	hTMEM16E WT apo (EMDB-77883) (PDB 36UZ)	hTMEM16E WT Ca^{2+}-bound (EMDB-78009) (PDB 37AM)	hTMEM16E R582I apo (EMDB-78021) (PDB 37AY)	hTMEM16E R582I Ca^{2+}-bound (EMDB-78017) (PDB 37AW)	hTMEM16E G503E Ca^{2+}-bound (EMDB-78028) (PDB 37BB)
Data collection and processing					
Magnification	×105,000	×105,000	×100,000	×105,000	×100,000
Voltage (kV)	300	300	200	300	200
Electron exposure (e–/Å^2)	51.43	52.53	40.00	47.07	40.00
Defocus range (μm)	-0.6 to -2.8	-0.6 to -2.8	-0.8 to -2.5	-0.6 to -2.5	-0.8 to -2.5
Pixel size (Å)	0.825	0.825	1.16	0.825	1.16
Symmetry imposed	C2	C2	C2	C2	C2
Micrographs	19,422	25,513	20,795	14,799	9,194
Initial particle images (no.)	3,608,575	2,877,350	2,294,980	4,834,784	1,052,943
Final particle images (no.)	398,669	305,199	176,556	91,132	151,158
Map resolution (Å)	3.20	3.0	3.5	3.20	4.11
FSC threshold	0.143	0.143	0.143	0.143	0.143
Map resolution range (Å)	2.9-4.1	2.8-4.5	3.3-4.9	3.0-4.6	3.8-6.6
Refinement					
Initial model used (PDB code)	N/A	36UZ	36UZ	37AM	37AM
Model resolution (Å)	3.4	3.0	3.7	3.2	4.66
FSC threshold	0.5	0.5	0.5	0.5	0.5
Model resolution range (Å)	28-3.20	34-3.0	40-3.5	29-3.20	33-4.11
Map sharpening *B* factor (Å^2)	-144.75	-125.707	-135.574	-128.256	-192.593
Model composition					
Non-hydrogen atoms	12,162	12,316	11,414	12,442	11,112
Protein residues	1,504	1,508	1,466	1,510	1,478
Ligands		6		6	6
B factors (Å^2)					
Protein	106.53	94.38	111.60	88.19	167.95
Ligand		88.162		92.89	193.32
R.m.s. deviations					
Bond lengths (Å)	0.002	0.004	0.004	0.003	0.004
Bond angles (°)	0.562	0.880	0.814	0.578	0.707
Validation					
MolProbity score	1.73	1.62	1.96	1.76	2.11
Clashscore	9.74	7.85	11.97	8.66	16.19
Poor rotamers (%)	0.00	0.00	0.00	0.00	0.00
Ramachandran plot					
Favored (%)	96.64	96.85	94.61	95.75	94.12
Allowed (%)	3.36	3.15	5.39	4.28	5.88
Disallowed (%)	0.00	0.00	0.00	0.00	0.00

Table 1 Cryo-EM data collection, refinement and validation statistics for WT, R582I and G503E TMEM16E