# **Supplementary information**

# The mechanism of RNA capping by SARS-CoV-2

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## The Mechanism of RNA Capping by SARS-CoV-2

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### This file contains:

Supplementary Fig. 1, Uncropped gels

Supplementary Tables 1 to 3

# Supplementary Fig. 1, Uncropped gels

#### Gel Figure 1a. ATP Coomassie



Gel Figure 1a. GTP Coomassie



#### Gel Figure 1a. UTP Coomassie



Gel Figure 1a. CTP Coomassie



#### Gel Figure 1b. Coomassie



Gel Figure 1a. ATP Autorad





Gel Figure 1a. UTP Autorad



Gel Figure 1a. CTP Autorad



Gel Figure 1b. Autorad





## gel in Fig. 2c















Gel Extended Figure 3a. GTP Coomassie



Gel Extended Figure 3a. GTP Autorad



Gel Extended Figure 3a. UTP Coomassie



Gel Extended Figure 3a. UTP Autorad





#### Gel Extended Data Fig. 4c



#### gel Extended Data fig. 4d







## Extended Data 5g









#### Gel Extended Data Fig. 8b



# Extended Data 9d



#### Gel Extended Figure 10d. Toluidine



Gel Extended Figure 10d. Autorad



# Supplementary Table 1. RNAs used in this study

RNA	Sequence
5'-pppRNA <sup>A19C 26</sup>	[ppp]ACCCCCCCCCCCCCCCC
5'-pppRNA <sup>LS10</sup>	[ppp]AUUAAAGGUU
5'-pppRNA <sup>LS2</sup>	[ppp]AU
5'-pppRNA <sup>LS3</sup>	[ppp]AUU
5'-pppRNA <sup>LS4</sup>	[ppp]AUUA
5'-pppRNA <sup>LS5</sup>	[ppp]AUUAA
5'-pppRNA <sup>LS6</sup>	[ppp]AUUAAG
5'-pppRNA <sup>LS20</sup>	[ppp]AUUAAAGGUUUAUACCUUCC
5'-pppRNA <sup>LS10_A1C</sup>	[ppp]CUUAAAGGUU
5'-pppRNA <sup>LS10_A1G</sup>	[ppp]GUUAAAGGUU
5'-pppRNA <sup>LS10_A1U</sup>	[ppp]UUUAAAGGUU
5'-pppRNA <sup>LS10_U2G</sup>	[ppp]AGUAAAGGUU
5'-pppRNA <sup>LS10_U2A</sup>	[ppp]AAUAAAGGUU
5'-pppRNA <sup>LS10_U2C</sup>	[ppp]ACUAAAGGUU

Magnification	81,000
Voltage (kV)	300
Electron exposure (e <sup>-</sup> Å <sup>-2</sup> )	54
Defocus range (µm)	-1.0 to -2.5
Pixel size (Å)	1.09
Symmetry imposed	C1
Initial particle images (no.)	4,196,806
Final particle images (no.)	39,985
Map resolution (Å)	3.2
FSC threshold	0.143
Refinement	
Initial model used (PDB code)	-
Model resolution (Å)	3.5
FSC threshold	0.5
Map sharpening <i>B</i> factor (Å <sup>-2</sup> )	-37
Nonhydrogen atoms	9,215
Protein residues	1150
Ligands	4
B factors (Å <sup>-2</sup> )	
Protein	67.4
Ligands	75.9
R.m.s. deviations	
Bond lengths (Å)	0.002
Bond angles (°)	0.453
MolProbity score	1.50
Clashscore	3.12
Poor rotamers (%)	0
Favored (%)	94.1
Allowed (%)	5.9
Disallowed (%)	0

# Supplementary Table 2. Data collection and refinement statistics

Oligo	Sequence	Use
PacI Forward	GGTTGAAGCAGTTAATTAAAGTTACACTTGTG	Fragment 1 and 3
1NtoA Reverse	GCAACAGGACTAAGCTCATTAGCCTGTAATTTGACAGC	Fragment 1
1NtoD Reverse	GCAACAGGACTAAGCTCATTGTCCTGTAATTTGACAGC	Fragment 1
2NtoA Reverse	GCAACAGGACTAAGCTCAGCATTCTGTAATTTGACAGC	Fragment 1
73KtoA Reverse	GAGAAAGTGTGTCTCGCAACTACAAAGTAAG	Fragment 1
MluI Reverse	CCTAAGTTGGCGTATACGCGTAATATATCTGGG	Fragment 2 and 3
1NtoA Forward	GCTGTCAAATTACAGGCTAATGAGCTTAGTCCTGTTGC	Fragment 2
1NtoD Forward	GCTGTCAAATTACAGGACAATGAGCTTAGTCCTGTTGC	Fragment 2
2NtoA Forward	GCTGTCAAATTACAGAATGCTGAGCTTAGTCCTGTTGC	Fragment 2
73KtoA Forward	CTTACTTTGTAGTTGCGAGACACACTTTCTC	Fragment 2

# Supplementary Table 3. Oligonucleotides used in the SARS-CoV-2 infection experiments