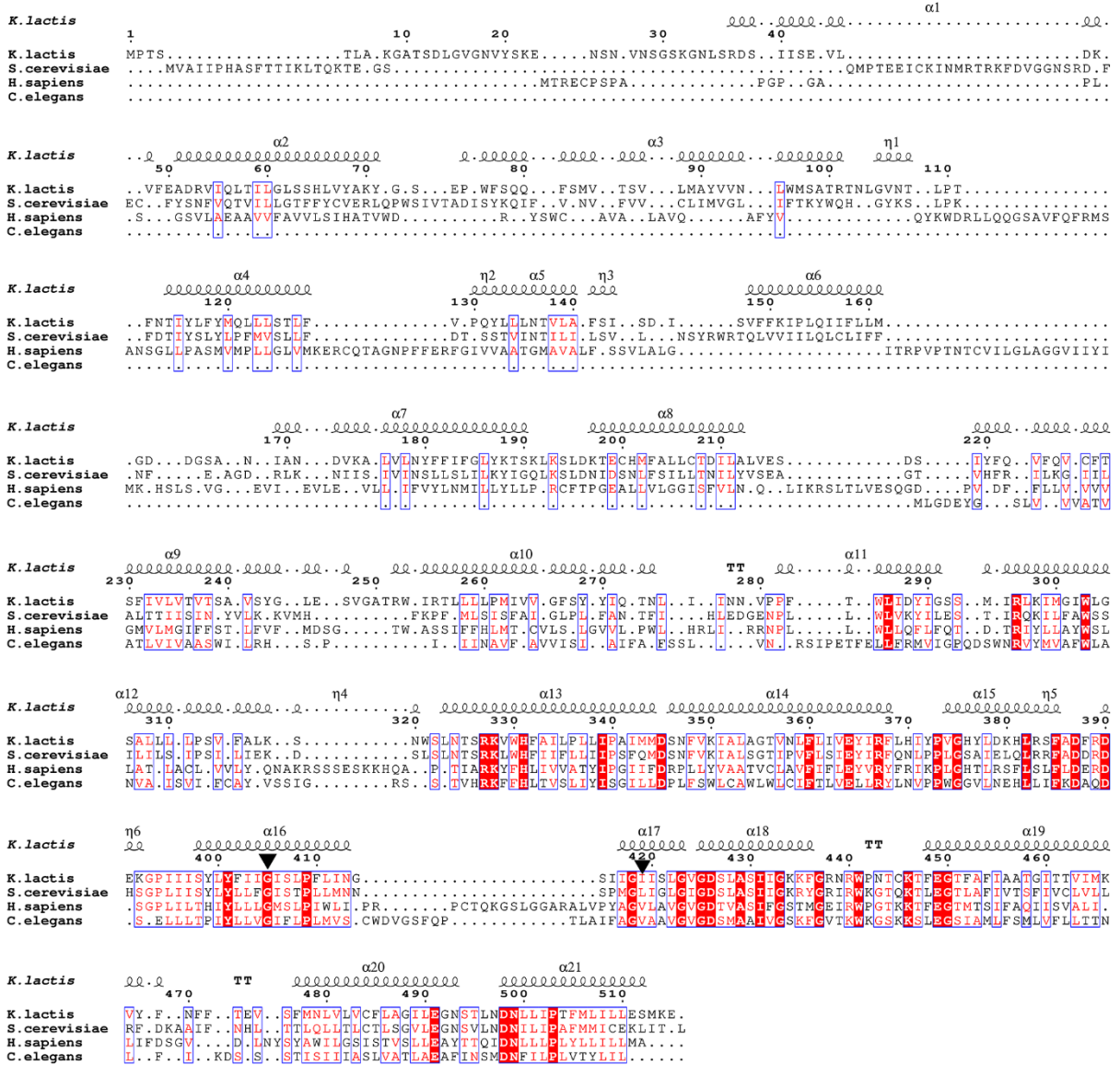


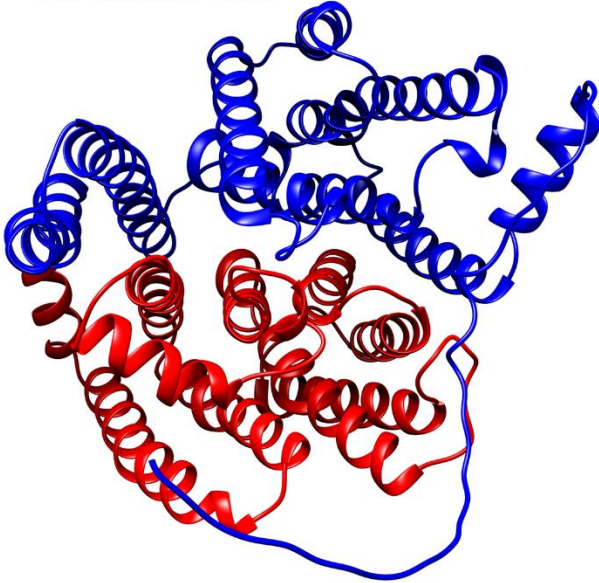
# S1 Fig.

**A**



**B**

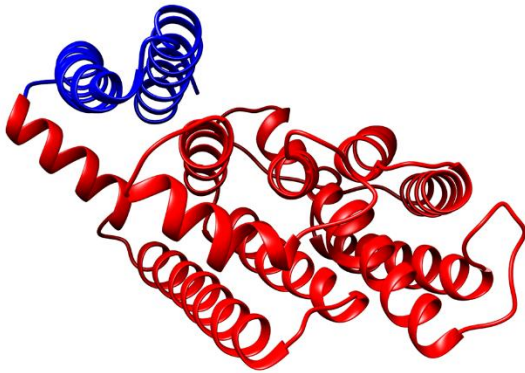
***K. lactis* DK**



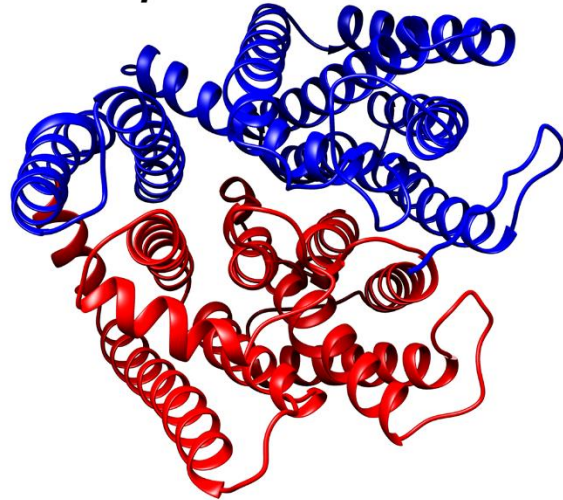
***S. cerevisiae* DK**



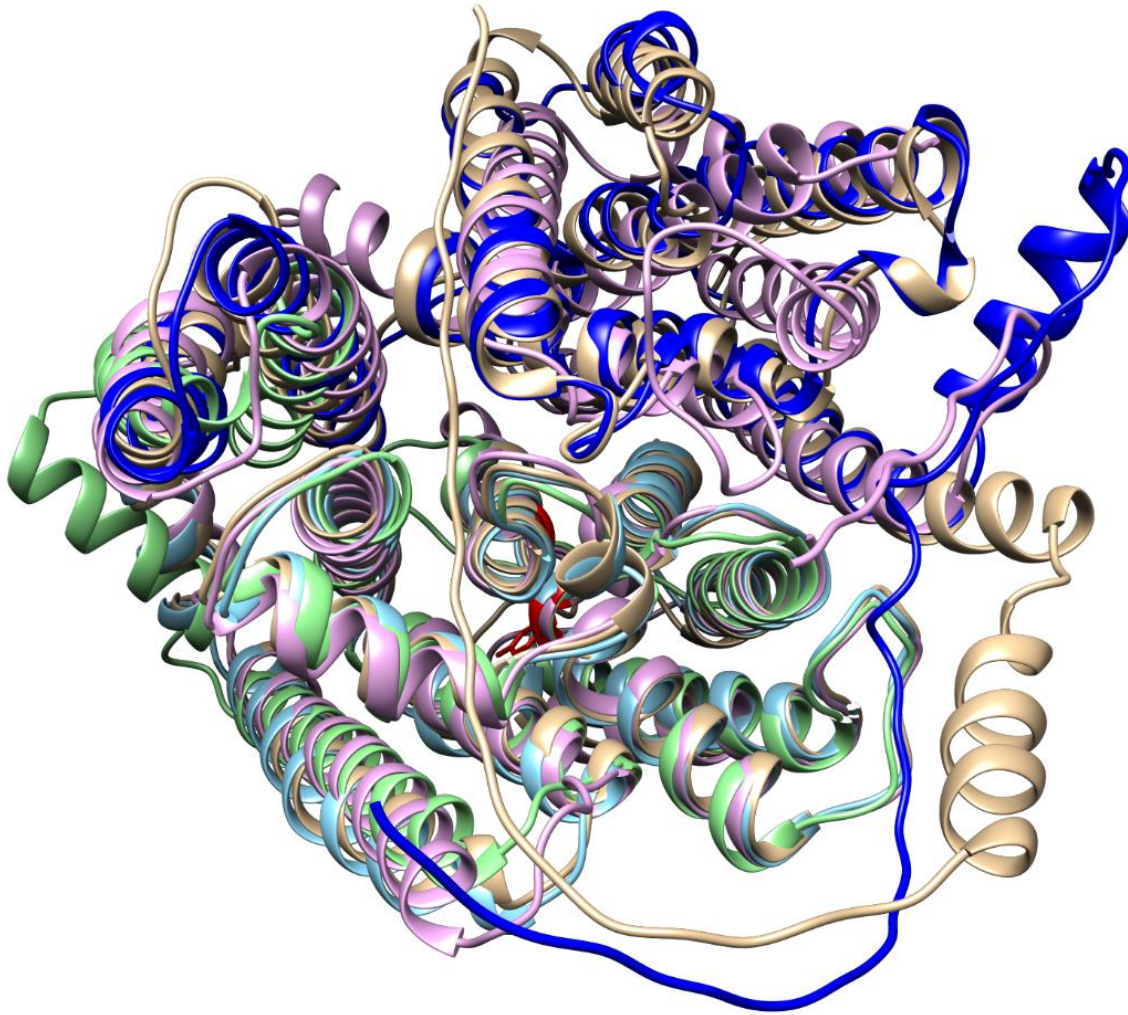
***C. elegans* DK**



***H. sapiens* DK**



C



**S1 Fig. Analysis of *K. lactis*, *S. cerevisiae*, *H. sapiens* and *C. elegans* DK sequence and structure similarities.** (A) Amino acid sequence alignment of *K. lactis*, *S. cerevisiae*, *H. sapiens* and *C. elegans* DK obtained from the alignment of AlphaFold3 3D models of appropriate proteins using UCSF Chimera tools. The aa residues G405, I419 which mutated in the *K.lactis* DK WSS mutant, and corresponding aa residues G407, L421 in *S.cerevisiae* WSGS mutant DK are marked with ▼. Representation of the alignment was carried out using ESPript3. (B) *K. lactis*, *S. cerevisiae*, *H. sapiens* and *C. elegans* DK 3D AF3 models obtained with AlphaFold3. The proposed N-terminal (blue) and C-terminal (red) domains are suggested based on evolutionary data. (C) Superimposed 3D structural models (obtained with AlphaFold3) of 4 dolichol kinases. *K.lactis* DK N-terminal – colored in blue and C-terminal domain – in sky blue, *S.cerevisiae* DK – in tan, *H.sapiens* – in plum, *C.elegans* – colored in light green. The aa residues G405, I419 which mutated in *K.lactis* DK WSS mutant, and aa residues G407, L421 which mutated in *S.cerevisiae* WSGS DK are marked in red.