

Figure S1: Summary of data processing. Processing workflow, exemplar micrograph, 2D classes, overall map, FSC curve and viewing distribution as calculated by cryoSPARC¹ for A TehA purified in GDN; B TehA purified in LMNG; C TehA purified in DDM and D TehA purified in OG.

Support Information

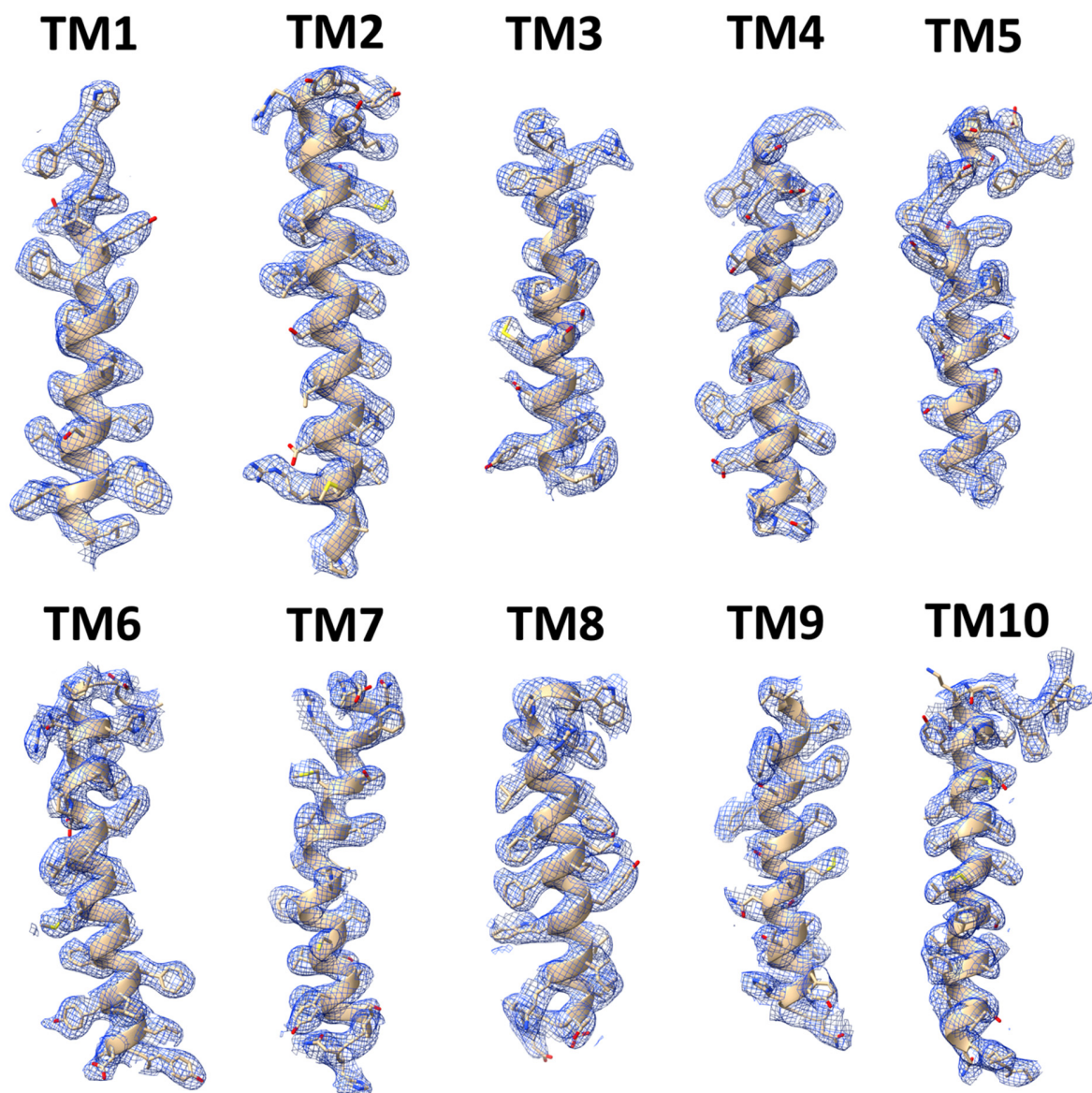


Figure S2 An example of the quality of the map for the *H*/TehA purified in OG.

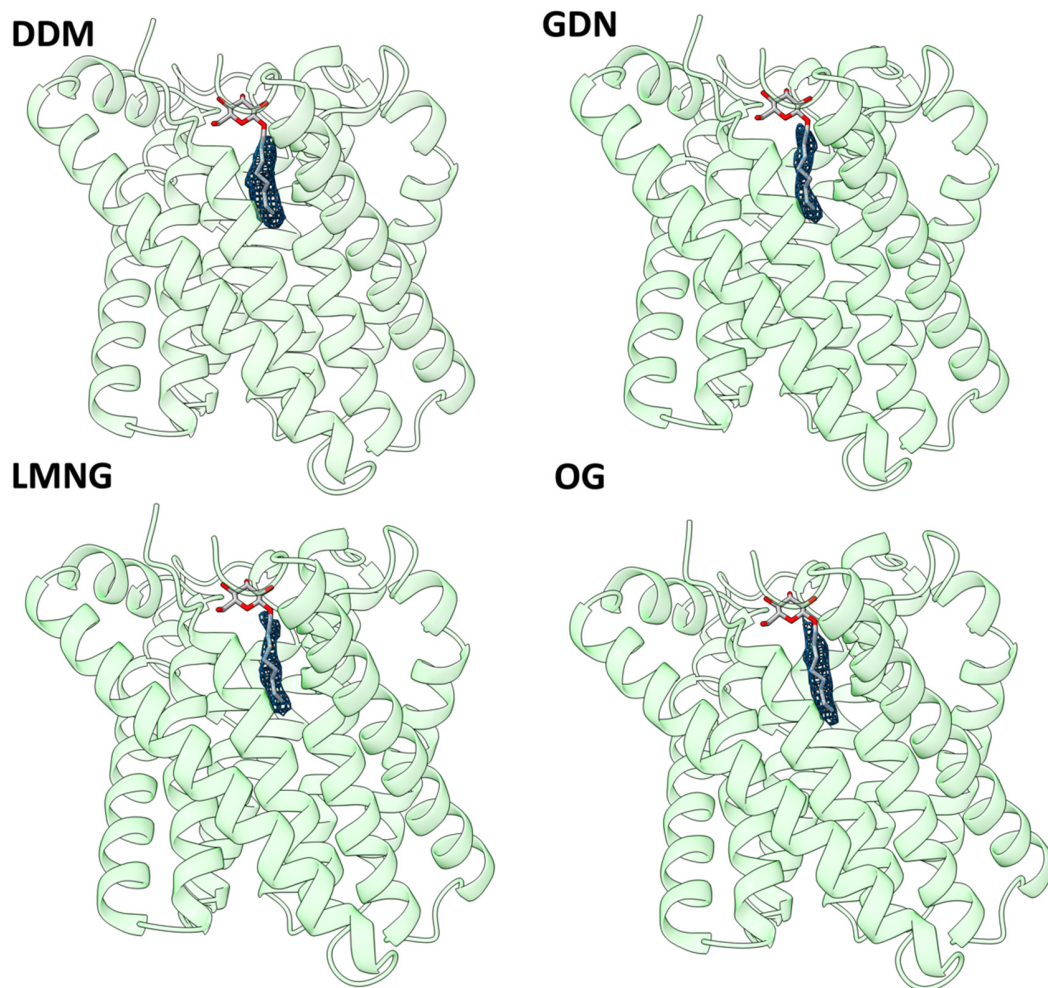


Figure S3 Comparing the cryo-EM maps of pore density with the room temperature structure rigidly fitted into the maps, transmembrane segments (TMs) are color-coded in green. Additionally, the OG molecule is represented as sticks, color-coded according to its heteroatoms, with the surrounding density map displayed as a blue mesh.

1. Punjani, A., Rubinstein, J. L., Fleet, D. J. & Brubaker, M. A. cryoSPARC: algorithms for rapid unsupervised cryo-EM structure determination. *Nat Methods* **14**, 290–296 (2017).