Supplementary Information

Electrophysiology assay for TAX-4 1G, TAX-4 2G, TAX-4 3G and DCM10

We generated four TAX-4 mutations, including three glycine-insertion mutations, TAX-4_1G, TAX-4_2G, and TAX-4_3G, and one disease-causing mutation DCM10 (R421W). Whole-cell current recording result (Fig. 1) showed that all these four mutants were unable to respond to a saturated concentration (100 μ M) of intracellular cGMP, indicating these mutations decoupled TAX-4 transduction.

<u>Protein purification and amphipol</u> <u>exchange for TAX-4 2G and DCM10</u>

TAX-4_2G and DCM10 mutant

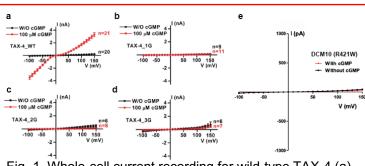


Fig. 1. Whole-cell current recording for wild-type TAX-4 (a), TAX-4_1G (b), TAX-4_2G (c), TAX-4_3G (d) and DCM10 (e) in HEK293T cells.

proteins were expressed in SF9 insect cells. Protein was purified with detergent and finally exchanged in amphipol. Gel filtration and SDS-PAGE results indicate that both TAX-4_2G and DCM10 samples are homogenous and good enough for cryo-EM study (Fig. 2).

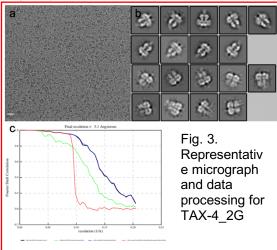
Image acquisition on F20 and processing for TAX-4 2G and DCM10

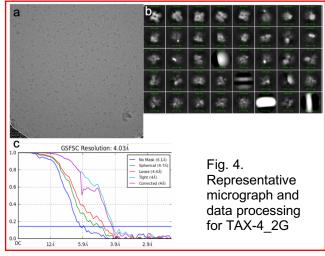
We prepared cryogenic grids using vitrobot machine (FEI) for TAX-4_2G and DCM10 proteins, and collected a 648-micrograph dataset and a 943-micrograph dataset for TAX-4_2G and DCM10 respectively on F20 microscope. After image processing using Relion and cryoSPARC, we got very promising 2D classification result for both samples. Representative views from 2D

TAX-4_2G peak

TAX-4_

classification showed clear 4-fold symmetry feature for both TAX-4_2G (Fig. 3b) and DCM10 (Fig. 4b). Through 3D refinement and post-processing, we were able to refine TAX-4_2G map to 5.1 Å resolution (Fig. 3c) and DCM10 to 4.03 Å resolution (Fig. 4c).





Grid availability and session request

We already have back-up grids for TAX-4_2G and DCM10. They are available for data collection on Titan Krios. For session request, we would like to apply for 4 sessions with 24 hours for each session.