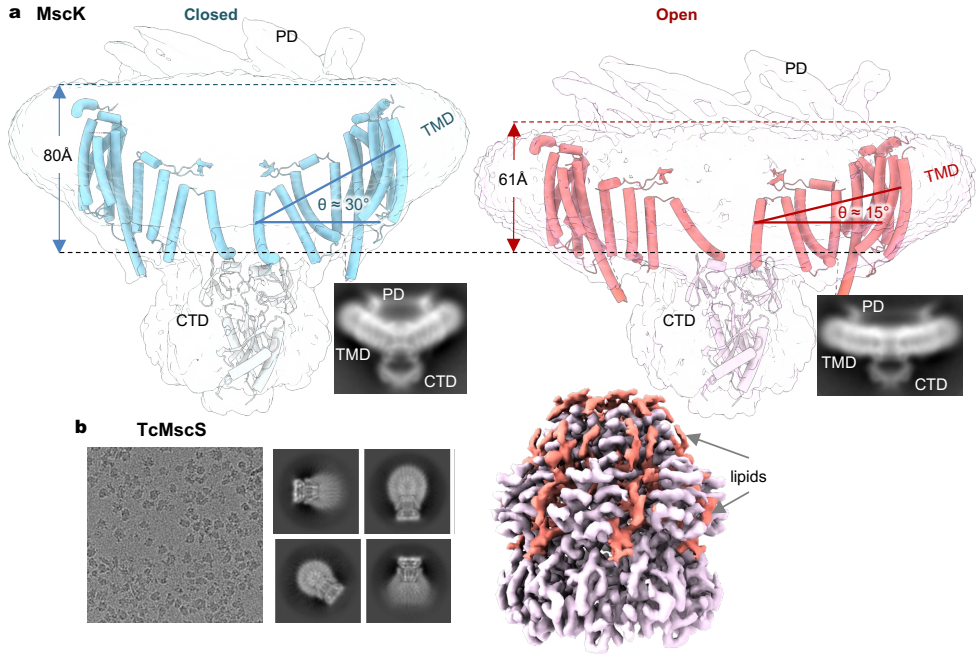

Fig. 1. Structural mechanisms of mechanosensitive channels. (**a**) Cryo-EM structures reveal the mechanotransduction mechanism in a potassium-dependent mechanosensitive channel, MscK (Reference: Mount et al., Nat Commun 2022). Only two opposing subunits are shown for clarity. Surfaces of the unsharpened maps indicate the positions of the periplasmic domain (PD), transmembrane domain (TMD), and cytoplasmic domain (CTD). Insets are 2D class averages illustrating the curvatures of the TMD. (**b**) Cryo-EM analysis of a miniature mechanosensitive channel TcMscS in the presumed closed state at ~3.2 angstrom resolution.

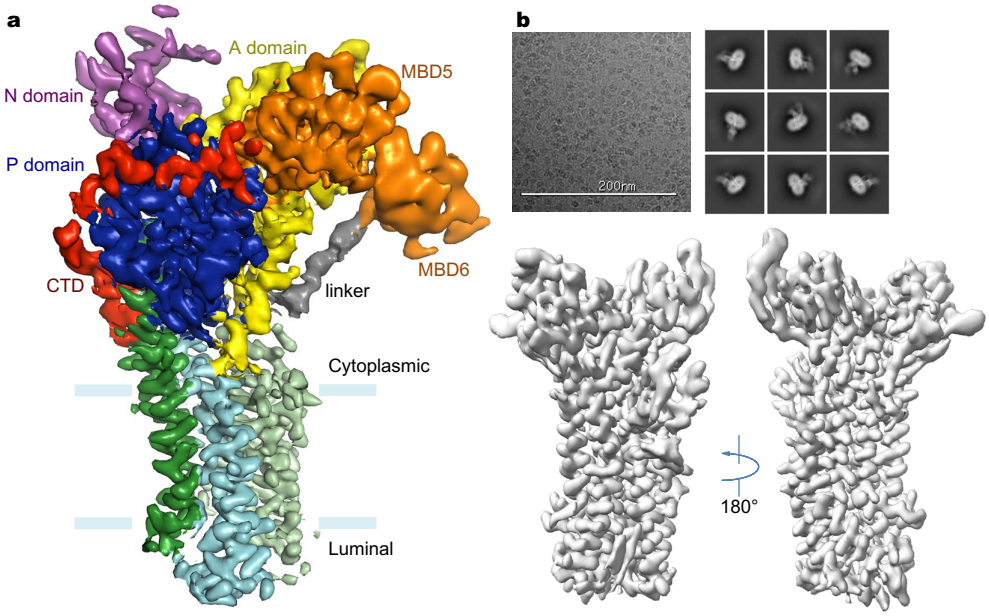

Fig. 2. Copper transporters ATP7A and ATP7B. (**a**) Cryo-EM structure of the Wilson's disease protein ATP7B at ~3.2 angstrom resolution (Reference: Bitter et al., *Sci Adv* 2022). (**b**) Preliminary cryo-EM analysis of the Menkes disease protein ATP7A in the apo state at ~3.4 angstrom resolution.

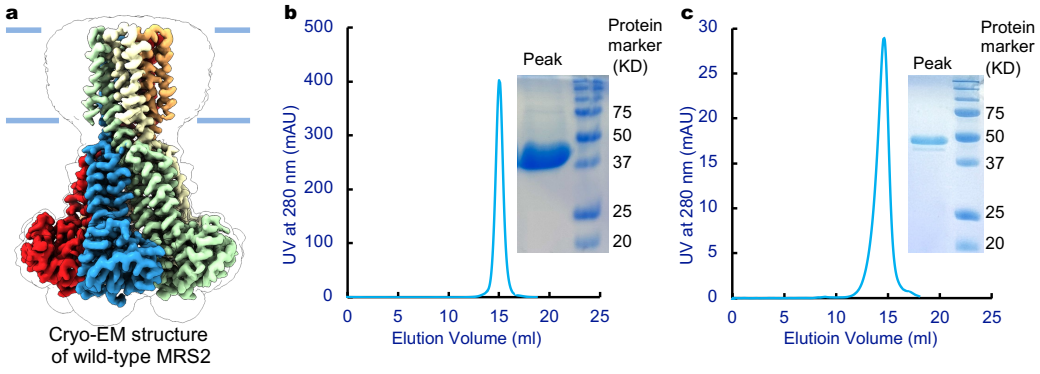

Fig. 3. Structural studies of MRS2/CorA channels. (**a**) cryo-EM structure of pentameric human MRS2 at ~3.0 angstrom resolution. (**b-c**) Isolation and identification of fungal MRS2/CorA proteins for structural and functional studies. The monodisperse peak near 15 ml from each size-exclusion chromatography indicated purified homogeneous channels, and the peak fraction was analyzed by SDS-PAGE (inset).