**Supplementary Information for**

# Refinement of AlphaFold2 Models against Experimental and Hybrid Cryo-EM Density Maps

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**Extension of Figure 3:** We provide additional Figures S1 and S2, in the style of Figures 1 and 2, for the two cases 23530-7LV9-B and 23208-7L6U-A described in Figure 3.

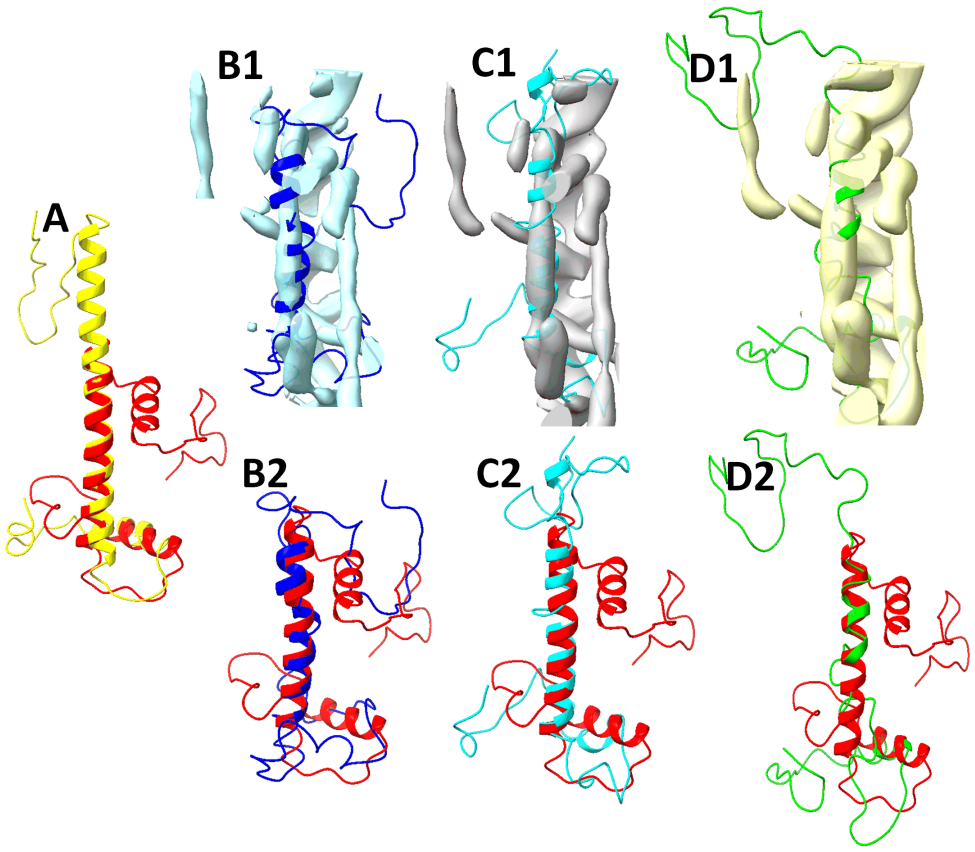


**Figure S1: Models obtained from AlphaFold2 and the refinements using Cryo-EM map 23530-7LV9-B (EMDB-PDB-chain ID) and hybrid density maps at 6Å and 8Å resolutions.** (A) Superposition of the protein structure (red, chain B of 7LV9) and the model obtained from AlphaFold2 (yellow). (B1) The box-cropped region of cryo-EM map 23530 (EMDB ID, cyan) superimposed with the model (blue) refined using Phenix and the cryo-EM map. (B2) Superposition of the structure (red, chain B of 7LV9) and the refined model (blue) using Phenix and the box-cropped cryo-EM map in B1. Hybrid maps of 6Å (gray in C1), 8Å (yellow in D1) resolutions are superimposed with the model refined from the corresponding map. The 6Å-map-refined model (Cyan ribbon in C1, C2) and 8Å-map-refined model (green in D1, D2) are superimposed with the structure (red) in C2 and D2.

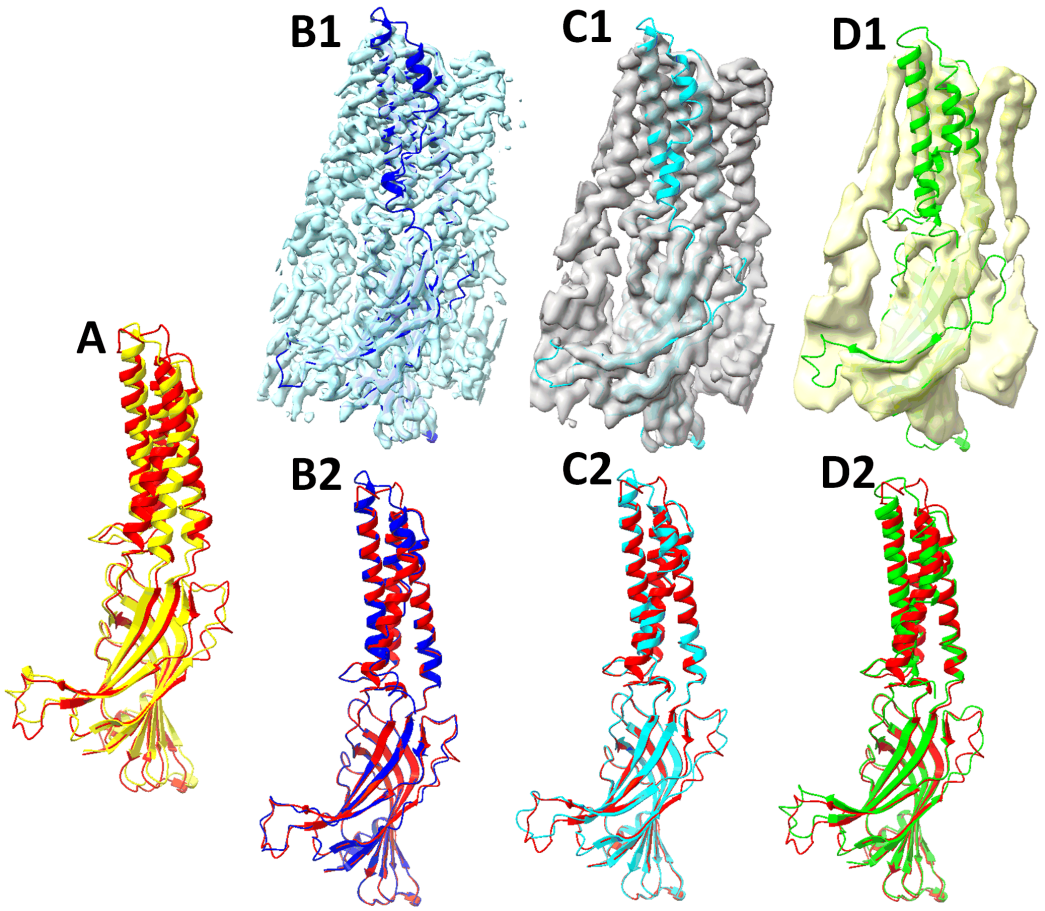


**Figure S2: Models obtained from AlphaFold2 and the refinements using Cryo-EM map 23208-7L6U-A (EMDB-PDB-chain ID) and hybrid density maps at 6Å and 8Å resolutions.** (A) Superposition of the protein structure (red, chain A of 7L6U) and the model obtained from AlphaFold2 (yellow). (B1) The box-cropped region of cryo-EM map 23208 (EMDB ID, cyan) superimposed with the model (blue) refined using Phenix and the cryo-EM map. (B2) Superposition of the structure (red, chain A of 7L6U) and the refined model (blue) using Phenix and the box-cropped cryo-EM map in B1. Hybrid maps of 6Å (gray in C1), 8Å (yellow in D1) resolutions are superimposed with the model refined from the corresponding map. The 6Å-map-refined model (Cyan ribbon in C1, C2) and 8Å-map-refined model (green in D1, D2) are superimposed with the structure (red) in C2 and D2.