

Table S1. Cryo-EM data collection and refinement statistics, Related to Figure 2.

Data collection				
Microscope	FEI Titan Krios			
Voltage (kV)	300			
Camera	Gatan K2 Summit			
Magnification	37,000			
Nominal defocus range (μm)	0.63-3.30			
Defocus mean \pm std (μm)	1.81 \pm 0.52			
Exposure time (s)	8			
Number of frames	80			
Dose rate ($\text{e}^-/\text{Pixel}/\text{s}$)	4.55			
Total dose ($\text{e}^-/\text{\AA}^2$)	58			
Pixel size (\AA)	0.79			
	Tilt angle			
Micrographs collected	0°	10°	20°	30°
	998	736	967	741
Micrographs processed	3368			
Total particles	401,889			
Reconstruction (RELION)				
	Pre-1r	Pre-2r		
Particles per classification	73,086	87,706		
Resolution, FSC 0.143	3.6	3.6		
FCS map-to-model (0.5)	3.6	3.6		
Map sharpening B-factor (\AA^2)	-75	-94		
Model composition				
Non-hydrogen atoms	21539	21276		
Protein residues	414	414		
RNA bases	829	818		
DNA bases	16	15		
Refinement (PHENIX)				
Refinement package	Real space refinement			
CC (volume)	0.80	0.79		
CC (mask)	0.82	0.80		
CC (peak)	0.75	0.73		
Rms deviations				
Bond length (\AA)	0.010	0.01		
Bond angles ($^\circ$)	1.154	1.21		
Validation				
Molprobrity score	2.24	2.33		
All-atom clashscore	13.72	15.30		
Rotamer outliers (%)	0.00	0.00		
C-beta deviations	0.00	0.00		
EM-Ringer score	2.89	2.53		
Ramachandran plot				
Outliers (%)	0.00	0.00		
Allowed (%)	11.76	13.73		
Favored (%)	88.24	86.27		