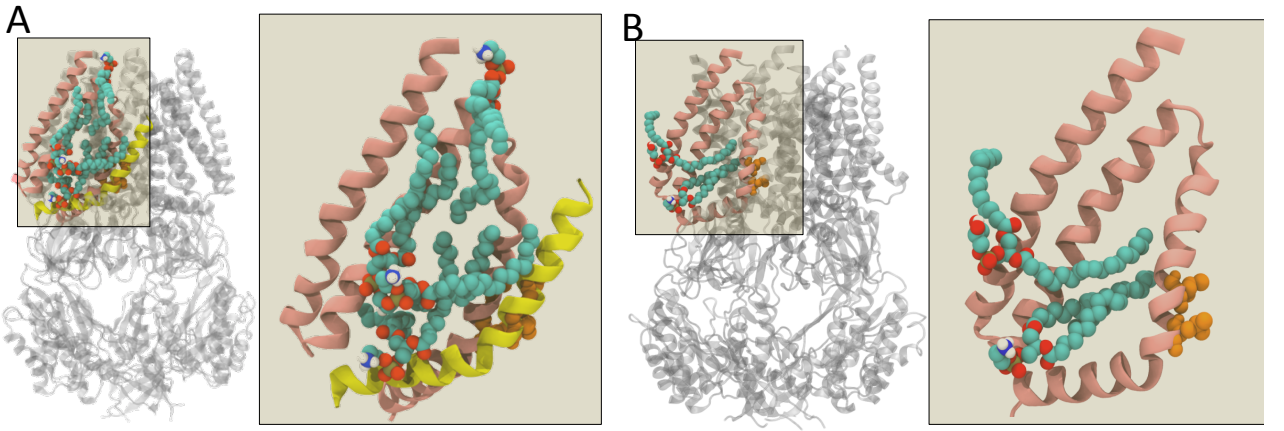
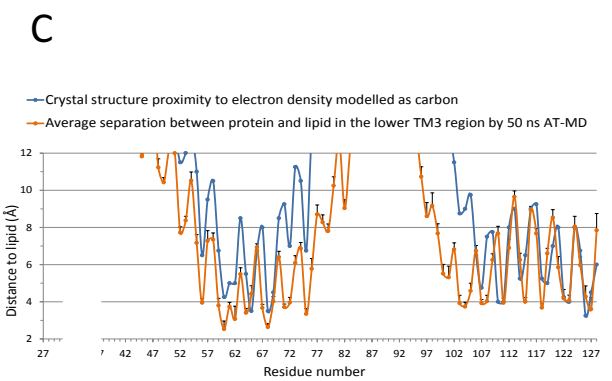
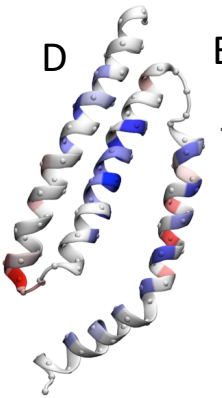
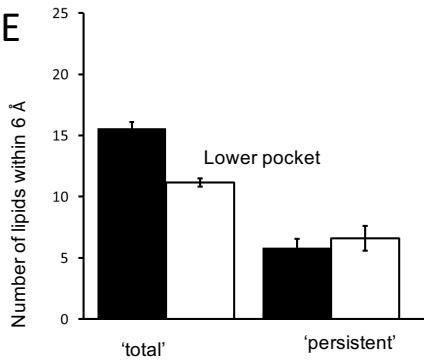
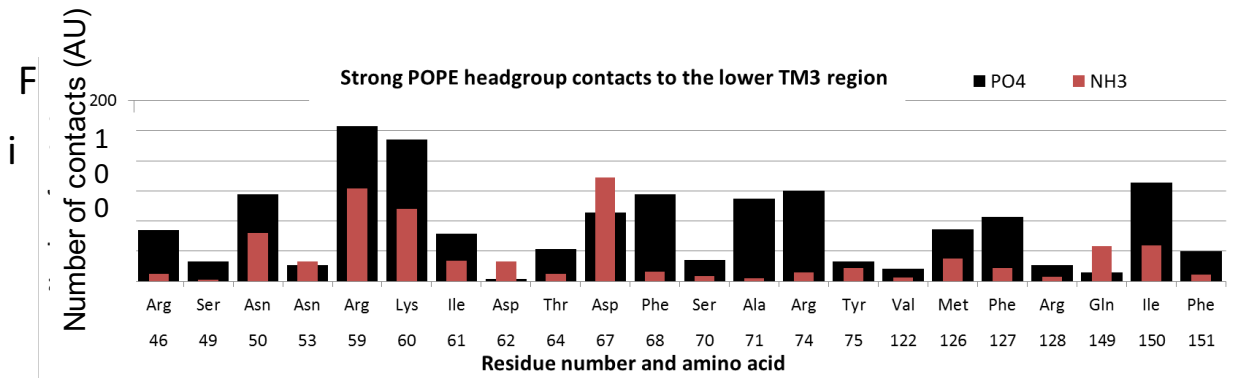

A
B

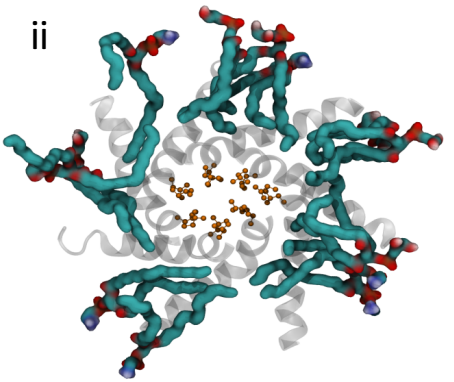

C
Crystal structure proximity to electron density modelled as carbon
Average separation between protein and lipid in the lower TM3 region by 50 ns AT-MD
Distance to lipid (Å)
Residue number

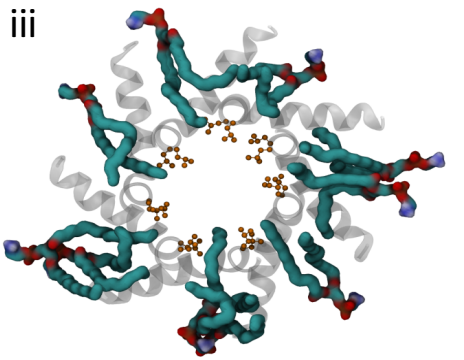

D


E
Number of lipids within 6 Å
Lower pocket
'total'
'persistent'


F
i
Strong POPE headgroup contacts to the lower TM3 region
PO4
NH3
Number of contacts (AU)
Arg Ser Asn Asn Arg Lys Ile Asp Thr Asp Phe Ser Ala Arg Tyr Val Met Phe Arg Gln Ile Phe
46 49 50 53 59 60 61 62 64 67 68 70 71 74 75 122 126 127 128 149 150 151
Residue number and amino acid

Residue


ii


iii