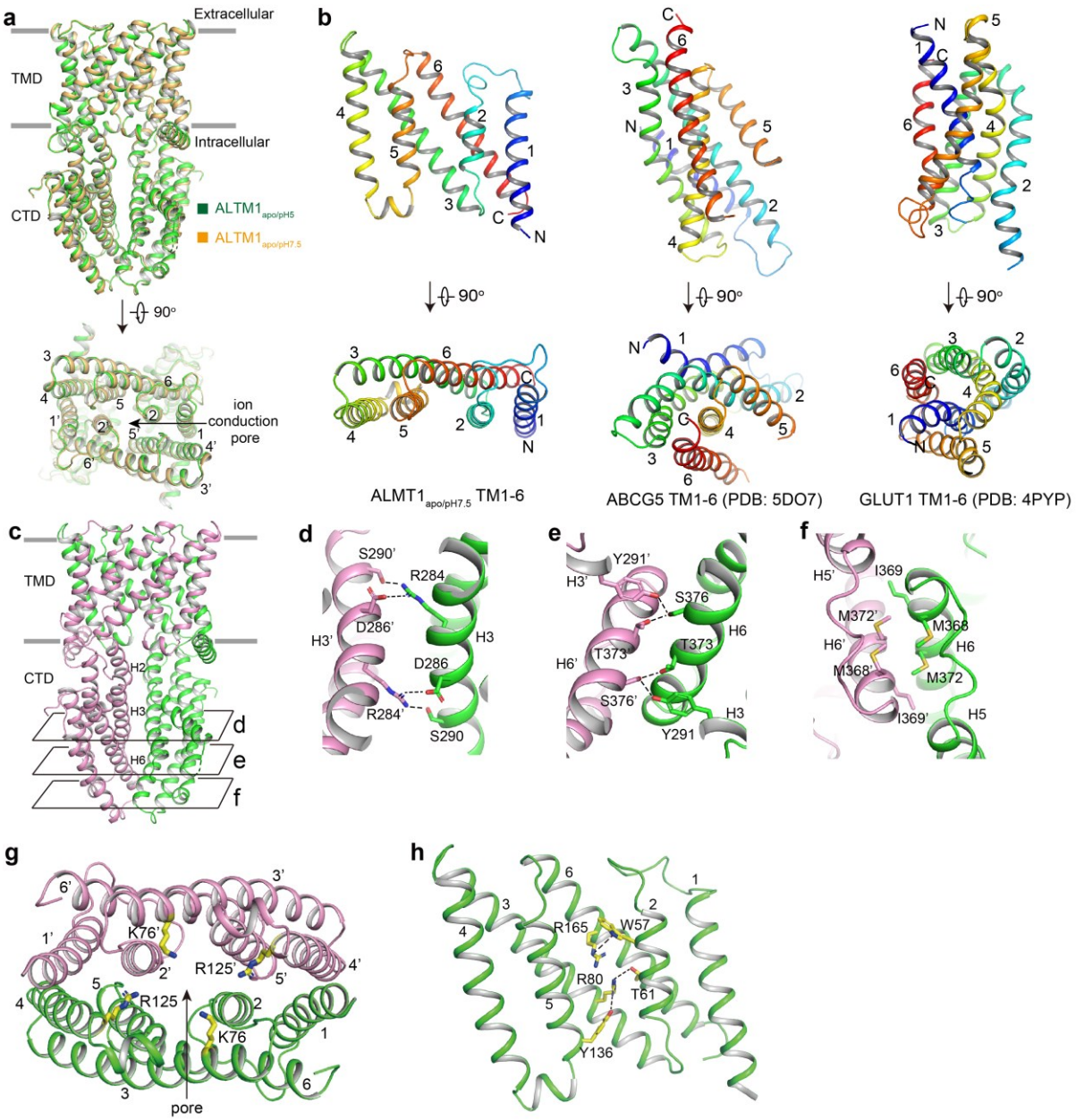

Fig. S5 Structures of the apo AtALMT1.

a, Structural alignment of $ALMT1_{apo/pH5}$ and $ALMT1_{apo/pH7.5}$. **b,** Side and top views of $ALMT1_{apo/pH7.5}$ (TM1–6), ABCG5 (TM1–6) and GLUT1 (TM1–6). ALMT1 displays different transmembrane helix arrangements in comparison with ABCG5 and GLUT1. The orientations of ABCG5 and GLUT1 are set based on their structural alignments with $ALMT1_{apo/pH7.5}$. **c**, Dimerization of the CTD in $ALMT1_{apo/pH5}$. **d,** Salt bridges and hydrogen bonds between two H3 helices. **e,** Hydrogen bonds stabilize the H3 and H6 helices. **f,** Hydrophobic interactions between two H6 helices. **g,** Positively charged residues localized at the intracellular entrance of the channel pore. **h,** Hydrogen bonds and the cation-π interaction stabilize the side-chain conformations of Arg80 and Arg165, respectively. **i,** Sequence alignment of *Arabidopsis thaliana* ALMT family and TaALMT1. Two highly conserved Arg and their interaction residues shown in **h** are highlighted with cyan boxes.