Table S1. Data collection, model refinement and validation. **Related to Figure 1.**

Data collection and processing	
Magnification	130,000
Voltage (kV)	300
Electron exposure (e–/Å^2)	~83
Defocus range (μm)	-1.0~-2.5
Pixel size (Å)	1.029
Symmetry imposed	C1
Initial particle images (no.)	1,590,810
Final particle images (no.)	721,844
Map resolution (Å)	3.20
FSC threshold	0.143
Refinement	
Initial model used (code)	6DDE
Model resolution (Å)	3.20
FSC threshold	0.143
Model resolution range (Å)	40-3.2
Map sharpening *B* factor (Å^2)	-180
Model composition	
Non-hydrogen atoms	10235
Protein residues	1284
Ligands	9
B factors (Å^2)	
Protein	122.5
Ligand	150.4
R.m.s. deviations	
Bond lengths (Å)	0.004
Bond angles (°)	0.882
Validation	
MolProbity score	1.41
Clashscore	4.98
Ramachandran plot	
Favored (%)	97.3
Allowed (%)	2.7
Disallowed (%)	0