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Supplemental Information

Cryo-EM Structure of an Extended SARS-CoV-2

Replication and Transcription Complex

Reveals an Intermediate State in Cap Synthesis

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Supplementary Tables

Table S1. Cryo-EM data statistics (Related to Figure 1).

	cap(-1)'-RTC
Data collection and processing	
Magnification	165,000
Voltage (kV)	300
Electron exposure (e ⁻ /Å ²)	60
Defocus range (μm)	-1.0 to -1.8
Pixel size (Å)	0.82
Symmetry imposed	C1
Initial particle images (no.)	529,558
Final particle images (no.)	67,540
Map resolution (Å)	2.83
FSC threshold	
Map resolution range (Å)	2.0 - 9.0
Refinement	
Model resolution (Å)	2.8
FSC threshold	0.143
Model resolution range (Å)	∞ to 2.8
Map sharpening <i>B</i> factor (Å ²)	-67.7
Model composition	
Non-hydrogen atoms	21,831
Protein residues	2654
Ligands	52
<i>B</i> factors (Å ²)	
Protein	51.7
Ligand	73.4
R.m.s. deviations	
Bond lengths (Å)	0.012
Bond angles (°)	0.87
Validation	
MolProbity score	3.13
Clashscore	18.7
Poor rotamers (%)	0.07
Ramachandran plot	
Favored (%)	91.2
Allowed (%)	8.8
Disallowed (%)	0

Table S2. Interactions of nsp9 with nsp12 and GDP (Related to Figure 3).

Molecule	Residue	Molecule	Residue
nsp9	N1	nsp12	F35, D36, I37, Y38, N39, D208
	N2		D36, I37, Y38, V204, T206, D221, R733
	E3		Y38, N39, D40
	L4		I223
	R74		T226
	N96		V231, P232, V233, Y289, D291
	L97		V233, R733
	G100		V202
	L103		I223, V231
	G104		I223
	A107		Q224
	N1	GDP	α -PO ₃

Table S3. Interactions of nsp13-2 with nsp8-1 and nsp12 (Related to Figure 5).

Molecule	Residue	Molecule	Residue
nsp13-2	S44	nsp8-1	M70
	V45		Q73
	P53		Y71, R75
	D56		T96
	L65		M62
	G67		M62
	M68		Q65
	I79		K58, L59, M62
	S80		L59
	L92		M67, M70, Y71
	Y93		nsp12
	N95	Y903, S904, V905	
	T96	M902, Y903, S904	

Table S4. Interactions of nsp13-2 and nsp13-1 (Related to Figure 5).

Molecule	Residue	Molecule	Residue
nsp13-2	R155	nsp13-1	Y253
	E156		Y253, P254
	V169		E244, Y246