Supplemental material

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Figure S1. Secondary structure prediction obtained with PSIPRED. Predicted α-helical segments are highlighted in gray (transmembrane segments), yellow, or green. Cation-conducting human pLGIC subunit sequences (top) and anion-conducting subunit sequences (bottom). PSIPRED, PSI-blast based secondary structure PREDiction 4pir (Buchan and Jones, 2019).
Figure S2. Charged amino acids in the MA helices. (A) X-ray structure of mouse 5-HT3AR (PDB ID: 4PIR; Hassaine et al., 2014) showing charged amino acids potentially involved in intersubunit salt bridges. (B) Zoomed-in view of salt bridges near the RRR motif. Distances from top to bottom: 8.2 Å, 3.8 Å, 3.6 Å, and 3.9 Å. (C) Multiple sequence alignment of MA helices with positively charged residues (cyan) and negatively charged residues (red) that provide the possibility for intersubunit salt bridges indicated.

References
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