

Extended Data Table 1 | Cryo-EM data collection, refinement and validation statistics

	hTRPV6-nanodiscs (EMDB-7120) (PDB 6BO8)	hTRPV6-amphipols (EMDB-7121) (PDB 6BO9)	hTRPV6-R470E (EMDB-7122) (PDB 6BOA)	rTRPV6* (EMDB-7123) (PDB 6BOB)
<b>Data collection and processing</b>				
Magnification	39,000x	39,000	105,000x	39,000x
Voltage (kV)	300	300	300	300
Electron exposure (e-/Å <sup>2</sup> )	67	67	67	67
Defocus range (μm)	1.5 to -3.5	-1.5 to -3.5	-1.5 to -3.5	-1.5 to -3.5
Pixel size (Å)	0.98	0.98	1.10	0.98
Symmetry imposed	C4	C4	C4	C4
Initial particle images (no.)	509,569	306,784	1,243,159	248,836
Final particle images (no.)	46,124	65,259	59,298	20,808
Map resolution (Å)	3.56	4.00	4.24	3.92
FSC threshold				
Map resolution range (Å)	2.5 to 6.0	2.5 to 6.0	2.5 to 6.0	2.5 to 6.0
<b>Refinement</b>				
Initial model used (PDB code)	5IWK	This study	This study	This study
Model resolution (Å)	3.56	4.00	4.24	3.92
FSC threshold				
Model resolution range (Å)	2.5 to 6.0	2.5 to 6.0	2.5 to 6.0	2.5 to 6.0
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	-165	-206	-239	-173
Model composition				
Non-hydrogen atoms	19,048	19,048	19,040	19,340
Protein residues	611	611	611	611
Ligands	N/A	N/A	N/A	N/A
<i>B</i> factors (Å <sup>2</sup> )				
Protein	182.9	242.8	122.0	184.2
Ligand	N/A	N/A	N/A	N/A
R.m.s. deviations				
Bond lengths (Å)	0.0079	0.0071	0.0101	0.0072
Bond angles (°)	1.33	1.3	1.46	1.37
Validation				
MolProbity score	1.97	2.06	2.22	1.98
Clashscore	7	8	5	7
Poor rotamers (%)	0.6	0.8	1.3	2.7
Ramachandran plot				
Favored (%)	88.96	87.95	88.75	88.55
Allowed (%)	11.04	12.05	11.25	11.15
Disallowed (%)	0.00	0.00	0.00	0.30