

Data collection and image processing Approximately 300 micrographs were collected on F20 at Columbia, from which 166,878 particles were picked and extracted for 2D classification (Fig. 1). 12,718 particles were chosen to reconstitute a final density map based on 2D and 3D classifications. The final density map was refined to 10.3 Å (Fig. 2A and 2B).

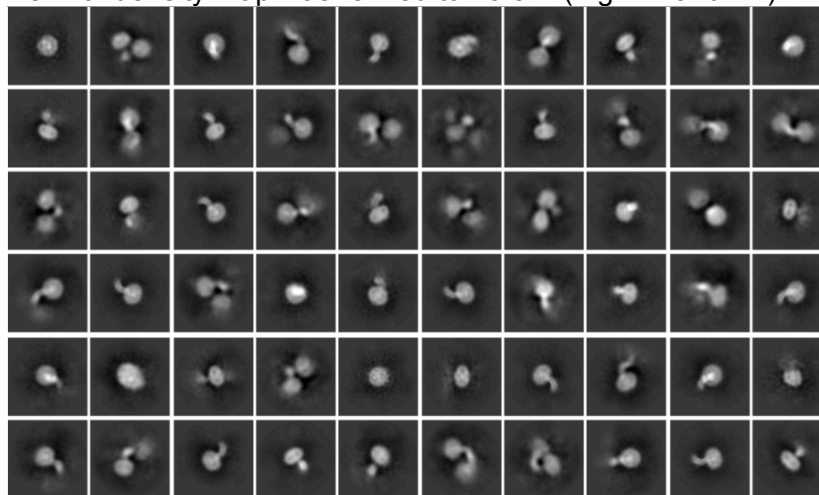


Figure 1. Selected 2D classes.

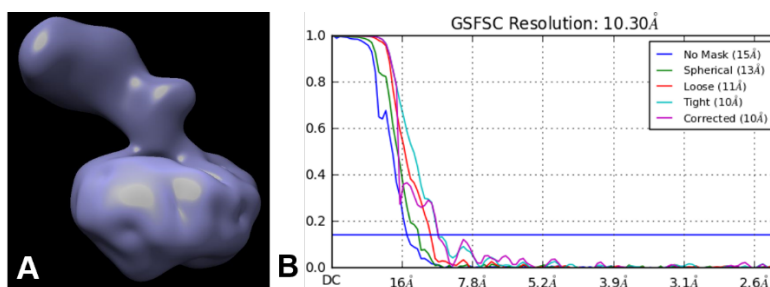


Figure 2. (A) The 3D density map of a mammalian GpHr. (B) Resolution estimation of the density map.

Modeling The template for the extracellular domain was derived from a protomer of a homotrimeric FSHR_{ED} crystal structure (PDB: 4MQW); while the template for the FSHR_{TM} domain was derived from a protomer of a homo-dimeric rhodopsin crystal structure in ground state (PDB: 1GZM). The protomers of FSHR_{ED} and FSHR_{TM} were fitted into our refined density map (Fig. 3A), which demonstrated that our mammalian GpHr alone formed a monomer (Fig. 3A, 3B and 3C).

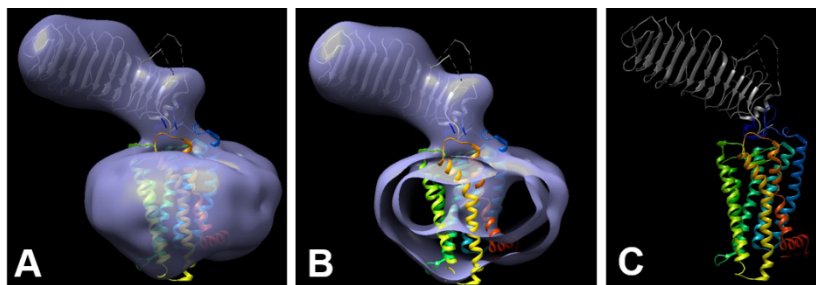


Figure 3. (A) Fitting our 3D model into the density map of a mammalian GpHr. (B) A clipped view of the density map to show the TM region. (C) Our 3D model of a mammalian GpHr. Gray color is the extracellular domain. Rainbow is the transmembrane domain, from which blue color indicated its N-terminus and red indicated the C-terminus.