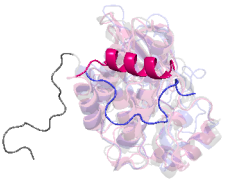
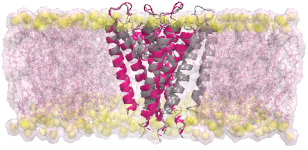
(a) **Hsp14**
PDB ID: 3AAC
RMSD = 0.589 Å

(b) **Abl kinase**
Active (in gray): PDB ID: 6XR6
RMSD = 0.927 Å
Inactive (in blue): PDB ID: 6XRG
RMSD = 1.421 Å



(c) **KcsA**
PDB ID: 1BL8
RMSD = 0.629 Å



(d)
ATP7B

(e)
DISC1

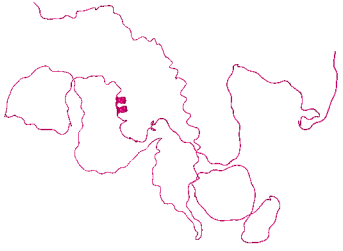


Fig 4: Protein structures predicted by the AlphaFold2 algorithm are presented for a diverse set of proteins. These include a chaperone, **HSP14 (a)**; an enzyme, Abselson tyrosine kinase, or **Abl (b)**; a transmembrane potassium channel, **KcSA (c)**;a transmembrane copper transporter, **ATP7B (d)**; and an intrinsically disordered protein, **DISC1 (e)**. Experimental structures, where available in the PDB database, are superimposed in grey, along with PDB ID and the backbone root mean squared deviations (RMSD, in Å units). For the transporters, the surrounding cellular membrane bilayer is putatively modeled, and depicted in yellow (lipid headgroups) and pink (aliphatic tails). The inability of AlphaFold2 to predict alternate (polymorphic) structures is demonstrated by the omission of the segment corresponding to the inactive state of Abl (see b; in blue)