

Figure 1: CryoEM structure of GIRK2 in nanodiscs. (A) Size-exclusion chromatography of the GIRK2 reconstituted discs. (B) and (C) are the representative cryo-EM image and 2D averages of GIRK2 in nanodisc. (D) CryoEM map of GIRK2 in nanodisc with well-resolved transmembrane (TMD) and cytoplasmic (CTD) domains.

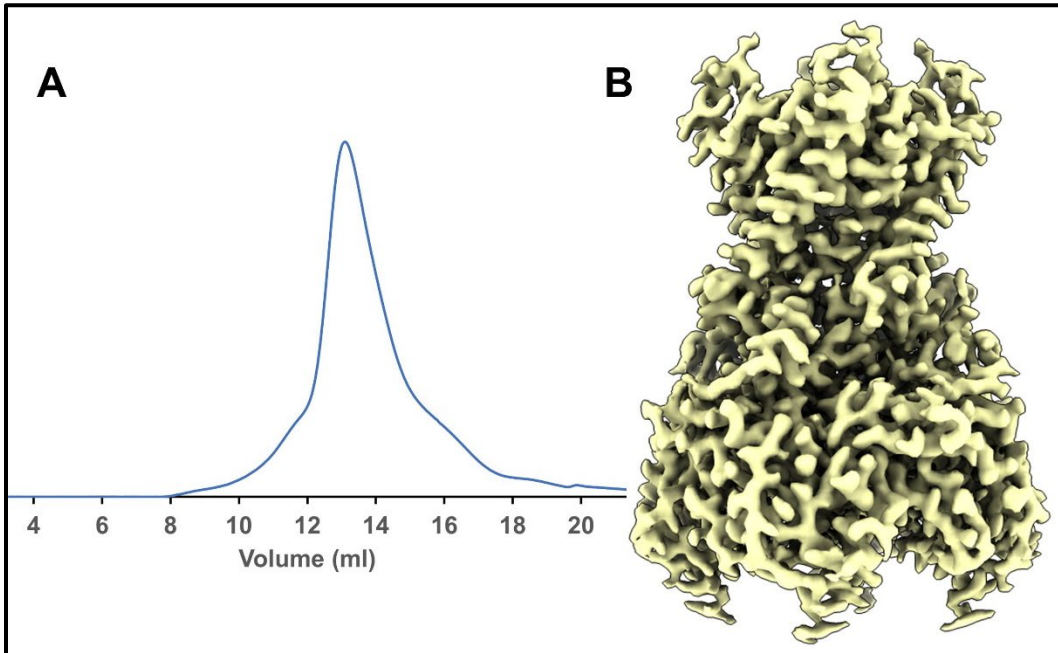


Figure 2: CryoEM structure of constitutive active GIRK2 K200Y mutant. (A) Size-exclusion chromatography. **(B)** CryoEM map of GIRK2 K200Y mutant obtained at 3.0Å.

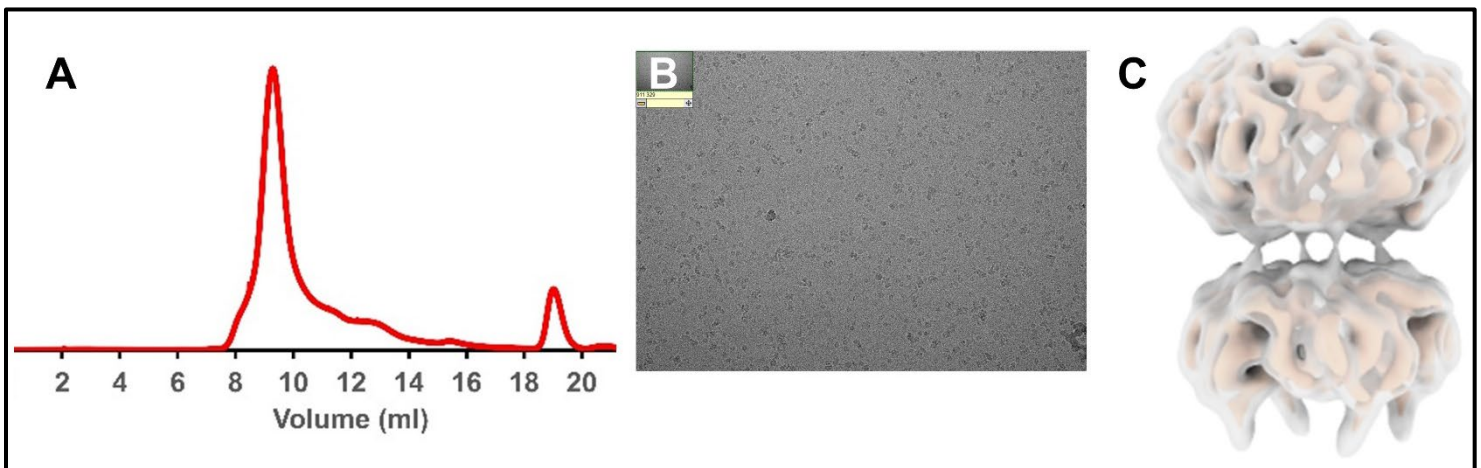


Figure 3: CryoEM structure of GIRK3. (A) Size exclusion chromatography. **(B)** Representative cryoEM image and **(C)** cryoEM structure of GIRK3.