Coronavirus genome replication and transcription processes are confined to viral-specific organelles formed from endoplasmic reticulum membranes (8, 9) during early-stage infection, and probably mitochondrial, endosomal, and Golgi membranes during viral particle assembly (8–10). Thus, nascent coronavirus mRNAs do not have access to the host mRNA capping and methylation machinery in the nucleus but instead encode their own capping machinery.

The viral replication helicase nsp13 also has 5’-RNA triphosphatase activity that removes the 5’-γ-phosphate from the nascent ppp-RNA (11). The RNA-dependent RNA polymerase nsp12 can then transfer a guanosine monophosphate to the 5′-end of the mRNA (12, 13), and this guanosine is then methylated by the nsp14-nsp10 heterodimer to generate N7-methylated Cap-0-RNA (m7GpppA1-RNA). Last, to form the Cap-1-RNA, a methyl group is transferred from S-adenosylmethionine (SAM) to the 2′-OH of the first adenine ribonucleotide. For coronaviruses, this last reaction is catalyzed by the 2′-O-methyltransferase (MTase), a heterodimeric complex of nsp16 with the activator nsp10 (Fig. 1A) (11, 14, 15). The coronavirus 2′-O-MTase is a validated antiviral drug target, because the formation of the nsp16-nsp10 complex can be blocked by peptides and protect mice from lethal challenge with mouse hepatitis virus (MHV) (16, 17).

Biochemical studies of the RNA MTases from SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV) demonstrated that methyl transfer is activated by divalent cations. SARS-CoV nsp14 is activated by Mn2+, but not by Mg2+ (11), whereas nsp16 can be activated by Mn2+ or Mg2+ and to a lesser extent by Ca2+ (11, 18–20). These data are consistent with known requirements for divalent cations by other viral RNA MTases, including dengue virus (DENV) NS5, which is stimulated by Mg2+ (21). Furthermore, studies of nsp16 from SARS-CoV and MERS-CoV have demonstrated that the methyl transfer reaction is most efficient in vitro with an RNA substrate composed of at least five ribonucleotides (11, 19, 20, 22). However, the role of metals in nsp16 catalysis and the influence of mRNA length on the reaction are not clear, particularly because no structures have been solved for any coronavirus nsp16 enzyme with bound metals or RNA. To support drug discovery efforts targeting nsp16, researchers around the globe have determined crystal structures of SARS-CoV-2 nsp16-nsp10 in complex with a variety of ligands (23–29), complementing prior structural biology observations for this enzyme from SARS-CoV and MERS-CoV (19, 20, 23).
This information has facilitated detailed examination of the SARS-CoV-2 2′-O-MTase and revealed conformational flexibility of loop 1 and loop8-n3-loop9, loops that border the Cap-0 binding site (25, 26). Despite this extensive structural information, a major gap exists in the understanding of the role of metal ions in the nsp16 2′-O-methyl transfer reaction and the position of ribonucleotides in the RNA binding groove because structures of the enzyme in complex with RNA and metals have not been reported. Herein, we present structures of the SARS-CoV-2 2′-O-MTase nsp16-nsp10 heterodimer in complex with substrates and products in the presence of divalent cations. Our structures reveal important information regarding interactions of nsp16 residues with the capped RNA, the influence of a coronavirus MTase-specific four-residue insert on the conformation of capped RNA, and the role of metal ions in 2′-O-methyl transfer.

RESULTS

SARS-CoV-2 nsp16 activity requires extended capped RNA and divalent cations

We launched this research by confirming that the SARS-CoV-2 2′-O-MTase activity requires divalent cations. We used a custom-synthesized Cap-0-RNA substrate composed of the N7-methylated guanosine (m7G) attached through a triphosphate bridge to a short RNA (AUUAAA), which matches the naturally occurring ribonucleotides at the 5′-end of SARS-CoV-2 mRNAs (31). At a concentration of 2 mM, both Mg2+ and Mn2+ increased MTase activity with this substrate (Fig. 1B). In contrast, 2 mM Ca2+ yielded only 50% of the activity observed with Mg2+, and Na+ did not stimulate activity at 3 mM (Fig. 1B). These data are consistent with observations for SARS-CoV nsp16 (11, 19, 20). The activity of SARS-CoV-2 nsp16 with the Cap-0-RNA substrate (m7GpppAUUAAA) was over 10 times higher than that with the Cap-0 analog (m7GpppA) (Fig. 1B).

Isothermal titration calorimetry (ITC) measurements showed that, although it is a poor substrate for catalysis, m7GpppA does bind to nsp16 alone (Kd = 6.6 ± 0.3 μM) with threefold higher affinity than to nsp16 alone (Kd = 28.0 ± 5.5 μM) (fig. S1, C and E, and table S1). In contrast, m7GpppG bound only to the nsp16-nsp10 heterodimer (m7GpppAUUAAA) was over 10 times higher than that with the Cap-0 analog (m7GpppA) (Fig. 1B).
Crystal structures of the nsp16-nsp10 heterodimer with capped RNA and metal ions

To gain insight into how metal ions stimulate catalysis, we took a structural biology approach. Crystals of nsp16-nsp10 in complex with SAM from different crystallization conditions were soaked with the custom-synthesized m’GpppAUUAAA substrate in the presence of Mg$^{2+}$ or Mn$^{2+}$. Multiple datasets were collected, and, ultimately, the three with the highest resolution and the best data statistics were selected for further analysis (table S2). Crystal #1 [Protein Data Bank (PDB) 7JYY] was soaked with substrates in the presence of 5 mM MgCl$_2$ for 1.5 hours. In this crystal, we observed Cap-0-RNA, SAM, and Mg$^{2+}$ (Fig. 1, C and D). Crystal #2 (PDB 7L6R) was soaked with substrates in the presence of 20 mM MnCl$_2$ for 6 hours. In this crystal, we observed Mn$^{2+}$ and products of the reaction, Cap-1-RNA and SAH, indicating that the methyl transfer occurred in the crystal (Fig. 1E). Crystal #3 (PDB 7L6T) was soaked with substrates in the presence of 500 mM MgCl$_2$ for 6 hours. In this crystal, we observed two Mg$^{2+}$ ions and the products Cap-1-RNA and SAH. The first Mg$^{2+}$ occupied the same metal binding site as in crystals #1 and #2, and the second Mg$^{2+}$ directly interacted with phosphate groups of the capped RNA (fig. S2). The capped RNAs in crystals #1 and #3 included the m’G cap, the first three ribonucleotides, and the phosphate group of A$_5$. Crystal #2 contained the m’G cap, the first four ribonucleotides, and the phosphate group of A$_5$.

Substrates are properly aligned when the capped short RNA is present

The superposition of the previously reported structure of SARS-CoV-2 nsp16-nsp10 with a Cap-0 analog [PDB 6WRZ (25)] and nsp16-nsp10 with Cap-0-RNA (PDB 7JYY, this study) revealed that they are very similar with a root mean square deviation of 0.33 Å (Fig. 2A). We previously showed that the cap-binding site, also called the high-affinity binding site (HBS), is bordered by flexible loops that adopt an open conformation upon Cap-0 analog binding (25). Interactions of the nsp16 residues with the Cap-0 analog and Cap-0-RNA are similar in both structures. The m’GpppA in the HBS is stabilized by stacking of the m’G and A$_1$ bases with Tyr$_{6828}$ and Tyr$_{6930}$ residues, respectively (Fig. 2A). The O2’ of the A$_1$ ribose interacts with the conserved nsp16 catalytic residues (19, 20) as well as with a conserved water molecule we previously identified (25). The interactions between Asn$_{6841}$, SAM, and O2’ from the A$_1$ are also consistent between these structures (Fig. 2B).

Of particular note was the space between the Tyr$_{6930}$ and Asp$_{6873}$ side chains, which is occupied by the A$_1$ base in the Cap-0 analog structure. In the Cap-0-RNA structure, this space accommodates the stacked bases of A$_1$ and U$_2$, with the U$_2$ base forcing repositioning of the A$_1$ ribonucleotide (Fig. 2A). Superposition of the Cap-0 and Cap-0-RNA structures revealed that this repositioning involves both a 0.6-Å shift of the A$_1$ base toward the side chain of Tyr$_{6930}$ without notable changes in the positions of Asn$_{6841}$ and Tyr$_{6930}$, as well as a 0.4-Å decrease in the distance between O2’ of A$_1$ and the SAM methyl group, which occurs without apparent changes in the position of catalytic residues (Fig. 2B). The movement and alignment of the A$_1$ O2’ atom toward the methyl group of SAM may explain why the additional ribonucleotides increase the efficiency of the methyl transfer reaction (33–35).

Fig. 2. The catalytic site of the SARS-CoV-2 2′-O-MTase. (A) The superposition of nsp16 with the Cap-0 analog (PDB 6WVN, pink) and nsp16 with the Cap-0-RNA (PDB 7JYY, green) structures with plotted electrostatic surface shown in blue (positive charge) and red (negative charge). Selected residues of nsp16, SAM, the Cap-0 analog, and Cap-0-RNA are labeled and shown as sticks. Carbons are in pink and green for Cap-0 analog and Cap-0-RNA, respectively, with oxygens in red, nitrogens in blue, and sulfurs in yellow. Repositioning of the A$_1$ base is marked with a curved arrow. (B) Catalytic residues of nsp16, Cap-0 analog, Cap-0-RNA, and conserved water for the same structures and same color scheme as in (A), with waters shown as small spheres in red and cyan for structures 6WVN and 7JYY, respectively. (C and D) Wall-eyed pseudo-stereo view of the active sites for complexes of (C) nsp16-nsp10 with Cap-0-RNA and SAM (PDB 7JYY) and (D) nsp16-nsp10 with Cap-1-RNA/SAH (PDB 7L6R). The catalytic site residues, SAM, and capped RNAs are labeled and shown as stick models with atoms colored in beige, green, and gray for carbons of nsp16, SAM, and capped RNA, respectively, with red for oxygens, blue for nitrogens, and yellow for sulfurs. Conserved catalytic waters are shown as cyan spheres, hydrogen bond interactions as black, dashed lines, and the omit [Fo-Fc] electron density maps contoured at the 3σ level as blue mesh. The methyl group of SAM and Cap-1-RNA are marked with black triangles.
Although the superposition of Cap-0 and capped RNA structures revealed differences in the position of the first adenosine, no deviations were observed between Cap-0-RNA and Cap-1-RNA conformations (Fig. 2, A and B), indicating that the A₁ base is not repositioned after the methyl transfer. The structures are essentially identical, with the only difference being the methyl group, which moves from SAM to the A₁ ribose hydroxyl group during methyl transfer (Fig. 2, C and D).

**Interaction of capped RNA ribonucleotides with residues of the low-affinity binding site**

The structures in complex with capped RNAs also revealed the importance of the low-affinity binding site (LBS) residues for the conformation of the mRNA in the catalytic site. The best resolved and most complete electron density for capped RNA was observed in crystal #2. The position of U₂ in the active site is "locked" by multiple interactions (Fig. 3A). The phosphate group of U₂ interacts with water molecules from the hydration sphere of the metal ion and the side-chain nitrogen of Lys⁶⁸⁷⁴, the O₂ atom of the U₂ base interacts with the main-chain nitrogen of Asp⁶⁸⁷₃, and the O₂' of the U₁ ribose makes direct interactions with one of the oxygens of the side chain of Asp⁶⁸⁷₃ (Fig. 3B). The phosphate group of U₃ interacts directly with the side-chain nitrogen of Lys⁶⁸⁷⁴ and forms water-mediated interactions with residues Asp⁶⁸⁷₃, Lys⁶⁸⁷₄, Met⁶⁸⁴⁰, and Asn⁶⁸⁴¹. The base of U₃ interacts directly with the main-chain oxygen and nitrogen atoms of Ala⁶⁸₃₂ and forms a water bridge interaction with the nitrogen of the main chain of Leu⁶₈₃₄. The whole nucleotide A₄ and phosphate group of A₅, the last ordered part of the capped RNA in the crystal #2 structure, are solvent exposed and connected to the protein by a hydrogen bond interaction between O4’ of the A₄ and the side-chain oxygen of Ser⁶⁸³¹ (Fig. 3B). The stacking interactions between bases of U₃ and A₄ define the position of the A₄ nucleotide.

It is unknown if the conformation of A₄ reflects the natural interaction of nucleotides or if a longer mRNA would form different contacts with the nsp16-nsp10 heterodimer. However, the position of m⁷G and first three nucleotides of the capped RNA closely match in all three structures and likely represent the accurate binding mode for this part of the capped RNA.

**Metal ions stabilize the capped RNA in the nsp16 active site**

The primary metal binding site is located near the HBS (Fig. 1C), with either Mg²⁺ or Mn²⁺ occupying the same site with similar interactions (Fig. 3, B and C). The metal ions make both direct and water-mediated interactions with side chains of nsp16 residues and the backbone of the capped RNA. The best electron density maps were observed for crystal #3 with two magnesium ions, both of which have near-ideal octahedral geometry (Fig. 3C). The Mg²⁺ in the primary metal binding site is coordinated in part by interactions with phosphate groups of the triphosphate bridge linking the cap to A₁, the phosphate group of U₂, and the ribose of U₃. The second Mg²⁺ directly interacts with the U₁ and A₄ phosphate group oxygens and through water molecules with the side-chain oxygens of the Asp⁶⁸⁷₃ and the side-chain nitrogen of Lys⁶⁸⁷₄ (Fig. 3C). Thus, the metal ion that occupies the primary metal binding site of nsp16 properly aligns capped RNA with SAM for an efficient methyl transfer reaction. The role of metal ions in facilitating orbital alignments for efficient catalysis has been demonstrated structurally for hydride transfer reactions (34). Structural evidence for the requisite orbital alignment of substrates in RNA 2'-O-MTases (33) and ribozymes (35) has also been observed.

Asp⁶⁸⁷₃ and Lys⁶⁸⁷₄ alter the backbone conformation of the capped RNA in coronaviruses

Comparison of the RNA binding site and the capped RNA conformation from the SARS-CoV-2 nsp16-nsp10 structure (PDB 7L6R) and the crystal structures of 2'-O-MTases with capped RNA for DENV NS5 [PDB 5D1O (21)], vaccinia virus (VACV) VP39 [PDB 1AV6 (36)], and human cap MTase hCMTr1 [PDB 4N48 (37)] revealed that the conformation of the m⁷G and the location of the cap-binding pockets relative to the active sites are markedly different (fig. S3, A to D). In the nsp16-nsp10 and VP39 structures, the N7'-methyl groups are nestled in the HBS pocket (fig. S3, A and C). In contrast, in NS5 and hCMTr1,
for which methylation at the $N^7$ position of the $G_0$ is not required for the 2′-O-MTase activity (37), the $N^7$-methyl groups are pointed toward the solvent (fig. S3, B and D). Although the m'G positions do not overlap, nucleotides $N_1$ and $N_2$ in all these structures are closely matched, which is consistent with the conserved mechanism of action and the structure of the catalytic site (Fig. 4A). In all but the nsp16-nsp10 structure, the $N_3$ nucleotide is sandwiched between the $N_2$ and $N_4$ by base stacking interactions, and these three nucleotides have limited interactions with the 2′-O-MTase residues of RNA binding grove. In the nsp16-nsp10 structure, all functional groups of the nucleotides $N_2$ and $N_3$ are involved in an integrated and complex network of hydrogen bond interactions with residues of the LBS. The $U_2$ base and the ribose directly interact with main-chain and side-chain atoms of Asp$^{6873}$. The Asp$^{6873}$ side chain occupies the space that is filled by $N_3$ in all other structures and forces the $U_3$ nucleotide to move to the opposite side of the RNA binding groove. The base of $U_3$ is involved in direct and water-mediated interactions with Ala$^{6832}$ and Leu$^{6834}$, while the phosphate group interacts with Lys$^{6874}$ (Fig. 3, B and C).

The superposition of SARS-CoV-2 nsp16-nsp10 (PDB 7JYY) with MERS-CoV [PDB 5YNM (38)] revealed almost identical conformations of the proteins and the promontory Asp$^{6873}$ and Lys$^{6874}$ residues, as well as the position of the Cap moiety (Fig. 4B). Alignment of the amino acid sequences of nsp16 from representative coronaviruses (Fig. 4C and fig. S4, A and B) showed that Asp$^{6873}$ is conserved across the coronaviruses, except for feline coronavirus (F-CoV). Structural alignment of nsp16 with NS5, VP39, and hCMTr1 revealed that two important residues, Asp$^{6873}$ and Lys$^{6874}$, are located in a four-residue loop that connects $\beta_1$ and $\alpha A$ (Fig. 4D). This four-residue insert is uniquely present in all coronavirus nsp16 MTases and is absent from other MTases (Fig. 4E).

To test the effect of this insert on nsp16 MTase activity, we prepared nsp16 proteins with D6873A or D6873G amino acid substitutions or with a deletion of Asp$^{6873}$ and Lys$^{6874}$ within the loop [$\Delta$(D$^{6873}$-K$^{6874}$)]. Overall, Mn$^{2+}$ stimulated the methyl transferase activity of nsp16 better than did Mg$^{2+}$ for both the wild-type and mutant nsp16 proteins (Fig. 5, A and B). At a 600 nM protein concentration in the presence of Mn$^{2+}$, we observed 10% of the maximum activity for all proteins, whereas only 2% activity was observed in the presence of Mg$^{2+}$. A similar pattern was detected when we measured values for maximum activity, which was reached at an enzyme concentration of 500 nM in the presence of Mn$^{2+}$ but required 1 µM enzyme in the presence of Mg$^{2+}$ (Fig. 5, A and B). The EC$_{50}$ (Half maximal effective concentration) values for activity of the D6873A and D6873G mutants in the presence of Mn$^{2+}$ were shifted higher than values obtained for the wild-type enzyme (Fig. 5C). These shifts in EC$_{50}$ values were more evident in the presence of Mg$^{2+}$. The $\Delta$(D$^{6873}$-K$^{6874}$) mutant showed much lower

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**Fig. 4. A four-residue loop in coronavirus nsp16 alters the orientation of the RNA substrate.** (A) Wall-eyed stereo view of the superimposed capped RNAs mapped on the electrostatic potential surface of SARS-CoV-2 2′-O-MTase. RNAs are shown as sticks in bright pink (SARS-CoV-2), cyan (DENV NS5), yellow (VACV VP39), and green (hCMTr1). The nucleotides are labeled with numbers starting from m'G (position 0); 3′ and 4′ correspond to U3 and A4 in the Cap-moiety residues, as well as the position of the Cap moiety (Fig. 4B). Alignment of the amino acid sequences of nsp16 from representative coronaviruses (Fig. 4C and fig. S4, A and B) showed that Asp$^{6873}$ is conserved across the coronaviruses, except for feline coronavirus (F-CoV). Structural alignment of nsp16 with NS5, VP39, and hCMTr1 revealed that two important residues, Asp$^{6873}$ and Lys$^{6874}$, are located in a four-residue loop that connects $\beta_1$ and $\alpha A$ (Fig. 4D). This four-residue insert is uniquely present in all coronavirus nsp16 MTases and is absent from other MTases (Fig. 4E).

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activity compared to the D6873A and D6873G mutants and the wild-type enzyme. At enzyme concentrations as high as 2 μM, the activity of Δ(D6873-K6874) reached only 45 and 65% of that of the wild-type max activity in the presence of Mn²⁺ or Mg²⁺, respectively. The results of activity assays support our structural finding regarding the importance of the four-residue loop that is unique for coronavirus nsp16 MTase as well as a preference for stimulation of the methyl transfer reaction by Mn²⁺.

**DISCUSSION**

In eukaryotes, 5′ capping and subsequent 2′-O-methylation events are essential for RNA metabolism and protection from cell innate immunity responses (39). Coronaviruses and other viruses have evolved entire RNA capping and methylation machineries to modify their own RNAs, thereby increasing the translation of viral proteins and promoting the evasion of host immune responses (7, 40, 41). For this reason, the viral 2′-O-MTases are suitable targets for drug development. Thus far, all proposed modeling of the Cap-RNA orientation in the LBS of nsp16-nsp10 (24, 26, 32) have relied on the crystal structures of DENV NS5, VACV VP39, and hCMTr1, indicating a knowledge gap for drug design.

The metal ion requirement for DENV, SARS-CoV, and MERS-CoV MTase activity is well known (11, 19, 20). However, the binding site of the metal ion and capped RNA has been shown only for the NS5 structure (21). In the NS5 structure, the Mg²⁺ ion directly interacts with all three phosphate groups that link the m⁷G with the A₁ and thus neutralizes the negative charge of the triphosphate group. Three additional interactions through its hydration sphere with the bases of the capped RNA help maintain stacking interactions and stabilize the single-stranded RNA helix in the A-form. The described Mg²⁺ is not involved in any direct hydrogen bond interactions with the residues of the 2′-O-MTase domain. In all SARS-CoV-2 nsp16 structures reported here, the metal ions that occupy the primary metal binding site directly interact with Asn⁶⁹⁹⁶. This direct interaction "pins" the metal ion to the negatively charged "nest." By neutralizing the negative charge, metal ions stabilize the unique conformation of the capped RNA and by direct interaction with Asn⁶⁹⁹⁶ help to hold the RNA in the RNA binding site for methyl transfer.

Metal ions tested in the activity assays had different effects on the methyl transfer efficiency of SARS-CoV-2 nsp16. Na⁺ has a lower charge and Ca²⁺ has longer metal-ligand distances than Mg²⁺ or Mn²⁺, which might yield a more extended capped RNA that is weakly attached to the binding site. We suspect that this is why Na⁺ and Ca²⁺ poorly stimulated the methyl transfer reaction in our assays. Mn²⁺ had been considered as the primary catalytic cofactor and is reported as an important additive for nsp16 activity assays (11, 19, 20, 22). The results of our biochemical assays, by contrast, showed that Mn²⁺ had the highest stimulation effect on the methyl transfer reaction, and maximum activity was reached at lower concentrations of enzyme. It was also reported that Mg²⁺ ions in micro- to millimolar concentrations can promote the cleavage of nucleic acids (42), suggesting that Mn²⁺ is preferable compared to Mg²⁺. In addition, Mn²⁺ has a higher reported concentration than Mg²⁺ in the endoplasmic reticulum and Golgi, where the SARS-CoV-2 replication vesicles...
are formed (43, 44). Together, these findings suggest that Mn$^{2+}$ is the natural cofactor for the methyl transfer reaction in SARS-CoV-2 and other coronaviruses. This information could be very helpful in the design of specific inhibitors to target the metal binding site and impair the activity of the complex.

Comparison of the RNA binding sites and the capped RNA conformations from the prior MTase structures of NS5, VP39, and HCMT1r1 with those of nsp16-nsp10 complexes revealed major differences between them. These four structures can be grouped into two classes: The $N'$ of the $m^7$G buried in the binding pocket, as observed in nsp16 and VP39, and $N'$ exposed to the solvent, as observed in NS5 and HCMT1r1. Despite these differences, the superposition of these structures revealed a close match for the positions and the conformations of the first and the second nucleotides of capped RNA. This observation is in line with the conserved mechanism of the 2'-O-MTase reaction. The major differences in the conformations of the RNA are located in the extended part of the capped RNA where it interacts with the residues of the LBS. In NS5, VP39, and HCMT1r1, the $N_3-N_2$ nucleotides of the capped RNA are stabilized by stacking interactions. In contrast, Asp$^{6873}$ in nsp16 alters the position of the $N_3$ and prevents the stacking of $N_3$ to $N_1-N_2$, and Lys$^{6874}$ stabilizes the position of the U$_3$ phosphate. All functional groups of the nucleotides $N_2$ and $N_3$ are involved in an integrated and complex network of hydrogen bond interactions with residues of the LBS. These distinct differences were found to affect catalysis with mutation of Asp$^{6873}$, leading to a reduced EC$_{50}$ and deletion of Asp$^{6873}$ and Lys$^{6874}$ from the loop shifting the EC$_{50}$ to the micromolar range.

A key advance of this work was the use of a custom-synthesized substrate RNA with ribonucleotides matched specifically to the sequences of the SARS-CoV-2 mRNA 5'-ends compared to earlier studies that used poly(C) RNA (11, 19). Use of this substrate, however, introduced a limitation of the studies due to precious amounts of the compound, which prevented maximizing the substrate concentration for kinetic and binding assays. However, we were able to determine the crystal structure of nsp16-nsp10 in complex with Cap-0-RNA and the product of the reaction, Cap-1-RNA. Cap-0-RNA was used to conduct biochemical assays at a fixed concentration of substrates to show the preference of the enzyme for Mn$^{2+}$ over Mg$^{2+}$, a requirement for the extended RNA, and the importance of the unique promontory loop in nsp16 for catalysis. These studies in total indicate that redirection of the RNA, which is also coordinated by metals, leads to proper alignment of substrates for efficient methyl transfer to the 2'-OH of the first adenosine, and that the presence of a unique four-residue insert (D$^{6873}$K$^{6874}$G$^{6875}$X$^{6876}$), which is conserved in all coronaviruses, is critical for catalysis. The absence of this insert in mammalian MTases makes this region a promising site for the design of selective RNA-like coronavirus-specific inhibitors.

**MATERIALS AND METHODS**

**Protein expression, purification, and crystallization**

Recombinant nsp16 and nsp10 proteins were purified from *Escherichia coli* and crystallized as previously described (25). DNA sequences for expression of mutant nsp16 protein were also generated by synthetic DNA in the same vector (Twist Biosciences) and purified following the prior established protocol (25). To form the nsp16-nsp10 heterodimers, the pure proteins were mixed at a 1:1 molar ratio at ~2 mg/ml in buffer [10 mM tris-HCl (pH 8.3), 500 mM NaCl, 1 mM tris(2-carboxyethyl) phosphate (TCEP), 2 mM MgCl$_2$, and 5% glycerol] and incubated for 1 hour, then dialyzed in crystallization buffer [10 mM tris-HCl (pH 7.5), 150 mM NaCl, 2 mM MgCl$_2$, 1 mM TCEP, and 5% glycerol] for 2 hours. SAM was added to a final concentration of 2 mM. Freshly purified preformed nsp16-nsp10 heterodimer was concentrated to 4.0 to 5.5 mg/ml and immediately set up for crystallization as 2-$\mu$l crystallization drops (1 $\mu$l protein:1 $\mu$l reservoir solution) in 96-well crystallization plates.

**MTase activity assays**

Custom-synthesized Cap-0-RNA (m$^7$GpppAUUAAA) was obtained from Bio-Synthesis Inc. (Lewisville, TX). Cap-0 analog (m$^7$GpppA) was obtained from New England Biolabs (catalog #S4105L). The MTase activity was measured using the MTase-Glo Methyltransferase bioluminescence assay (Promega) (45) according to the manufacturer’s protocol in a suitable solution for SARS-CoV-2 MTase: 20 mM tris-HCl (pH 8.0), 1 mM EDTA, 100 nM nsp16-nsp10 heterodimer, 1 $\mu$M excess of nsp10, 5 $\mu$M SAM, 300 nM Cap-0-RNA or Cap-0 analog, and 2 mM MgCl$_2$, MnCl$_2$, CaCl$_2$, or 3 mM NaCl as indicated. The reactions were incubated for 1 hour at 37°C and stopped with 0.5% trifluoroacetic acid. The detection solution from the kit was then added, and the mixture was further incubated for 30 min at room temperature, followed by the addition of the developing solution. Luminescence was measured using a TECAN Safire2 microplate reader in arbitrary units and normalized assigning 100% to the activity in the presence of Mg$^{2+}$ and Cap-0-RNA. The average and the SD of three measurements in two independent experiments using different protein purifications (n = 6) were plotted as a histogram using GraphPad Prism v9.

For determination of EC$_{50}$, the assay was modified for a 384-well plate format at the Northwestern University High Throughput Analysis Laboratory. Each nsp16-nsp10 heterodimer complex was serially diluted in solution as detailed above using the Mosquito robot. Reactions were initiated by addition of the substrates (5 $\mu$M SAM and 1 $\mu$M Cap-0-RNA) using the Mantis liquid handler. After 1 hour at 37°C, the reactions were coupled with the detection and developing solutions using Mantis liquid handler and incubated as described above. Luminescence was measured in a TECAN Infinite M1000. The blank was defined as containing all reagents except Cap-0-RNA, and this value was subtracted for each corresponding point. The values were then reported as the percentage of MTase activity compared to the wild type under the same conditions. Assays were conducted in triplicate, and the experiment was independently repeated (n = 6). EC$_{50}$ and the standard error were calculated using four-parameter logistic curve in GraphPad Prism v9 at 95% confidence interval.

**Isothermal titration calorimetry**

Binding affinity was determined using a MicroCal PEAQ-ITC system (Malvern, Worcestershire, UK) at 25°C. The sample cell volume was 200 $\mu$l, and the total syringe volume was 40 $\mu$l. For each titration, the first injection was performed using 0.4 $\mu$l, which was then followed by 18 additional injections at 2 $\mu$l per injection. The first injection was considered a void and was automatically removed from data analysis. Each injection was spaced by 120 s after a 60-s initial delay. SARS-CoV-2 samples of nsp10, nsp16, and nsp16-nsp10 were individually loaded into the sample cell and then titrated with either SAH, SAM, m$^7$GpppA Cap analog or the m$^7$GpppG Cap analog as described above. The values were then reported as the percentage of MTase activity compared to the wild type under the same conditions. Assays were conducted in triplicate, and the experiment was independently repeated (n = 6). EC$_{50}$ and the standard error were calculated using four-parameter logistic curve in GraphPad Prism v9 at 95% confidence interval.
The capped RNA has a 5′-5′ triphosphate linkage between m^7^G and A1 with noncanonical RNA backbone geometry, which resulted in low RNA backbone scores in MolProbity reports. All structures were deposited to Validated SARS-CoV-2–related structural models of potential drug targets (https://covid19.bioreproducibility.org/) and to the Protein Data Bank (www.rcsb.org/) with the assigned PDB 7JYY (crystal #1), 7L6R (crystal #2), and 7L6T (crystal #3). Flexible parts of the structure, alternative side-chain conformations, and partial water molecules were fit into electron density maps at a lower σ level, which resulted in overall high real-space R-value Z-score (RSRZ) scores for all structures. All figures with models of the structures were created in PyMOL open source version 2.1 (53); the diagram showing protein and capped RNA interactions was created in LigPlot+ (54).

**Structural, sequence alignment, and phylogenetic analysis**

The PDB coordinates of SARS-CoV-2 nsp16 and nsp10 were analyzed using the FATCAT (55), POSA (56), and DALI (57) servers to perform structural alignments with MERS-CoV, N55, hCMTr1, and VP39 cap RNA MTases. Generated PDB files were downloaded from the servers and modeled in PyMOL open source version 2.1. The protein sequence of 2′-O-MTases was obtained from the National Center for Biotechnology Information database: F-CoV (AGT52079), murine hepatitis virus (MHV; YP_009915686.1), human coronavirus (HKU1; YP_460023.1), human coronavirus 229E (H-CoV-229E; AGT21344.1:6464-6763), infectious bronchitis virus (IBV; NP_066134.1:6328-6629), DENV nonstructural protein NS5 (NS5, NP_739590.2), Homo sapiens (hCMTr1, BAA07893.3 KIAA0082), and VACV VP39 (VP39, NC_006998.1). The multiple sequence alignment was performed using Clustal-O (www.ebi.ac.uk/Tools/msa/clustalo/) and merged with the coordinates of the structure with PDB code 7JYY using ESPript 3. x (58). The phylogenetic tree was created using MacVector and processed in iTol (https://itol.embl.de).

**SUPPLEMENTARY MATERIALS**

stke.sciencemag.org/cgi/content/full/14/689/eaab2071/DC1

Figs. S1 to S4

Tables S1 and S2

References (59–60)

View/request a protocol for this paper from Bio-protocol.

**REFERENCES AND NOTES**

1. E. Dong, H. Du, L. Gardner, An interactive web-based dashboard to track COVID-19 in real time. Lancet Infect. Dis. 20, 533–534 (2020).
2. A. E. Gorbalenya, L. Enjuanes, J. Ziebuhr, E. J. Snijder, Nidovirales: Evolving the largest RNA virus genome. Virus Res. 117, 17–37 (2006).
3. J. Cui, F. Li, Z. L. Shi, Origin and evolution of pathogenic coronaviruses. Nat. Rev. Microbiol. 17, 181–192 (2019).
8. I. Fernandez de Castro, J. J. Fernandez, D. Barajas, P. D. Nagy, C. Risco, Three-dimensional minasov et al., Sci. Signal. 14, eabh2071 (2021) 29 June 2021

9. E. J. Snijder, R. W. A. L. Limpens, A. H. de Wilde, A. W. M. de Jong, J. C. Zevenhoven-Dobbe, 17. Y. Wang, Y. Sun, A. Wu, S. Xu, R. Pan, C. Zeng, X. Jin, X. Ge, Z. Shi, T. Ahola, Y. Chen, D. Guo, 13. L. Yan, J. Ge, L. Zheng, Y. Zhang, Y. Gao, T. Wang, Y. Huang, S. Gao, M. Li, Z. Liu, 19. Y. Chen, C. Su, M. Ke, X. Jin, L. Xu, Z. Zhang, A. Wu, Y. Sun, Z. Yang, P. Tien, T. Ahola, 16. M. Ke, Y. Chen, A. Wu, Y. Sun, C. Su, H. Wu, X. Jin, Y. Chen, L. Wei, Y. Wang, X. Ma, J. A. Pan, D. Guo, 20. E. Decroly, C. Debarnot, F. Ferron, M. Bouvet, B. Coutard, I. Imbert, L. Gluais, N. Papageorgiou, 25. M. Rosas-Lemus, G. Minasov, L. Shuvalova, N. L. Inniss, O. Kiryukhina, J. Brunzelle, 24. P. Krafcikova, J. Silhan, R. Nencka, E. Boura, Structural analysis of the SARS-CoV-2 transcriptome. Proc. Natl. Acad. Sci. U.S.A. 118, e1200170118 (2021).

S. Daffis, K. Jafferis, E. Schreier, J. Li, S. Yoon, E. Tett, Y. L. Lin, S. Schneller, R. Zust, H. Dong, V. Thiel, G. C. Sen, V. Fensterl, W. B. Klimstra, T. C. Piersson, R. M. Boller, M. Gale Jr., P. Y. Shi, S. M. Diamond, 2′-O-methylation of the viral mRNA cap evades host restriction by ITI family members. Nature 468, 452–456 (2010).

I. Fernandez de Castro, J. J. Fernandez, D. Barajas, P. D. Nagy, C. Risco, Three-dimensional modeling of the coronavirus replication organelle: Tracking down RNA synthesis. PLoS Biol. 18, e3000715 (2020).

Vuwanathan, A. Misra, S.-H. Chan, S. Qi, N. Dai, S. Arya, L. Martinez-Sobrido, Y. K. Gupta, A metal ion orients mRNA to ensure accurate 2′-riboosyl methylation of the first nucleotide of the SARS-CoV-2 genome. bioRxiv, 2021.03.12.435174 (2021).

S. Kellokumpu, H. Zieg, S. A. Goueli, Methytransferase-Glu: A universal, bioluminescent and homogenous assay for monitoring all classes of methyltransferases. Epigenomics 8, 321–339 (2016).

M. Wilamowski, D. A. Sherrill, G. Minasov, Y. Kim, L. Shuvalova, A. Lavrens, R. Chard, N. Maltesa, R. Jedrzejczak, M. Rosas-Lemus, N. Saint, I. T. Foster, K. Michalska, K. J. F. Satchell, A. Joachimak, 2′-O-methylation of RNA cap in SARS-CoV-2 captured by crystallography. Proc. Natl. Acad. Sci. U.S.A. 118, e1200170118 (2021).

S. Kellokumpu, H. Zieg, S. A. Goueli, Methytransferase-Glu: A universal, bioluminescent and homogenous assay for monitoring all classes of methyltransferases. Epigenomics 8, 321–339 (2016).
53. W. L. DeLano, Pymol: An open-source molecular graphics tool. CCP4 News. Protein Crystallogr. 40, 82–92 (2002).
54. R. A. Laskowski, M. B. Swindells, LigPlot+: Multiple ligand-protein interaction diagrams for drug discovery. J. Chem. Inf. Model. 51, 2778–2786 (2011).
55. Y. Ye, A. Godzik, FATCAT: A web server for flexible structure comparison and structure similarity searching. Nucleic Acids Res. 1, W582–W585 (2004).
56. Z. Li, P. Natarajan, Y. Ye, T. Hrabe, A. Godzik, POSA: A user-driven, interactive multiple protein structure alignment server. Nucleic Acids Res. 42, W240–W245 (2014).
57. L. Holm, P. Rosenström, Dali server: Conservation mapping in 3D. Nucleic Acids Res. 38, W545–W549 (2010).
58. X. Robert, P. Gouet, Deciphering key features in protein structures with the new ENDscript server. Nucleic Acids Res. 42, W320–W324 (2014).
59. M. S. Weiss, Global indicators of X-ray data quality. J. Appl. Cryst. 34, 130–135 (2001).
60. P. A. Karplus, K. Diederichs, Linking crystallographic model and data quality. Science 336, 1030–1033 (2012).

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Data and materials availability: Structures reported are available from the RCSB Protein Data Bank (www.rcsb.org) and from covid19.bioreproducibility.org with accession numbers 7JYY, 7L6R, and 7L6T. Recombinant protein expression plasmids are available from www.beiresources.org under their standard material transfer agreement. All other data needed to evaluate the conclusions in the paper are in the paper or in the Supplementary Materials. This work is licensed under a Creative Commons Attribution 4.0 International (CC BY 4.0) license, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. To view a copy of this license, visit https://creativecommons.org/licenses/by/4.0/. This license does not apply to figures/photos/artwork or other contents included in the article that are credited to a third party; obtain authorization from the rights holder before using such material.

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