



**Figure S4.** Alignment of the CTEs of the Cdc3, Cdc11, Cdc12 and Shs1 orthologs from various yeast species. CLUSTAL-W (THOMPSON *et al.* 1994) was used to align the orthologous septin sequences (residue numbers in parentheses) from: Sc, *Saccharomyces cerevisiae*; Ag, *Ashbya gossypii*; Ca, *Candida albicans*; Cg, *Candida glabrata*; Dh, *Debaryomyces hansenii*; Kl, *Kluyveromyces lactis*; Lt, *Lachancea thermotolerans*; Vp, *Vanderwaltozyma polyspora*; and, Zr, *Zygosaccharomyces rouxii*. Position of  $\alpha$ -helix VI (purple cylinder) of the GTP-binding domain is based on sequence homology and modeling (MCMURRAY AND THORNER 2008) against the crystal structures of human septins (SIRAJUDDIN *et al.* 2007); position of the most strongly predicted 4-3 hydrophobic repeat (yellow cylinder), a potential coiled-coil forming segment, is based on algorithms described in (VERSELE *et al.* 2004; BARTH *et al.* 2008). Various deletions (red boxes; (residues removed indicated) of the "linker" sequence between  $\alpha$ -helix VI and the coiled-coil segment in the corresponding *S. cerevisiae* septin were constructed. Cdc10 is not shown because it does not possess a CTE of significant length.