

Supplementary Table 1. Cryo-EM data collection, refinement and validation statistics. The transmembrane domain (TM) and T1 domain were refined separately, using each corresponding Focused Refinement map. The models were merged at the final step, using the Overall map as alignment guide.

	#1 Kv1.3 with 4 Overall map (EMD-57536) (PDB 30BF)	#1.1 Kv1.3 with 4 TM Focused Refinement (EMD-57533)	#1.2 Kv1.3 with 4 T1 Focused Refinement (EMD-57535)	#2 Kv1.3 with 7 Overall map (EMDB-58170) (PDB 30ZB)	#2.1 Kv1.3 with 7 TM Focused Refinement (EMDB-57753)	#2.2 Kv1.3 with 7 T1 Focused Refinement (EMDB-57754)
Data collection and processing						
Magnification	130KX			165KX		
Voltage (kV)	300			300		
Electron exposure (e-/Å ²)	60			50		
Defocus range (µm)	0.5-3			0.5-3		
Pixel size (Å)	0.926			0.726		
Symmetry imposed	C4			C4		
Initial particle images (no.)	3280710			5735462		
Final particle images (no.)	127851			277705		
Map resolution (Å)	2.95	2.87	2.89	2.79	2.66	2.82
FSC threshold	0.143	0.143	0.143	0.143	0.143	0.143
Map resolution range (Å)	1.9-3.7	1.9-3.7	1.9-3.7	1.9-3.7	1.9-3.7	1.9-3.7
Map sharpening B factor (Å ²)						
		Residues 208 - 491	Residues 104 - 207		Residues 208 - 491	Residues 104 - 207
Refinement						
Initial model used (PDB code)		7SSY	7SSY		7SSY	7SSY
Model composition						
Non-hydrogen atoms		7855	3580		7891	3580
Protein residues		976	416		976	416
Ligands		3 K ⁺ 4 4			3 K ⁺ 4 7	
<i>B</i> factors (Å ²)						
Protein		85	137		59	103
Ligand		80			53	
R.m.s. deviations						
Bond lengths (Å)		0.003	0.002		0.004	0.003
Bond angles (°)		0.534	0.571		0.545	0.561
Validation						
MolProbity score		1.60	1.62		1.42	1.48
Clashscore		5.67	4.54		7.48	4.68
Poor rotamers (%)		1.75	1.82		1.05	2.08
Ramachandran plot						
Favored (%)		97.48	96.81		98.32	98.04
Allowed (%)		2.52	3.19		1.68	1.96
Disallowed (%)		0	0		0	0