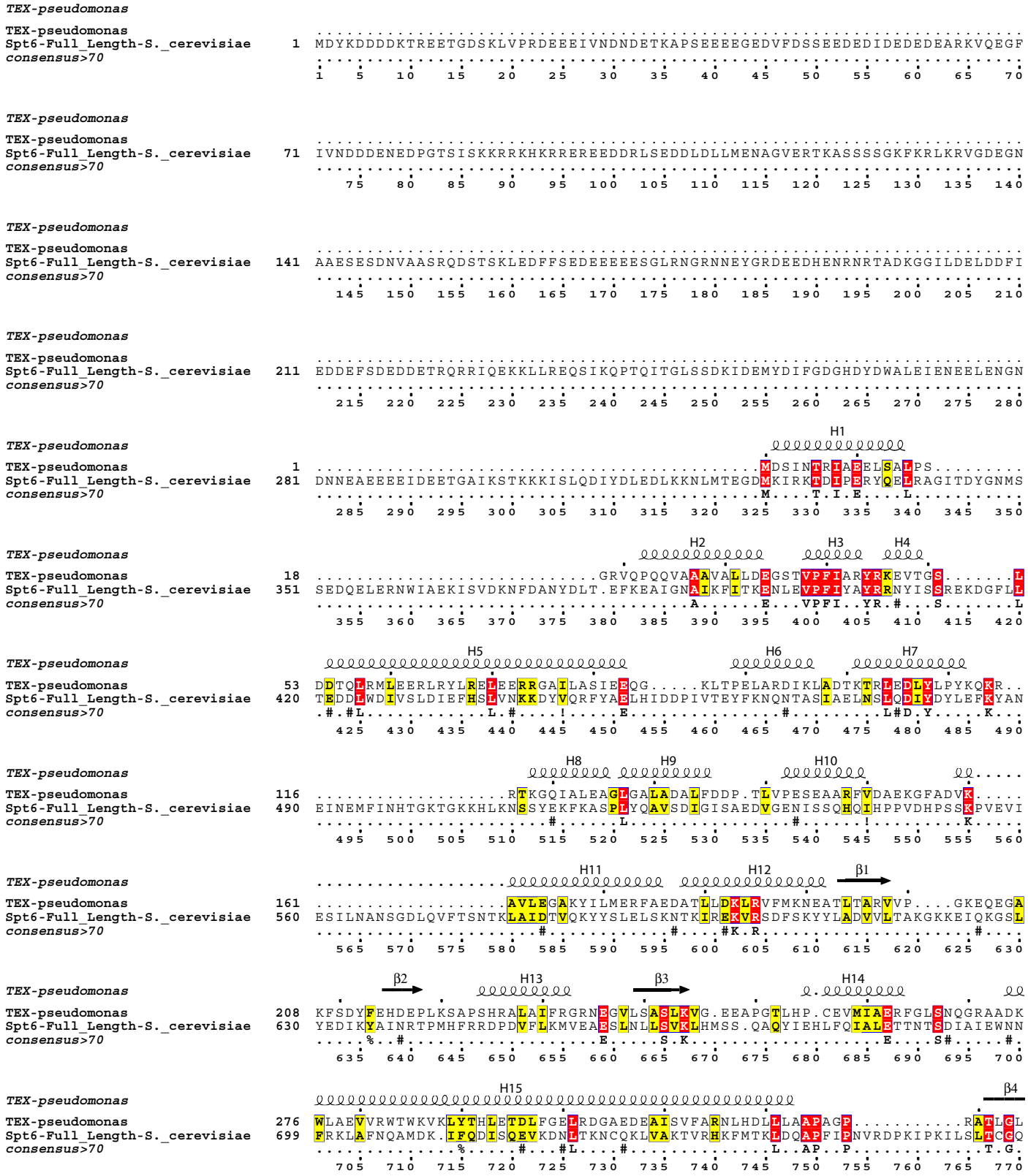Figure S4. Amino acid sequence alignment of Tex (*P. aeruginosa*) and Spt6 (*S. cerevisiae*). Observed Tex secondary structure is indicated above the Tex sequence. Highlighted regions indicate identical (red) and similar (yellow) residues. Sequence alignment was performed using ClustalW.[1] Figure was created using ESPript.[2]