

Table 1: Cryo-EM data collection, processing and validation statistics

	pH 7.0 SMA-cASIC1a (EMD-21380) (PDB-6VTK)	pH 8.0 SMA-cASIC1a (EMD-21381) (PDB-6VTL)
<i>Data collection/processing</i>		
Microscope	Krios (NCCAT)	Krios (PNCC)
Camera	K2	K3
Magnification	105,000	105,000
Voltage (kV)	300	300
Exposure time (s)	7.25	2
Frames (no.)	48	50
Electron exposure (e ⁻ /Å ²)	45-50	40-50
Defocus range (µm)	-0.8 – -2.6	-0.8 – -2.6
Pixel size (Å)	1.096	0.648
Initial micrographs (no.)	3,396	1,946
Micrographs used (no.)	3,221	1,946
Particles picked (no.)	1,874,332	608,152
2D-cleaned particles (no.)	327,268	57,209
<i>Final Refinement</i>		
Symmetry imposed	C3	C3
Final particles (no.)	121,140	48,338
Map resolution (Å)	2.8	3.7
FSC threshold	0.143	0.143
<i>Model statistics</i>		
Initial model used (PDB code)	4NYK	5WKU
Model resolution (Å)	3.1	4.0
FSC threshold	0.5	0.5
Map sharpening <i>B</i> factor (Å ²)	99	121
Model composition		
Non-hydrogen atoms	10686	10242
Protein residues	1338	1338
Ligands	6	6
<i>B</i> factors (Å)		
Protein	69.42	32.15
Ligand	89.03	124
R.m.s. deviations		
Bond lengths (Å)	0.005	0.004
Bond angles (°)	0.834	0.807
Validation		
MolProbity score	1.29	1.54
Clashscore	3.10	5.90
Poor rotamers (%)	0.0	0.0
Ramachandran plot		
Favored (%)	96.85	96.62
Allowed (%)	3.15	3.38
Disallowed (%)	0.0	0.0