

Table S2: Cryo-EM data collection, refinement and validation statistics

	hTRPC6 (EMD-6856) (PDB 5YX9)	hTRPC3 (EMD-6911) (PDB 5ZBG)
Data collection and processing		
Magnification	37,500×	37,500×
Voltage (kV)	300	300
Electron exposure (e ⁻ /Å ²)	50	50
Defocus range (μm)	-1.0 to -3.0	-1.0 to -3.0
Pixel size (Å)	1.33	1.37
Symmetry imposed	<i>C4</i>	<i>C4</i>
Initial particle images (no.)	326,026	625,074
Final particle images (no.)	53,528	22,220
Map resolution (Å)	3.8	4.4
FSC threshold	0.143	0.143
Refinement		
Model resolution (Å)	3.8	4.4
FSC threshold	0.143	0.143
Model resolution range (Å)	3.8	4.4
Map sharpening <i>B</i> factor (Å ²)	-166.8	-176.2
Model composition		
Non-hydrogen atoms	21,348	21,276
<i>B</i> factors (Å ²)		
Non-hydrogen atoms	146.94	214.84
R.m.s. deviations		
Bond lengths (Å)	0.003	0.005
Bond angles (°)	0.637	0.686
Validation		
MolProbity score	2.11	2.38
Clashscore	8.66	7.44
Poor rotamers (%)	2.1	4.78
Ramachandran plot		
Favored (%)	94.19	92.71
Allowed (%)	5.66	6.99
Disallowed (%)	0.15	0.30