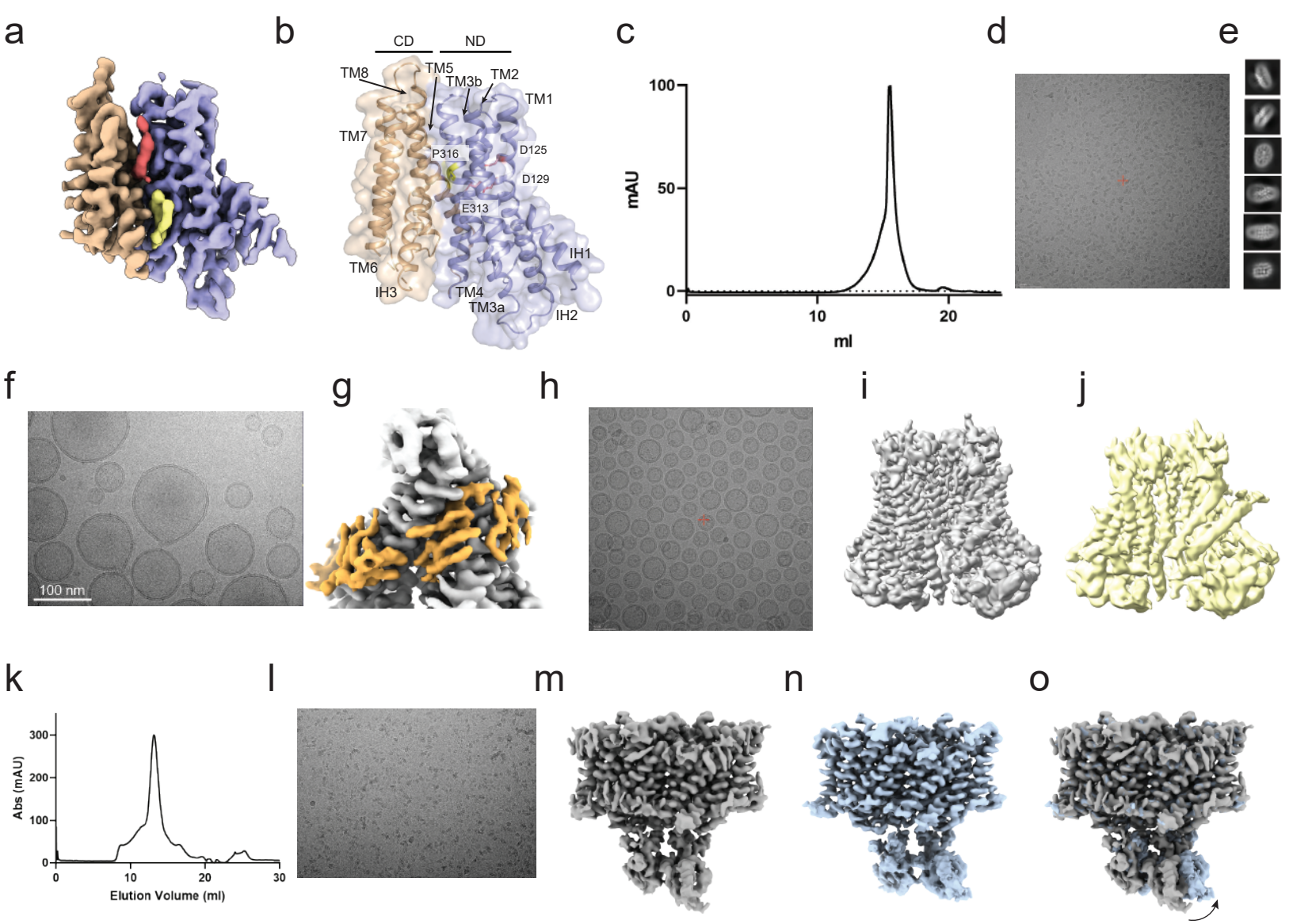

Figure 1 a) CryoEM density of hXkr4 in LMNG-CHS detergent micelles. The ND repeat is colored in pale blue, the CD repeat in wheat. Associated lipid-like densities are shown in yellow (inner leaflet) and red (outer leaflet). b) The structure of hXkr4 viewed from the plane of the membrane. The protein surface is shown as transparent and the atomistic model is shown in ribbon with the ND repeat in pale blue, the CD repeat in wheat. Functionally important residues are colored and shown in stick representation. c) Size Exclusion Chromatograph (SEC) profile of hXkr4 in MSP1E3 nanodiscs formed from POPC lipids. d) Representative micrograph of hXkr4 in nanodiscs. e) Representative 2D classes of hXkr4 nanodiscs obtained from an overnight data collection of a Glacios 200 kV microscope. f) Representative micrograph of DOPC/DOPG afTMEM16 proteoliposomes. g) 2.7 Å resolution cryoEM density of Ca^{2+} bound afTMEM16 in liposomes (gray) and of lipids at the groove (yellow). h) Representative micrograph of POPC/POPG hTMEM16F proteoliposomes. i-j) CryoEM density maps of Ca^{2+} bound hTMEM16F in proteoliposomes with a closed groove at 2.9 Å resolution (i, gray) and with a remodeled groove at 3.5 Å resolution (j, yellow). k-l) SEC profile (k) and micrographs (l) of purified hCLC-1 in 0 Cl^-. m-o) CryoEM maps of CLC-1 in 0 Cl^- in known conformation (m, gray) and in a new state (n, cyan) with a rotated cytosolic domain (o). Arrow denotes direction of rotation from the known state to the new one.