

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

Dataset	nsp13-RTC (CHAPSO)		
	nsp13 <sub>1</sub> -RTC	nsp13 <sub>2</sub> -RTC	(nsp13 <sub>2</sub> -RTC) <sub>2</sub>
<b>Sample ID</b>	nsp13 <sub>1</sub> -RTC	nsp13 <sub>2</sub> -RTC	(nsp13 <sub>2</sub> -RTC) <sub>2</sub>
<b>EMDB</b>	EMD-22270	EMD-22160	EMD-22271
<b>PDB</b>		6XEZ	
<b>Data collection and processing</b>			
Microscope	FEI Titan Krios	FEI Titan Krios	FEI Titan Krios
Voltage (kV)	300	300	300
Detector	Gatan K3	Gatan K3	Gatan K3
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	64	64	64
Defocus range (µm)	-0.8 to -2.5	-0.8 to -2.5	-0.8 to -2.5
Data collection mode	Counting Mode	Counting Mode	Counting Mode
Nominal Magnification	81,000x	81,000x	81,000x
Pixel size (Å)	1.1	1.1	1.1
Symmetry imposed	C1	C1	C1
Initial particle images (no.)	1447307	1447307	1447307
Final particle images (no.)	17345	58942	11771
Map resolution (Å) - FSC threshold 0.143	4.0	3.5	7.9
Map resolution range (Å)	3.2-7.6	2.8-7.1	4.0-10.3
<b>Refinement</b>			
Initial model used (PDB code)		6YYT/6JYT	
Map sharpening B factor (Å <sup>2</sup> )	-60.7	-76.8	-417.7
Model composition			
Non-hydrogen atoms		21,744	
Protein residues		2,563	
Nucleic acid residues (RNA)		70	
Ligands		8 Zn <sup>2+</sup> , 3 Mg <sup>2+</sup> , 3 CHAPSO, 3 ADP, 2 AF <sub>3</sub>	
B factors (Å <sup>2</sup> )			
Protein		50.08	
Nucleic acid		75.64	
Ligands		89.8	
R.m.s. deviations			
Bond lengths (Å)		0.01	
Bond angles (°)		0.945	
Validation			
MolProbity score		3.20	
Clashscore		19.89	

Poor rotamers (%)	10.77
Ramachandran plot	
Favored (%)	86.91
Allowed (%)	13.01
Disallowed (%)	0.08