

**BACKGROUND**

STARD4 is a member of the StAR-related domain protein family and binds cholesterol for intracellular transport.

**AIM**

Describing the region responsible for membrane binding in STARD4

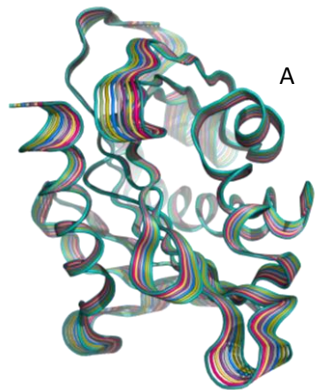


Figure 3 : **Flexibility within the membrane binding region of the STARD4 protein.** Figure 3-A showing protein flexibility in mode 8. Figure 3-B showing protein flexibility as fluctuation of atomic displacement.

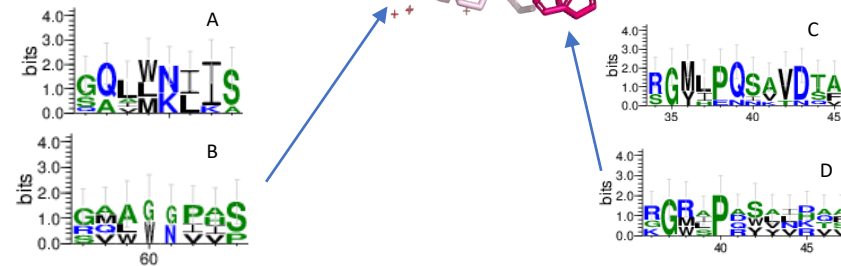
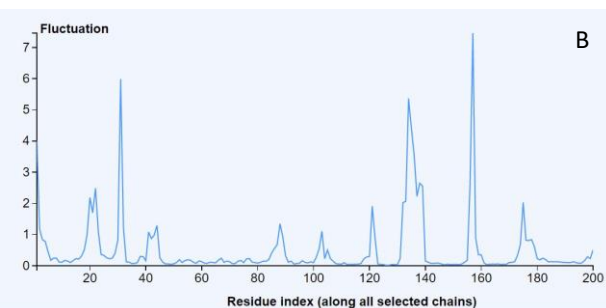


Figure 1 : **STARD4 protein structure and membrane binding sites.** Membrane binding sites show low conservation in between the STARD proteins(B,D), but higher in between different species(A, C).

By Marthe Dalsplass  
Supervisor : Nathalie Reuter  
Institutt for Biovitenskap

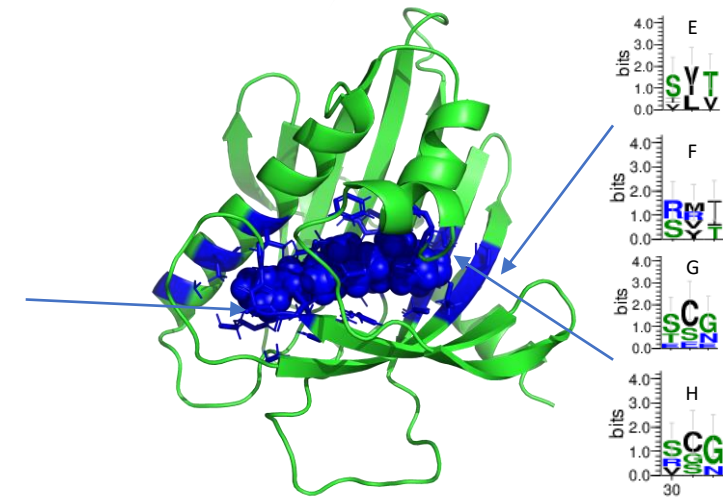
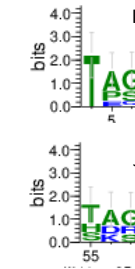
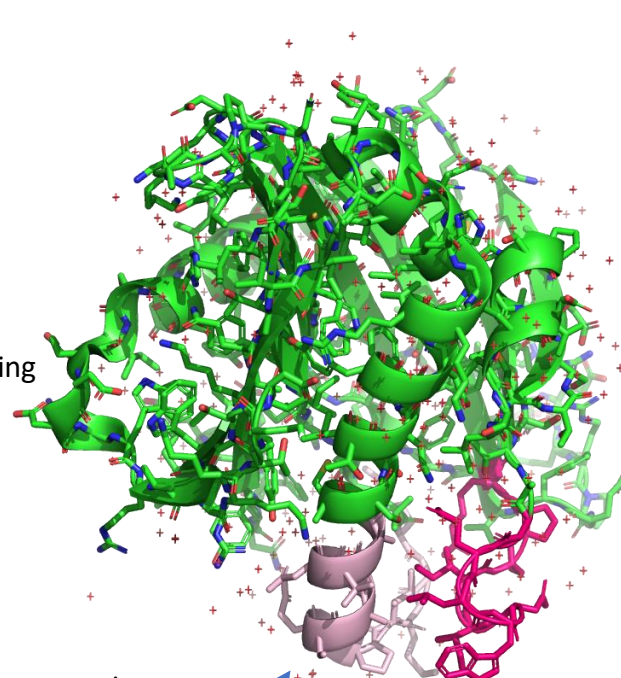


Figure 2 : **Cholesterol binding site in different species and STARD proteins.** Ligand binding sites shows higher conservation in the SCG amino acid group than other areas of the binding site, both in between species(E, G, I) and proteins in the STARD family(F, H, J).

**CONCLUSION**

Low conservation in both membrane and ligand binding sites between species and other STARD family proteins.

Flexibility is shown to be low near membrane binding sites, but high in the ligand binding site coding to the bottom of the binding cavity (Figure 3-B). Flexibility in TAG region of the ligand binding site is connected to the membrane binding site(Fig.1-A) and affects the ligands ability to enter and leave the binding site. Most flexibility is found in areas coding for the opposite side of the protein from the membrane binding site.

**REFERENCES**

- Lingchen Tan et al, Structural (2019) 466-472
- Louise H Wong et al, Lipid transfer (2019)

