Extended Data Table 1: Cryo-EM data collection, refinement and model statistics.

	#1 *Ec*ZorAB WT (EMDB-18751) (PDB 8QYD)	#2 *Ec*ZorA$^{E86A/E89A}$ZorB (EMD-18754) (PDB 8QYH)	#3 *Ec*ZorA$^{\Delta 359-592}$ZorB (EMD-18756) (PDB 8QYK)	#4 *Ec*ZorA$^{\Delta 435-729}$ZorB (EMD-18766) (PDB 8QYY)
Data collection and processing				
Microscope	Titan Krios G2			
Magnification (nominal)	96,000x			
Voltage (kV)	300			
Total exposure ($e^-/Å^2$)	40.01	38.00	41.00	41.00
Exposure fractions (no.)	40			
Pixel size (Å)	0.832	0.832	0.832	0.832
Symmetry imposed	C1			
Movies used (no.)	7,700	3,203	3,181	1008
Final particles (no.)	227,728	97,005	278,186	62,926
Box size (pixels)	500	500	500	500
Map resolution (Å) (FSC 0.143)	2.67	2.40	2.07	2.56
Refinement				
Refinement resolution (FSC map vs. model (masked)=0.143) (Å)	2.60	2.40	2.10	2.50
Model composition				
Non-hydrogen atoms	16,154	15,925	16,182	14,829
Protein residues	1,892	1,837	1,817	1,717
Water molecules	313	484	866	313
B-factors (mean; $Å^2$)				
Protein	89.70	90.46	64.60	84.84
Solvent	88.61	50.89	34.01	44.93
R.m.s. deviations				
Bond lengths (Å)	0.006	0.008	0.008	0.009
Bond angles (°)	0.874	1.025	1.373	1.339
CC (mask)	0.86	0.85	0.85	0.84
Validation				
MolProbity score	1.46	1.46	1.42	1.45
Poor rotamers (%)	0.12	0.12	0.19	0.00
Ramachandran plot				
Favored (%)	98.30	98.63	98.56	98.12
Allowed (%)	1.7	1.37	1.44	1.88
Disallowed (%)	0.00	0.00	0.00	0.00

	#5 *Ec*ZorD Apo form (EMD-18747) (PDB 8QY7)	#6 *Ec*ZorD + ATP-r-S (EMD-18750) (PDB 8QYC)	#7 *Ec*ZorC Apo from (EMD-18948) (PDB 8R68)
Data collection and processing			
Microscope	Titan Krios G2		
Magnification (nominal)	96,000x		
Voltage (kV)	300		
Total exposure ($e^-/Å^2$)	40.00	38.00	39.50
Exposure fractions (no.)	40		
Pixel size (Å)	0.832	0.832	0.832
Symmetry imposed	C1		
Movies used (no.)	1,750	1,213	5,209
Final particles (no.)	332,426	211,477	168,569
Box size (pixels)	400	400	256
Map resolution (Å) (FSC 0.143)	2.66	2.75	3.55
Refinement			
Refinement resolution (FSC map vs. model (masked)=0.143) (Å)	2.60	2.70	3.50
Model composition			
Non-hydrogen atoms	7,168	7,199	3,240
Protein residues	893	893	391
Water molecules	n/a	n/a	n/a
B-factors (mean; $Å^2$)			
Protein	27.26	26.87	64.60
Solvent	n/a	n/a	n/a
R.m.s. deviations			
Bond lengths (Å)	0.018	0.004	0.003
Bond angles (°)	1.706	0.767	0.648
CC (mask)	0.85	0.81	0.52
Validation			
MolProbity score	1.90	1.459	2.11
Poor rotamers (%)	0.00	0.26	0.30
Ramachandran plot			
Favored (%)	96.72	96.95	94.43
Allowed (%)	3.28	3.05	5.57
Disallowed (%)	0.00	0.00	0.00