

Table S1. Cryo-EM data collection, refinement, and validation statistics. Related to the STAR Methods

	rNa _v 1.5 _C (EMDB code: EMD-20951) (PDB code: 6UZ3)	rNa _v 1.5 _C -flecainide (EMDB code: EMD-20949) (PDB code: 6UZ0)
Data collection and processing		
Magnification	130,000	130,000
Voltage (kV)	300	300
Electron exposure (e-/Å ²)	60	60
Defocus range (µm)	1.0 – 2.5	1.0 – 3.0
Pixel size (Å)	1.056	1.056
Symmetry imposed	C1	C1
Initial particle images (no.)	2,188,972	2,369,854
Final particle images (no.)	106,104	513,604
Map resolution (Å)	3.50	3.24
FSC threshold	0.143	0.143
Map resolution range (Å)	3.3 – 6.0	3.0-5.0
Refinement		
Initial model used (EMDB code)		
Model resolution (Å)	3.85	3.50
FSC threshold	0.5	0.5
Model resolution range (Å)	3.3 – 6.0	3.0-5.0
Map sharpening <i>B</i> factor (Å ²)	-60	-60
Model composition		
Non-hydrogen atoms	9463	9565
Protein residues	1125	1138
Ligand	21	26
<i>B</i> factors (Å ²)		
Protein	105.6	56.5
Ligand	89.3	61.0
R.m.s. deviations		
Bonds (Å)	0.008	0.006
Angles (°)	0.914	0.799
Validations		
MolProbity score	2.46	2.20
Poor rotamers (%)	0.32	0.10
Ramachandran plot		
Favored (%)	88.30	90.94
Allowed (%)	11.43	8.79
Disallowed (%)	0.27	0.27