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## **Supplemental Information**

### **Structural Basis for RNA Replication**

#### **by the SARS-CoV-2 Polymerase**

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Number	Constructs	Oligonucleotide sequences
1	T33-1/P10	GGGAGAUGAAAGUCUCCA <b>CCUGUG</b> UCGUCGAAA
2	T33-2/P10	GGGAGAUGAAAGUCUCCA <b>GCAUAU</b> UCGUCGAAA
3	T33-3/P10	GGGAGAUGAAAGUCUCCA <b>CCGGG</b> GUCGUCGAAA
4	T33-4/P10	GGGAGAUGAAAGUCUCCA <b>CCGUGU</b> UCGUCGAAA
5	T33-5/P10	GGGAGAUGAAAGUCUCCA <b>CCUUUU</b> UCGUCGAAA
6	T33-6/P10	GGGAGAUGAAAGUCUCCA <b>GGUCUC</b> UCGUCGAAA
7	T31/P8	GGGAGAUGAAAGUCUCCA <b>GGUCUC</b> GUGGAAA
8	T34/P10	GGGAGAUGAAAGUCUCCA <b>GGCUCUC</b> UCGUCGAAA
9	T35/P10	GGGAGAUGAAAGUCUCCA <b>GGUCUCUC</b> UCGUCGAAA
10	T36/P10	GGGAGAUGAAAGUCUCCA <b>GGCUCUCUC</b> UCGUCGAAA
11	T37/P10	GGGAGAUGAAAGUCUCCA <b>GGUCUCUCUC</b> UCGUCGAAA
12	T33-7/P10	GGGAGAUGAAAGUCUCCA <b>GGUCUCUCUC</b> UCGUCGAAA
N/A	P10	UGUUCGACGA
N/A	P8	UGUCCGA

**Table S1. Oligonucleotide sequences information, Related to STAR Methods.**

	Pre-translocated catalytic complex			Post-translocated catalytic complex
	Overall	Conformation I	Conformation II	
<b>PDB entry</b>	7C2K	N/A	N/A	7BZF
<b>EMDB entry</b>	EMD-30275	EMD-30283	EMD-30284	EMD-30252
<b>Data collection and processing</b>				
Magnification	165,000	165,000	165,000	165,000
Voltage (keV)	300	300	300	300
Electron exposure (e <sup>-</sup> /Å <sup>2</sup> )	60.00	60.00	60.00	60.00
Defocus range (μm)	-2.0 to -1.0	-2.0 to -1.0	-2.0 to -1.0	-1.8 to -1.0
Pixel size (Å)	0.82	0.82	0.82	0.82
Symmetry imposed	C1	C1	C1	C1
Initial particle images (no.)	1,330,896	1,330,896	1,330,896	1,235,162
Final particle images (no.)	103,159	65,463	37,696	119,662
Map global resolution (Å)	2.93	3.03	3.12	3.26
Global resolution FSC threshold	0.143	0.143	0.143	0.143
Map sharpening <i>B</i> factor (Å <sup>2</sup> )	97.6	86.1	76.4	99.0
Map local resolution range (Å)	1.8-7.5	1.8-10.0	1.8-10.0	2.0-8.0
Model resolution (Å)	2.8	N/A	N/A	3.2
FSC threshold	0.143	N/A	N/A	0.143
Model resolution range (Å)	∞ to 2.8	N/A	N/A	∞ to 3.2
<b>Model composition</b>				
Non-hydrogen atoms	10,692	N/A	N/A	9,932
Protein residues	1,256	N/A	N/A	1,200
Nucleotide residues	31	N/A	N/A	19
Ligands	3	N/A	N/A	2
<b><i>B</i> factors (Å<sup>2</sup>)</b>				
Protein	45.91	N/A	N/A	51.33
Nucleotide	78.99	N/A	N/A	74.57
Ligand	22.30	N/A	N/A	42.29
<b>R.m.s. deviations</b>				
Bond lengths (Å)	0.005	N/A	N/A	0.004
Bond angles (°)	0.645	N/A	N/A	0.988
CC(mask)	0.90	N/A	N/A	0.78
CC(box)	0.79	N/A	N/A	0.73
<b>Validation</b>				
MolProbity score	1.71	N/A	N/A	2.09
Clashscore	7.25	N/A	N/A	11.67
Poor rotamers (%)	0.00	N/A	N/A	0.00
<b>Ramachandran plot</b>				
Favored (%)	95.51	N/A	N/A	91.50
Allowed (%)	4.49	N/A	N/A	8.50
Disallowed (%)	0.00	N/A	N/A	0.00
<b>Model coverage</b>				
Chain A	A1~V907; D910~T929	N/A	N/A	A1~T896; T912~T929
Chain B	S76~N192	N/A	N/A	K72~N192
Chain C	P0~C72	N/A	N/A	S1~I68
Chain D	A53~A191	N/A	N/A	K127~A191

**Table S2. Cryo-EM data statistics, Related to Figures 2, 3, 4, 5 and 7.**