Table S1. Cryo-EM data collection, refinement and validation statistics

	MouseTRPC4 (EMD-6901) (PDB 5Z96)
Data collection and processing	
Magnification	40,607
Voltage (kV)	300
Electron exposure (e–/Å^2)	52.8
Defocus range (μm)	1.5-3.0
Pixel size (Å)	1.23
Symmetry imposed	*C4*
Initial particle images (no.)	381,165
Final particle images (no.)	232,858
Map resolution (Å)	3.3
Refinement	
Initial model used (PDB code)	*de novo*
Model resolution (Å)	3.3
Model composition	
Non-hydrogen atoms	21,506
Protein residues	2,608
Ligands	13
R.m.s. deviations	
Bond lengths (Å)	0.01
Bond angles (°)	1.11
Validation	
MolProbity score	1.83
Ramachandran plot	
Favored (%)	97.39
Allowed (%)	2.08
Disallowed (%)	0.53