

## SUPPLEMENTARY TABLE

Supplementary Table 1. Cryo-EM data collection and refinement statistics.

	<b>Apo-EMC</b> <b>EMD-35906</b> <b>PDB 8J0N</b>	<b>EMC-VDAC1</b> <b>EMD-35907</b> <b>PDB 8J0O</b>
<b>Data collection and processing</b>		
EM equipment	FEI Titan Krios	FEI Titan Krios
Magnification	81,000	81,000
Voltage (kV)	300	300
Detector	Gatan K3	Gatan K3
Pixel size (Å)	1.09	1.09
Electron dose (e-/Å <sup>2</sup> )	50	50
Defocus range (µm)	-1.2 to -2.5	-1.2 to -2.5
<b>Reconstruction</b>		
Software	Relion 3.0, cryoSPARC	Relion 3.0, cryoSPARC
Number of used particles	693,381	455,504
Final resolution (Å)	3.47	3.32
FSC threshold	0.143	0.143
Map sharpening B-factor (Å <sup>2</sup> )	-120.0	-122.9
<b>Model building</b>		
Software	Coot 0.89	Coot 0.89
<b>Refinement</b>		
Software	Phenix 1.20.1	Phenix 1.20.1
Map CC	0.70	0.72
<b>Model composition</b>		
Protein residues	2,301	2,627
Protein atoms	18,475	20,986
<b>Validation</b>		
R.M.S deviations		
Bond lengths (Å)	0.010	0.014
Bond angles (°)	0.948	1.083
Ramachandran plot (%)		
Preferred region	91.50	91.37
Allowed region	8.23	8.36
Outlier region	0.26	0.27
MolProbity score	2.01	2.13
Clashscore (all-atom)	9.72	12.97
Poor rotamers (%)	0.75	0.40