

Figure 1. Preliminary data for enzyme-Fab complex. A) SEC profile with and without Fab. B) Micrograph and 2D class averages. C) Initial 3D ab initio model.

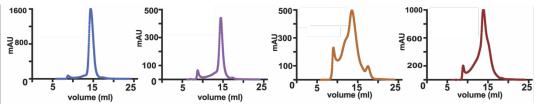


Figure 2. SEC profiles of four different ion channel samples ready for single particle cryo-EM analysis.

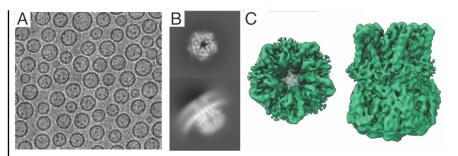


Figure 3. Cryo-EM studies of BEST1 in liposomes. A) Micrograph of liposome preparation. B) 2D class averages. C) Initial 3D reconstruction.

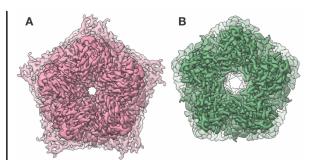


Figure 4. 3D reconstructions of the human BEST1 channel, in detergent, reveal closed (A) and open (B) conformations.

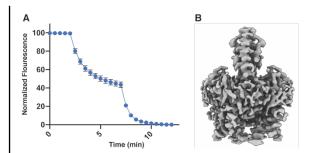


Figure 5. Preliminary data for K2P channel. A) Fluorescence-based ion flux assay demonstrating that purified K2P is active (time dependent decrease in fluorescence is indicative of ion flux). B) Initial 3D reconstruction of K2P from single particle analysis.