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(12) **United States Patent**  
**Akinc et al.**(10) **Patent No.:** US 12,391,945 B2  
(45) **Date of Patent:** Aug. 19, 2025(54) **CORONAVIRUS IRNA COMPOSITIONS AND METHODS OF USE THEREOF**(71) Applicants: **Alnylam Pharmaceuticals, Inc.**, Cambridge, MA (US); **Vir Biotechnology, Inc.**, San Francisco, CA (US)(72) Inventors: **Akin Akinc**, Needham, MA (US); **James D. McIninch**, Burlington, MA (US); **Yesseinia Anglero-Rodriguez**, Cambridge, MA (US); **Mark K. Schlegel**, Boston, MA (US); **Christy M. Hebner**, San Francisco, CA (US); **Florian A. Lempp**, San Francisco, CA (US)(73) Assignees: **Alnylam Pharmaceuticals, Inc.**, Cambridge, MA (US); **Vir Biotechnology, Inc.**, San Francisco, CA (US)

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**Related U.S. Application Data**

(63) Continuation of application No. 17/321,561, filed on May 17, 2021, now Pat. No. 11,208,660, which is a continuation of application No. PCT/US2021/024038, filed on Mar. 25, 2021.

(60) Provisional application No. 63/124,910, filed on Dec. 14, 2020, provisional application No. 63/019,481, filed on May 4, 2020, provisional application No. 63/001,580, filed on Mar. 30, 2020, provisional application No. 62/994,907, filed on Mar. 26, 2020.

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**C12N 15/113** (2010.01)(52) **U.S. Cl.**  
CPC ..... **C12N 15/1131** (2013.01); **C12N 2310/14** (2013.01); **C12N 2310/315** (2013.01); **C12N 2310/321** (2013.01); **C12N 2310/322** (2013.01); **C12N 2310/3515** (2013.01)(58) **Field of Classification Search**  
CPC ..... C12N 2310/14; C12N 2310/315; C12N 2310/321; C12N 2310/322; C12N 2310/3515; C12N 2310/343

See application file for complete search history.

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*Primary Examiner* — Kimberly Chong(74) *Attorney, Agent, or Firm* — McCarter & English, LLP; Maria Laccotripe Zacharakis; Deborah L. Nagle(57) **ABSTRACT**

The present invention relates to RNAi agents, e.g., dsRNA agents, targeting the coronavirus genome. The invention also relates to methods of using such RNAi agents to inhibit expression of a coronavirus genome and to methods of treating or preventing a coronavirus-associated disease in a subject.

**22 Claims, 7 Drawing Sheets****Specification includes a Sequence Listing.**

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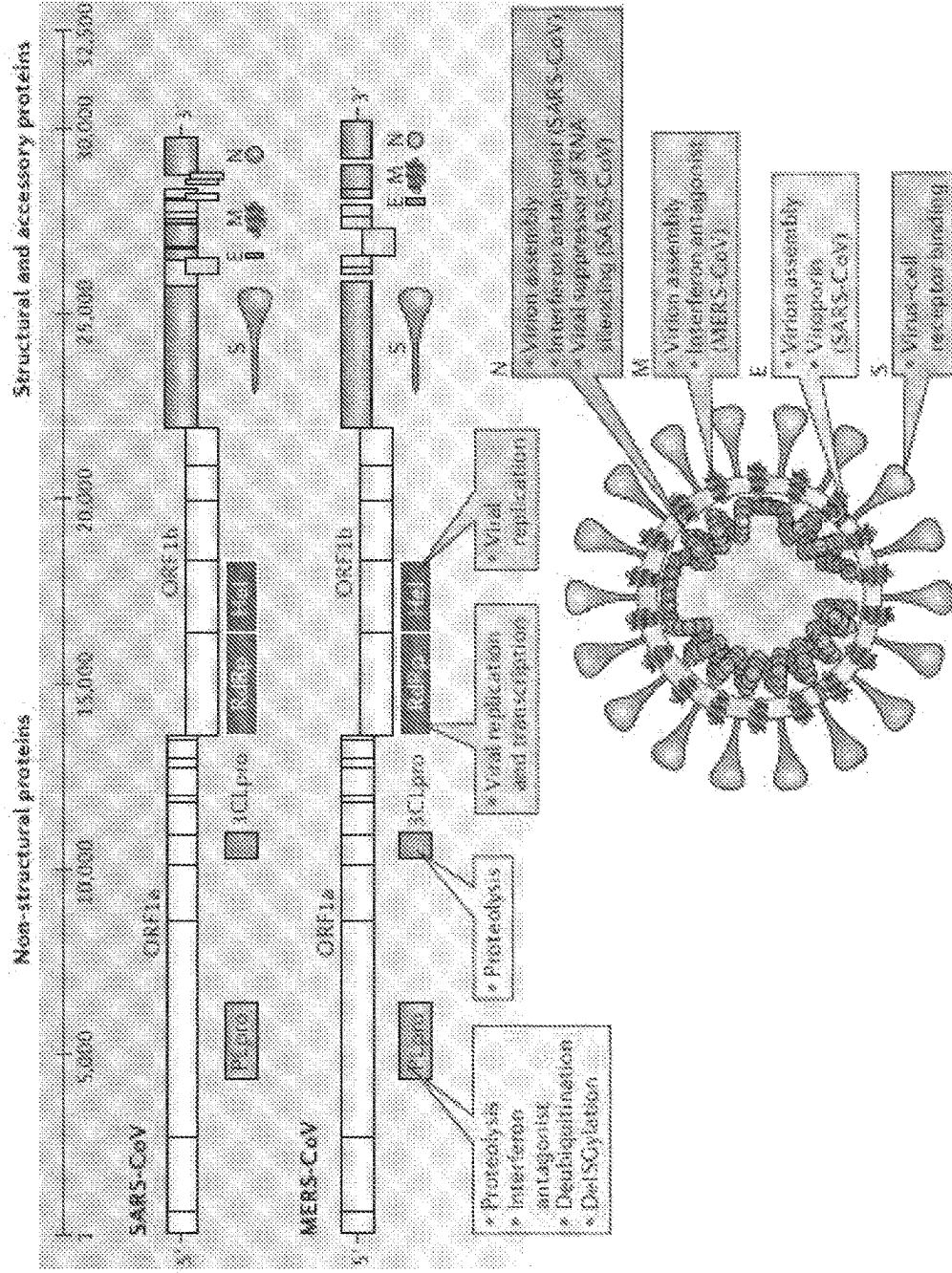


Figure 1

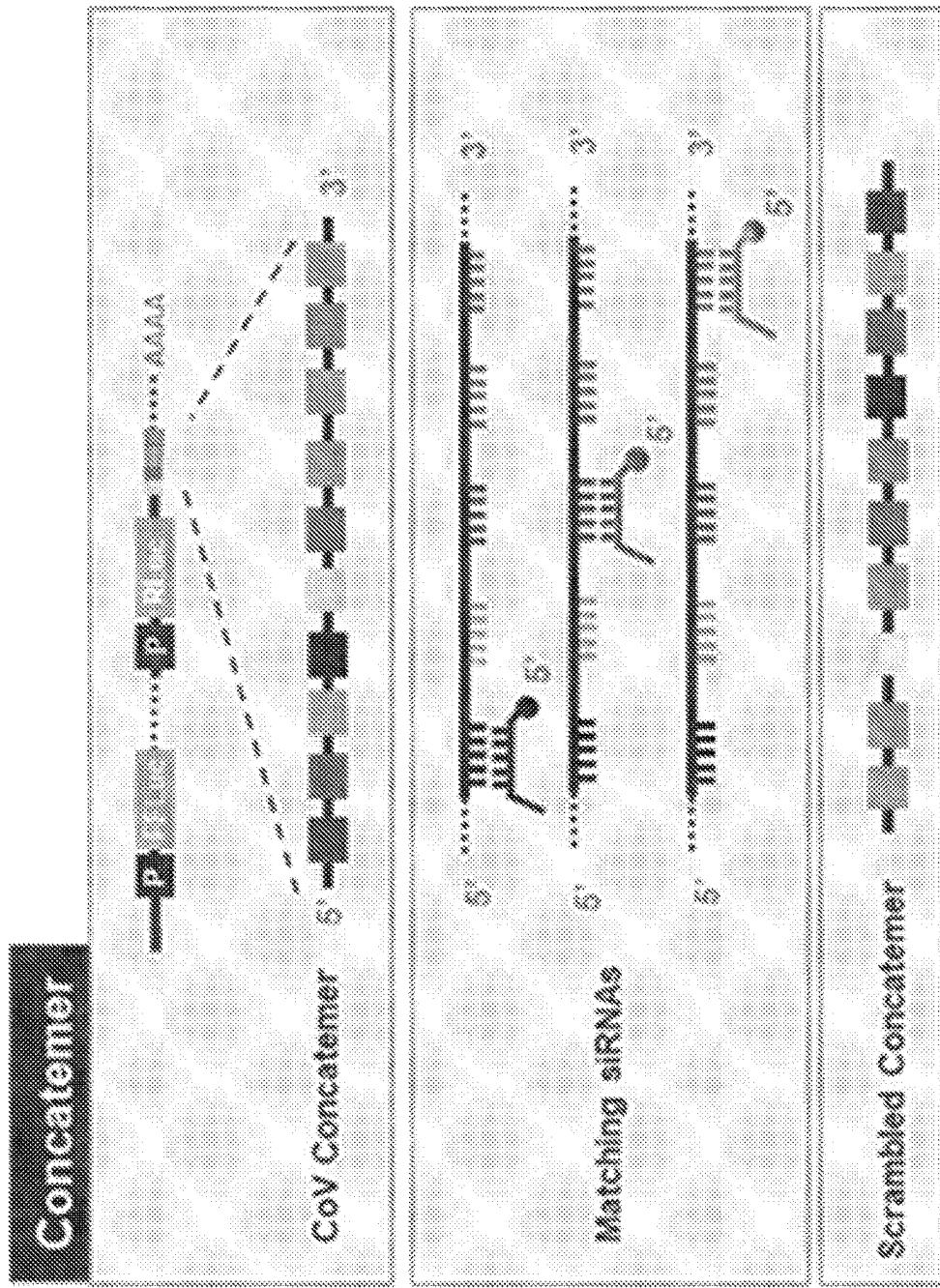


Figure 2

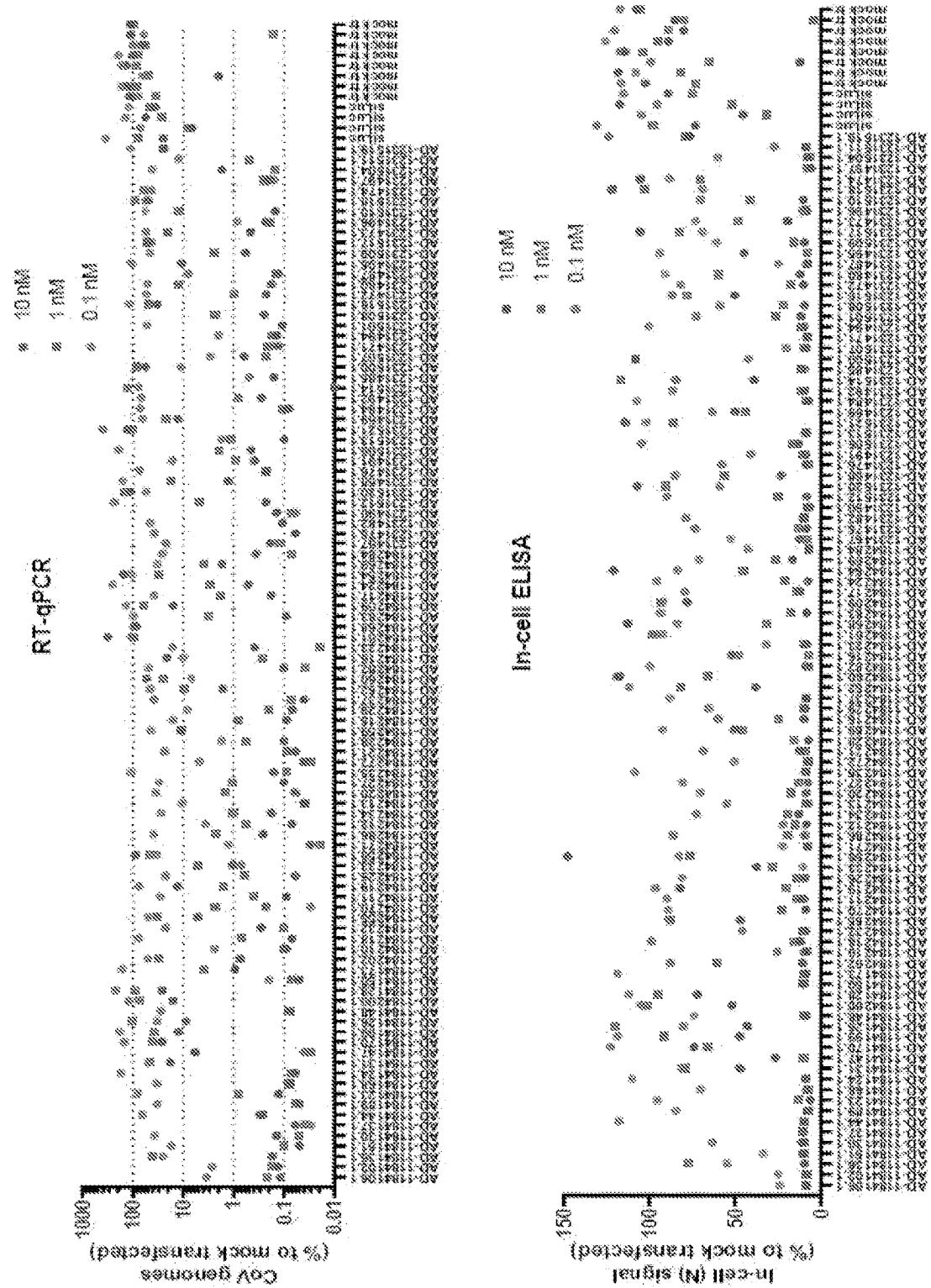


Figure 3

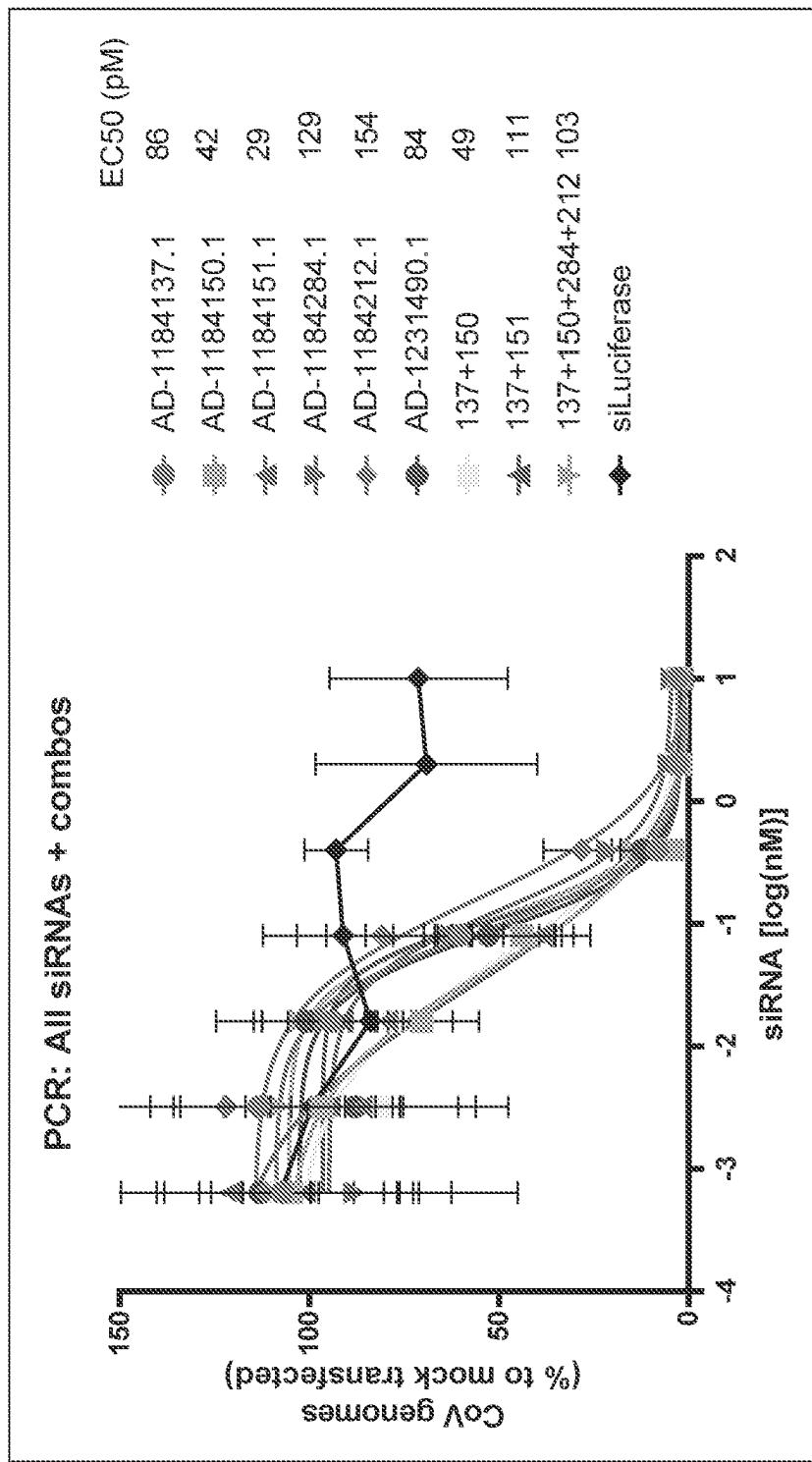


Figure 4.

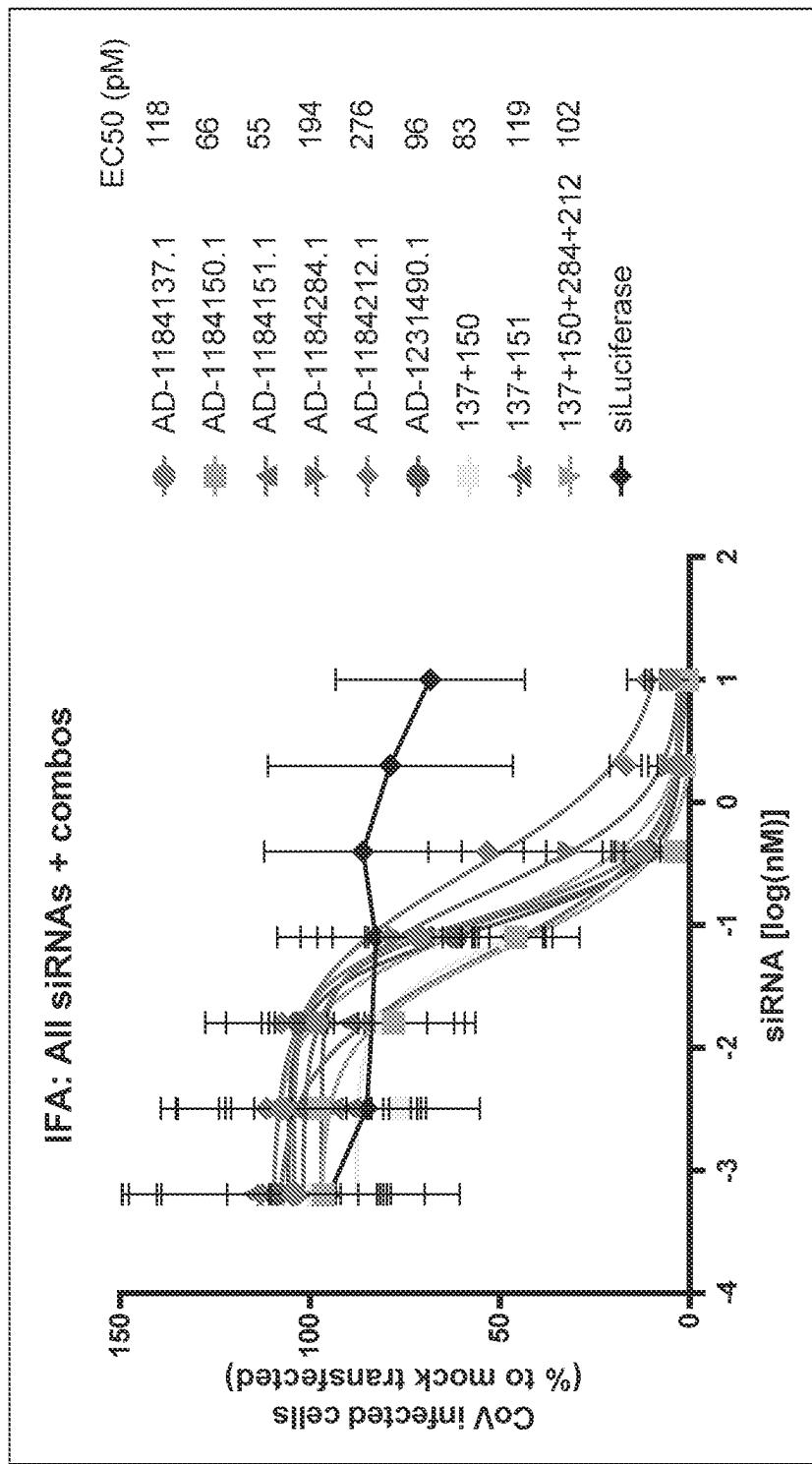
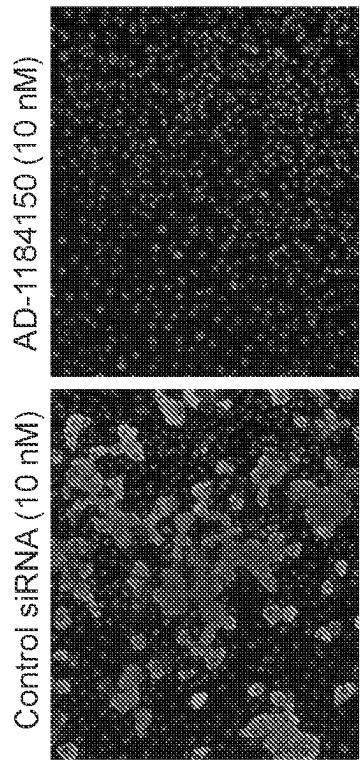


Figure 5



IFC  
SARS-CoV-2  
nucleocapsid protein  
(red stain)

Figure 6

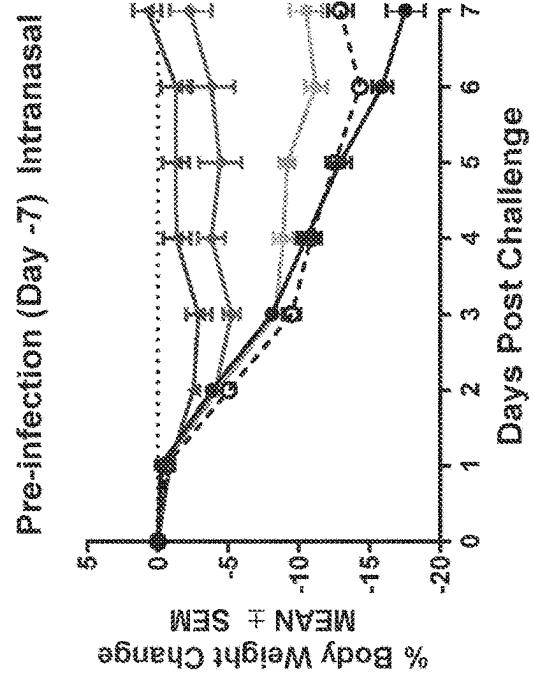


Figure 7

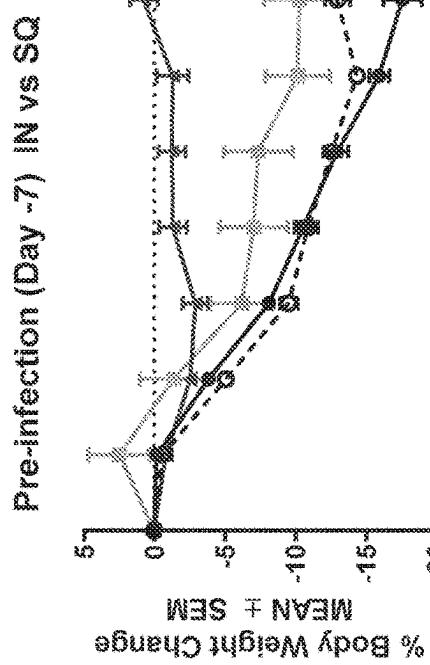


Figure 8

**1**
**CORONAVIRUS RNA COMPOSITIONS AND METHODS OF USE THEREOF**
**RELATED APPLICATIONS**

This application is a continuation of U.S. patent application Ser. No. 17/321,561, filed May 17, 2021, which is a 35 § U.S.C. 111(a) continuation application which claims the benefit of priority to PCT/US2021/024038, filed on Mar. 25, 2021, which, in turn, claims the benefit of priority to U.S. Provisional Application No. 62/994,907, filed on Mar. 26, 2020; U.S. Provisional Application No. 63/001,580, filed on Mar. 30, 2020; U.S. Provisional Application No. 63/019,481, filed on May 4, 2020; and U.S. Provisional Application No. 63/124,910, filed on Dec. 14, 2020. The entire contents of each of the foregoing applications are incorporated herein by reference.

**SEQUENCE LISTING**

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Oct. 29, 2021, is named 121301\_12206\_SL.txt and is 577,274 bytes in size.

**BACKGROUND OF THE INVENTION**

Coronaviruses (CoV) are a large family of viruses that cause diseases in mammals and birds. Coronaviruses constitute the subfamily Orthocoronavirinae, in the family Coronaviridae. They are enveloped viruses with a positive-sense single-stranded RNA genome and a nucleocapsid of helical symmetry. The genome size of coronaviruses ranges from approximately 27 to 34 kilobases. The name coronavirus is derived from the Latin corona, meaning "crown" or "halo", which refers to the characteristic appearance reminiscent of a crown or a solar corona around the virions (virus particles) when viewed under two-dimensional transmission electron microscopy, due to the surface covering in club-shaped protein spikes.

Coronaviruses can cause illness ranging from the common cold to more severe diseases. For example, infections with the human coronavirus strains CoV-229E, CoV-OC43, CoV-NL63 and CoV-HKU1 usually result in mild, self-limiting upper respiratory tract infections, such as a common cold, e.g., runny nose, sneezing, headache, cough, sore throat or fever (Zumla A. et al., *Nature Reviews Drug Discovery* 15(5): 327-47, 2016; Cheng V. C., et al., *Clin. Microbial. Rev.* 20: 660-694, 2007; Chan J. F. et al., *Clin. Microbial. Rev.* 28: 465-522, 2015). Other infections may result in more severe diseases such as Middle East Respiratory Syndrome (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS-CoV), diseases associated with pneumonia, severe acute respiratory syndrome, kidney failure and death.

MERS-CoV and SARS-CoV have received global attention over the past decades owing to their ability to cause community and health-care-associated outbreaks of severe infections in human populations. MERS-CoV is a viral respiratory disease that was first reported in Saudi Arabia in 2012 and has since spread to more than 27 other countries, according to the World Health Organization (de Groot, R. J. et al., *J. Virol.* 87: 7790-7792, 2013). SARS was first reported in Asia in 2003, and quickly spread to about two dozen countries before being contained after about four months (Lee N. et al., *N. Engl. J. Med.* 348: 1986-1994,

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2003; Peiris J. S. et al., *Lancet* 36: 1319-1325, 2003). Detailed investigations found that SARS-CoV was transmitted from civet cats to humans and MERS-CoV from dromedary camels to humans (Cheng V. C., et al., *Clin. Microbial. Rev.* 20: 660-694, 2007; Chan J. F. et al., *Clin. Microbial. Rev.* 28: 465-522, 2015).

A recent outbreak of respiratory disease caused by a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was first identified in Wuhan City, China. 10 This disease, named by the World Health Organization as coronavirus disease 2019 ("COVID-19"), presents a major threat to public health worldwide. As of Feb. 24, 2020, there were more than 79,000 confirmed cases and 2,600 deaths across the world.

15 Coronaviruses pose major challenges to clinical management because many questions regarding transmission and control remain unanswered. Moreover, there is currently no vaccine to prevent infections by coronavirus, and there are no specific antiviral treatments available or proven to be effective to treat or prevent coronavirus infection in subjects.

20 Accordingly, there exists an immediate need for therapeutics to treat coronavirus infections.

**BRIEF SUMMARY OF THE INVENTION**

The present disclosure provides RNAi agent compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA genome and RNA transcripts of coronavirus genes. The coronavirus genome may be within a cell, e.g., a cell within a subject, such as a human. The present disclosure also provides methods of using the RNAi agent compositions of the disclosure for inhibiting the expression of a coronavirus genome or for treating a subject 30 who would benefit from inhibiting or reducing the expression of a coronavirus genome, e.g., a subject having a coronavirus-associated disorder, e.g., a subject having a coronavirus infection, e.g., a subject having Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or 35 Middle East Respiratory Syndrome (MERS-CoV).

Accordingly, in one aspect, the instant disclosure provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of a coronavirus genome, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of the nucleotide sequence of SEQ ID NO:1, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:1, and the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion 40 of the nucleotide sequence of SEQ ID NO:2, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:2; and wherein the sense strand or the antisense strand is conjugated to one or more lipophilic moieties.

In another aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of coronavirus genome in a cell, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of the nucleotide sequence of SEQ ID NO:2, or a

nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:2, and the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO:1, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:1; and wherein the sense strand or the antisense strand is conjugated to one or more lipophilic moieties.

In one aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of coronavirus genome in a cell, comprising a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a region complementary to part of an mRNA encoding a coronavirus genome (SEQ ID NO:1), wherein each strand independently is 14 to 30 nucleotides in length; and wherein the sense strand or the antisense strand is conjugated to one or more lipophilic moieties.

In another aspect, the present invention provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of coronavirus genome in a cell, comprising a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a region complementary to part of a reverse complement of an mRNA encoding a coronavirus genome (SEQ ID NO:2), wherein each strand independently is 14 to 30 nucleotides in length; and wherein the sense strand or the antisense strand is conjugated to one or more lipophilic moieties.

In yet another aspect, the present invention provides a double stranded RNAi agent for inhibiting expression of a coronavirus genome in a cell, comprising a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the antisense nucleotide sequences in any one of Tables 2-5, wherein each strand independently is 14 to 30 nucleotides in length; and wherein the sense strand or the antisense strand is conjugated to one or more lipophilic moieties.

In one embodiment, the sense strand or the antisense strand is a sense strand or an antisense strand selected from the group consisting of any of the sense strands and antisense strands in any one of Table 2-5. In one embodiment, the sense strand or the antisense strand is selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1184210, AD-1184270, AD-1184233, AD-1184271, AD-1184212, AD-1184228, AD-1184223, AD-1231490, AD-1231513, AD-1231485, AD-1231507, AD-1231471, AD-1231494, AD-1231496, and AD-1231497. In another embodiment, the sense strand or the antisense strand is selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1231490, AD-1231513, AD-1231485, AD-1231471, AD-1231496, and AD-1231497. In one embodiment, the sense strand or the antisense strand is selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137 and AD-1184150. In one embodiment, the sense strand and the antisense strand are the sense strand and antisense strand of AD-1184137. In another embodiment, the sense strand and the antisense strand are the sense strand and antisense strand of AD-1184150.

In one embodiment, both the sense strand and the antisense strand is conjugated to one or more lipophilic moieties.

In one embodiment, the lipophilic moiety is conjugated to one or more positions in the double stranded region of the dsRNA agent.

In one embodiment, the lipophilic moiety is conjugated via a linker or a carrier.

<sup>10</sup> In one embodiment, lipophilicity of the lipophilic moiety, measured by log K<sub>ow</sub>, exceeds 0.

In one embodiment, the hydrophobicity of the double-stranded RNAi agent, measured by the unbound fraction in a plasma protein binding assay of the double-stranded RNAi agent, exceeds 0.2.

<sup>15</sup> In one embodiment, the plasma protein binding assay is an electrophoretic mobility shift assay using human serum albumin protein.

<sup>20</sup> In one embodiment, the dsRNA agent comprises at least one modified nucleotide.

In one embodiment, no more than five of the sense strand nucleotides and no more than five of the nucleotides of the antisense strand are unmodified nucleotides

<sup>25</sup> In another embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand comprise a modification.

In one embodiment, at least one of the modified nucleotides is selected from the group a deoxy-nucleotide, a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-O-alkyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a 5'-phosphorothioate group, a nucleotide comprising a 5'-methylphosphonate group, a nucleotide comprising a 5' phosphate or 5' phosphate mimic, a nucleotide comprising vinyl phosphonate, a nucleotide comprising adenosine-glycol nucleic acid (GNA), a nucleotide comprising thymidine-glycol nucleic acid (GNA)-S-Isomer, a nucleotide comprising 2-hydroxymethyl-tetrahydrofuran-5-phosphate, a nucleotide comprising 2'-deoxythymidine-3'-phosphate, a nucleotide comprising 2'-deoxyguanosine-3'-phosphate, a 2'-O hexadecyl nucleotide, a nucleotide comprising a 2'-phosphate, a cytidine-2'-phosphate nucleotide, a guanosine-2'-phosphate nucleotide, a 2'-O-hexadecyl-cytidine-3'-phosphate nucleotide, a 2'-O-hexadecyl-adenosine-3'-phosphate nucleotide, a 2'-O-hexadecyl-guanosine-3'-phosphate nucleotide, a 2'-O-hexadecyl-uridine-3'-phosphate nucleotide, a 5'-vinyl phosphonate (VP), a 2'-deoxyadenosine-3'-phosphate nucleotide, a 2'-deoxycytidine-3'-phosphate nucleotide, a 2'-deoxyguanosine-3'-phosphate nucleotide, a 2'-deoxythymidine-3'-phosphate nucleotide, a 2'-deoxyuridine nucleotide, and a <sup>50</sup> terminal nucleotide linked to a cholestry derivative and a dodecanoic acid bisdecylamide group; and combinations thereof.

<sup>65</sup> In another embodiment, modified nucleotide is selected from the group consisting of a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, 3'-terminal deoxy-thymine nucleotides (dT), a locked nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-al-

kyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide.

In another embodiment, the modified nucleotide comprises a short sequence of 3'-terminal deoxy-thymine nucleotides (dT).

In yet another embodiment, the modifications on the nucleotides are 2'-O-methyl modifications, 2'-deoxy-modifications, and 2'fluoro modifications.

In one embodiment, the dsRNA agent further comprises at least one phosphorothioate internucleotide linkage.

In one embodiment, the dsRNA agent comprises 6-8 phosphorothioate internucleotide linkages.

In one embodiment, each strand is no more than 30 nucleotides in length.

In one embodiment, at least one strand comprises a 3' overhang of at least 1 nucleotide.

In another embodiment, at least one strand comprises a 3' overhang of at least 2 nucleotides.

The double stranded region may be 15-30 nucleotide pairs in length; 17-23 nucleotide pairs in length; 17-25 nucleotide pairs in length; 23-27 nucleotide pairs in length; 19-21 nucleotide pairs in length; or 21-23 nucleotide pairs in length.

Each strand of the dsRNA agent may be has 19-30 nucleotides in length; 19-23 nucleotides in length; or 21-23 nucleotides in length.

In one embodiment, one or more lipophilic moieties are conjugated to one or more internal positions on at least one strand.

In one embodiment, the one or more lipophilic moieties are conjugated to one or more internal positions on at least one strand via a linker or carrier.

In one embodiment, the internal positions include all positions except the terminal two positions from each end of the at least one strand.

In another embodiment, the internal positions include all positions except the terminal three positions from each end of the at least one strand.

In another embodiment, the internal positions exclude a cleavage site region of the sense strand.

In yet another embodiment, the internal positions include all positions except positions 9-12, counting from the 5'-end of the sense strand.

In one embodiment, the internal positions include all positions except positions 11-13, counting from the 3'-end of the sense strand.

In one embodiment, the internal positions exclude a cleavage site region of the antisense strand.

In one embodiment, the internal positions include all positions except positions 12-14, counting from the 5'-end of the antisense strand.

In one embodiment, the internal positions include all positions except positions 11-13 on the sense strand, counting from the 3'-end, and positions 12-14 on the antisense strand, counting from the 5'-end.

In one embodiment, the one or more lipophilic moieties are conjugated to one or more of the internal positions selected from the group consisting of positions 4-8 and 13-18 on the sense strand, and positions 6-10 and 15-18 on the antisense strand, counting from the 5'end of each strand.

In one embodiment, the one or more lipophilic moieties are conjugated to one or more of the internal positions selected from the group consisting of positions 5, 6, 7, 15, and 17 on the sense strand, and positions 15 and 17 on the antisense strand, counting from the 5'-end of each strand.

In one embodiment, the positions in the double stranded region exclude a cleavage site region of the sense strand.

In one embodiment, the sense strand is 21 nucleotides in length, the antisense strand is 23 nucleotides in length, and the lipophilic moiety is conjugated to position 21, position 20, position 15, position 1, position 7, position 6, or position 5 2 of the sense strand or position 16 of the antisense strand.

In one embodiment, the lipophilic moiety is conjugated to position 21, position 20, position 15, position 1, or position 7 of the sense strand.

In one embodiment, the lipophilic moiety is conjugated to position 21, position 20, or position 15 of the sense strand.

In one embodiment, the lipophilic moiety is conjugated to position 20 or position 15 of the sense strand.

In one embodiment, the lipophilic moiety is conjugated to position 16 of the antisense strand.

In one embodiment, the lipophilic moiety is an aliphatic, alicyclic, or polycyclic compound.

In one embodiment, the lipophilic moiety is selected from the group consisting of lipid, cholesterol, retinoic acid, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-bis-O(hexadecyl)glycerol, geranylloxyhexanol, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine.

In one embodiment, the lipophilic moiety contains a saturated or unsaturated C4-C30 hydrocarbon chain, and an optional functional group selected from the group consisting of hydroxyl, amine, carboxylic acid, sulfonate, phosphate, thiol, azide, and alkyne.

In one embodiment, the lipophilic moiety contains a saturated or unsaturated C6-C18 hydrocarbon chain.

In one embodiment, the lipophilic moiety contains a saturated or unsaturated C16 hydrocarbon chain.

In one embodiment, the saturated or unsaturated C16 hydrocarbon chain is conjugated to position 6, counting from the 5'-end of the strand.

In one embodiment, the lipophilic moiety is conjugated via a carrier that replaces one or more nucleotide(s) in the 40 internal position(s) or the double stranded region.

In one embodiment, the carrier is a cyclic group selected from the group consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuranyl, and decalinyl; or is an acyclic moiety based on a serinol backbone or a diethanolamine backbone.

In one embodiment, the lipophilic moiety is conjugated to the double-stranded iRNA agent via a linker containing an ether, thioether, urea, carbonate, amine, amide, maleimide-thioether, disulfide, phosphodiester, sulfonamide linkage, a product of a click reaction, or carbamate.

In one embodiment, the lipophilic moiety is conjugated to 55 a nucleobase, sugar moiety, or internucleosidic linkage.

In one embodiment, the lipophilic moiety or a targeting ligand is conjugated via a bio-cleavable linker selected from the group consisting of DNA, RNA, disulfide, amide, functionalized monosaccharides or oligosaccharides of galactosamine, glucosamine, glucose, galactose, mannose, and combinations thereof.

In one embodiment, the 3' end of the sense strand is protected via an end cap which is a cyclic group having an amine, said cyclic group being selected from the group 65 consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolo-

lidinyl, isothiazolidinyl, quinoxaliny, pyridazinonyl, tetrahydrofuranyl, and decalinyl.

In one embodiment, the dsRNA agent further comprises a targeting ligand that targets a liver tissue.

In one embodiment, the targeting ligand is a GalNAc conjugate.

In one embodiment, the dsRNA agent further comprises a terminal, chiral modification occurring at the first internucleotide linkage at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp configuration or Sp configuration.

In one embodiment, the dsRNA agent further comprises a terminal, chiral modification occurring at the first and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In one embodiment, the dsRNA agent further comprises a terminal, chiral modification occurring at the first, second and third internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In one embodiment, the dsRNA agent further comprises a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the third internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In one embodiment, the dsRNA agent further comprises a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In one embodiment, the dsRNA agent further comprises a phosphate or phosphate mimic at the 5'-end of the antisense strand.

In one embodiment, the phosphate mimic is a 5'-vinyl phosphonate (VP).

In one embodiment, the base pair at the 1 position of the 5'-end of the antisense strand of the duplex is an AU base pair.

In one embodiment, the sense strand has a total of 21 nucleotides and the antisense strand has a total of 23 nucleotides.

In one embodiment, the sense strand comprises the 10 nucleotide sequence 5'-UAACAAUGUUGCUUUU-CAAAC-3' (SEQ ID NO: 5) and the antisense strand comprises the nucleotide sequence 5'-GUUUGAAAAGCAA-CAUUGUUAGU-3' (SEQ ID NO: 6).

In another embodiment, the sense strand comprises the 15 nucleotide sequence 5'-ACUGUACAGUCUAAAAU-GUCA-3' (SEQ ID NO: 7) and the antisense strand comprises the nucleotide sequence 5'-UGACAUUUUAGACU-GUACAGUGG-3' (SEQ ID NO: 8).

In one embodiment, the sense strand comprises the sense 20 strand nucleotide sequence 5'-usasaca(Ahd)UfgUfUfGfc-uuucaasa-3' (SEQ ID NO: 9) and the antisense strand comprises the nucleotide sequence 5'-VPusUfsuugA-faaagcaaCfaUfuguasgsu-3' (SEQ ID NO: 10), wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexadecyl-adenosine-3'-phosphate; and VP is Vinyl-phosphonate.

In another embodiment, the sense strand comprises the nucleotides sequence 5'-ascugu(Ahd)CfaGfUfCfuaaaau-guscsa-3' (SEQ ID NO: 11) and the antisense strand comprises the nucleotide sequence 5'-VPusGfsacaUfuuuuaga-cUfgUfacagusgs-3' (SEQ ID NO: 12), wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexadecyl-adenosine-3'-phosphate; and VP is Vinyl-phosphonate.

The present invention further provides cells, pharmaceutical compositions for inhibiting expression of a coronavirus genome, and pharmaceutical composition comprising a lipid 40 formulation comprising the dsRNA agents of the invention.

In one aspect, the present invention provides a composition comprising two or more, e.g., 2, 3, or 4, double stranded RNAi agents for inhibiting expression of coronavirus genome in a cell, wherein each double stranded RNAi agent independently comprises a sense strand and an antisense strand forming a double stranded region, wherein each of the sense strands independently comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of the nucleotide sequence of SEQ ID NO:1, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:1, and each of the antisense strands independently comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO:2, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:2.

In another aspect, the present invention provides a composition comprising two or more, e.g., 2, 3, or 4, double stranded ribonucleic acid (dsRNA) agents for inhibiting expression of coronavirus genome in a cell, wherein each dsRNA agent independently comprises a sense strand and an antisense strand forming a double stranded region, wherein each of the sense strands independently comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of the nucleotide

sequence of SEQ ID NO:2, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:2, and each of the antisense strands independently comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO:1, or a nucleotide sequence having at least 90% nucleotide sequence identity to a portion of the nucleotide sequence of SEQ ID NO:1.

In yet another aspect, the present invention provides a composition comprising two or more, e.g., 2, 3, or 4, double stranded ribonucleic acid (dsRNA) agents for inhibiting expression of coronavirus genome in a cell, wherein each dsRNA agent independently comprises a sense strand and an antisense strand forming a double stranded region, wherein each of the antisense strands independently comprises a region complementary to part of an mRNA encoding a coronavirus genome (SEQ ID NO:1), wherein each of the sense strands or each of the antisense strands are independently 14 to 30 nucleotides in length.

In one aspect, the present invention provides a composition comprising two or more, e.g., 2, 3, or 4, double stranded ribonucleic acid (dsRNA) agents for inhibiting expression of coronavirus genome in a cell, wherein each dsRNA agent independently comprises a sense strand and an antisense strand forming a double stranded region, wherein each of the antisense strands independently comprises a region complementary to part of a reverse complement of an mRNA encoding a coronavirus genome (SEQ ID NO:2), wherein each of the sense strands or each of the antisense strands are independently 14 to 30 nucleotides in length.

In another aspect, the present invention provides a composition comprising two or more, e.g., 2, 3, or 4, double stranded RNAi agents for inhibiting expression of a coronavirus genome in a cell, wherein each double stranded RNAi agent independently comprises a sense strand and an antisense strand forming a double stranded region, wherein each of the antisense strands independently comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the antisense nucleotide sequences in any one of Tables 2-5, wherein each of the sense strands or each of the antisense strands are independently 14 to 30 nucleotides in length.

In one embodiment, each of the sense strands or each of the antisense strands is a sense strand or an antisense strand independently selected from the group consisting of any of the sense strands and antisense strands in any one of Table 2-5.

In another embodiment, each of the sense strands or each of the antisense strands is a sense strand or an antisense strand independently selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1184210, AD-1184270, AD-1184233, AD-1184271, AD-1184212, AD-1184228, AD-1184223, AD-1231490, AD-1231513, AD-1231485, AD-1231507, AD-1231471, AD-1231494, AD-1231496, and AD-1231497.

In yet another embodiment, each of the sense strands or each of the antisense strands is a sense strand or an antisense strand of a duplex independently selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1231490, AD-1231513, AD-1231485, AD-1231471, AD-1231496, and AD-1231497.

In one embodiment, each of the sense strands and each of the antisense strands is a sense strand and an antisense strand of a duplex independently selected from the group consisting of AD-1184137 and AD-1184150.

In one embodiment, at least one of said sense strands or at least one of said antisense strands is independently conjugated to one or more lipophilic moieties

In one embodiment, all of the sense strands or all of the antisense strand of each of the dsRNA agents are independently conjugated to one or more lipophilic moieties.

In one embodiment, each lipophilic moiety is independently conjugated to one or more positions in the double stranded region of the dsRNA agent.

10 In one embodiment, each lipophilic moiety is independently conjugated via a linker or a carrier.

In one embodiment, lipophilicity of each lipophilic moiety, measured by log Kow, independently exceeds 0.

In another embodiment, the hydrophobicity of each 15 double-stranded RNAi agent, measured by the unbound fraction in a plasma protein binding assay of the double-stranded RNAi agent, independently exceeds 0.2.

In one embodiment, the plasma protein binding assay is an electrophoretic mobility shift assay using human serum albumin protein.

20 In one embodiment, each of the dsRNA agents independently comprises at least one modified nucleotide.

In one embodiment, each sense strand and each antisense strand of each dsRNA agent independently comprises no 25 more than five unmodified nucleotides.

In one embodiment, all of the nucleotides of each sense strand and all of the nucleotides of each antisense strand independently comprise a modification.

In one embodiment, at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-O-allyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramide, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a 5'-phosphorothioate group, a nucleotide comprising a 5'-methylphosphonate group, a nucleotide comprising a 5'

30 phosphate or 5' phosphate mimic, a nucleotide comprising vinyl phosphonate, a nucleotide comprising adenosine-glycol nucleic acid (GNA), a nucleotide comprising thymidine-glycol nucleic acid (GNA)S-Isomer, a nucleotide comprising 2-hydroxymethyl-tetrahydrofuran-5-phosphate, a nucleotide comprising 2'-deoxythymidine-3'-phosphate, a nucleotide comprising 2'-deoxyguanosine-3'-phosphate, a 2'-O hexadecyl nucleotide, a nucleotide comprising a 2'-phosphate, a cytidine-2'-phosphate nucleotide, a guanosine-2'-phosphate nucleotide, a 2'-O-hexadecyl-cytidine-3'-phosphate nucleotide, a 2'-O-hexadecyl-adenosine-3'-phosphate nucleotide, a 2'-O-hexadecyl-guanosine-3'-phosphate nucleotide, a 2'-O-hexadecyl-uridine-3'-phosphate nucleotide, a 5'-vinyl phosphonate (VP), a 2'-deoxyadenosine-3'-phosphate nucleotide, a 2'-deoxycytidine-3'-phosphate nucleotide, a 2'-deoxyguanosine-3'-phosphate nucleotide, a 2'-deoxythymidine-3'-phosphate nucleotide, a 2'-deoxyuridine nucleotide, and a terminal nucleotide linked to a cholesterol derivative and a dodecanoic acid bisdecylamide group; and combinations thereof.

35 40 45 50 55 60 65 70 75 80 85 90 95 100

In another embodiment, the modified nucleotide is independently selected from the group consisting of a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleo-

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tide, 3'-terminal deoxy-thymine nucleotides (dT), a locked nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide.

In yet another embodiment, the modified nucleotide comprises a short sequence of 3'-terminal deoxy-thymine nucleotides (dT).

In one embodiment, the modifications on the nucleotides are each independently selected from the group consisting of 2'-O-methyl modifications, 2'-deoxy-modifications, or 2'fluoro modifications.

In one embodiment, at least one of the dsRNA agents further comprises at least one phosphorothioate internucleotide linkage.

In one embodiment, at least one of the dsRNA agents comprises 6-8 phosphorothioate internucleotide linkages.

In one embodiment, each strand of each dsRNA agent is independently no more than 30 nucleotides in length.

In one embodiment, at least one strand of at least one dsRNA agent independently comprises a 3' overhang of at least 1 nucleotide.

In another embodiment, at least one strand of at least one dsRNA agent independently comprises a 3' overhang of at least 2 nucleotides.

In one embodiment, the double stranded region of each dsRNA agent is independently 15-30 nucleotide pairs in length.

In another embodiment, the double stranded region of each dsRNA agent is independently 17-23 nucleotide pairs in length.

In yet another embodiment, the double stranded region of each dsRNA agent is independently 17-25 nucleotide pairs in length.

In one embodiment, double stranded region of each dsRNA agent is independently 23-27 nucleotide pairs in length.

In another embodiment, the double stranded region of each dsRNA agent is independently 19-21 nucleotide pairs in length.

In one embodiment, the double stranded region of each dsRNA agent is independently 21-23 nucleotide pairs in length.

In one embodiment, each strand of each dsRNA agent independently has 19-30 nucleotides.

In another embodiment, each strand of each dsRNA agent independently has 19-23 nucleotides.

In yet another embodiment, wherein each strand of each dsRNA agent independently has 21-23 nucleotides.

In one embodiment, each dsRNA agent comprises one or more lipophilic moieties independently conjugated to one or more internal positions on at least one strand.

In one embodiment, the one or more lipophilic moieties are each independently conjugated to one or more internal positions on at least one strand via a linker or carrier.

In one embodiment, each of the internal positions independently include all positions except the terminal two positions from each end of the at least one strand.

In one embodiment, each of the internal positions independently include all positions except the terminal three positions from each end of the at least one strand.

In one embodiment, each of the internal positions independently exclude a cleavage site region of the sense strand.

In one embodiment, each of the internal positions independently include all positions except positions 9-12, counting from the 5'-end of the sense strand.

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In one embodiment, each of the internal positions independently include all positions except positions 11-13, counting from the 3'-end of the sense strand.

In one embodiment, each of the internal positions independently exclude a cleavage site region of the antisense strand.

In one embodiment, each of the internal positions independently include all positions except positions 12-14, counting from the 5'-end of the antisense strand.

<sup>10</sup> In another embodiment, each of the internal positions independently include all positions except positions 11-13 on the sense strand, counting from the 3'-end, and positions 12-14 on the antisense strand, counting from the 5'-end.

<sup>15</sup> In one embodiment, each of the one or more lipophilic moieties are independently conjugated to one or more of the internal positions selected from the group consisting of positions 4-8 and 13-18 on the sense strand, and positions 6-10 and 15-18 on the antisense strand, counting from the 5'end of each strand.

<sup>20</sup> In another embodiment, the one or more lipophilic moieties are each independently conjugated to one or more of the internal positions selected from the group consisting of positions 5, 6, 7, 15, and 17 on the sense strand, and positions 15 and 17 on the antisense strand, counting from the 5'-end of each strand.

In one embodiment, each of the positions in the double stranded region independently exclude a cleavage site region of the sense strand.

<sup>30</sup> In one embodiment, each of the sense strands is independently 21 nucleotides in length, each of the antisense strands is independently 23 nucleotides in length, and each of the lipophilic moieties is independently conjugated to position 21, position 20, position 15, position 1, position 7, position 6, or position 2 of the sense strand or position 16 of the antisense strand.

In one embodiment, each of the lipophilic moieties is independently conjugated to position 21, position 20, position 15, position 1, or position 7 of the sense strand.

<sup>40</sup> In another embodiment, each of the lipophilic moieties is independently conjugated to position 21, position 20, or position 15 of the sense strand.

In yet another embodiment, each of the lipophilic moieties is independently conjugated to position 20 or position 15 of the sense strand.

In one embodiment, each of the lipophilic moieties is independently conjugated to position 16 of the antisense strand.

<sup>50</sup> In one embodiment, each of the lipophilic moieties is independently an aliphatic, alicyclic, or polycyclic compound.

In one embodiment, each of the lipophilic moieties is independently selected from the group consisting of lipid, cholesterol, retinoic acid, cholic acid, adamantine acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-bis-O (hexadecyl)glycerol, geranylgeranyl, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, 03-(oleoyl)lithocholic acid, 03-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine.

<sup>60</sup> In one embodiment, each of the lipophilic moieties independently contains a saturated or unsaturated C4-C30 hydrocarbon chain, and an optional functional group selected from the group consisting of hydroxyl, amine, carboxylic acid, sulfonate, phosphate, thiol, azide, and alkyne.

<sup>65</sup> In one embodiment, each of the lipophilic moieties independently contains a saturated or unsaturated C6-C18 hydrocarbon chain.

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In one embodiment, each of the lipophilic moieties independently contains a saturated or unsaturated C16 hydrocarbon chain.

In one embodiment, each of the saturated or unsaturated C16 hydrocarbon chain is independently conjugated to position 6, counting from the 5'-end of the strand.

In one embodiment, each of the lipophilic moieties is independently conjugated via a carrier that replaces one or more nucleotide(s) in the internal position(s) or the double stranded region.

In one embodiment, each of the carriers is independently a cyclic group selected from the group consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuranyl, and decalinyl; or is an acyclic moiety based on a serinol backbone or a diethanolamine backbone.

In one embodiment, each of the lipophilic moieties is independently conjugated to the double-stranded siRNA agent via a linker containing an ether, thioether, urea, carbonate, amine, amide, maleimide-thioether, disulfide, phosphodiester, sulfonamide linkage, a product of a click reaction, or carbamate.

In one embodiment, each of the lipophilic moieties is independently conjugated to a nucleobase, sugar moiety, or internucleosidic linkage.

In one embodiment, each of the lipophilic moieties or one or more targeting ligands is independently conjugated via a bio-cleavable linker selected from the group consisting of DNA, RNA, disulfide, amide, functionalized monosaccharides or oligosaccharides of galactosamine, glucosamine, glucose, galactose, mannose, and combinations thereof.

In one embodiment, the 3' end of at least one of the sense strands is independently protected via an end cap which is a cyclic group having an amine, said cyclic group being selected from the group consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuranyl, and decalinyl.

In one embodiment, at least one of the dsRNA agents further comprises a targeting ligand that targets a liver tissue.

In one embodiment, each of the targeting ligands is independently a GalNAc conjugate.

In one embodiment, at least one of the dsRNA agents further comprises a terminal, chiral modification occurring at the first internucleotide linkage at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp configuration or Sp configuration.

In another embodiment, at least one of the dsRNA agents further comprises a terminal, chiral modification occurring at the first and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

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In yet another embodiment, at least one of the dsRNA agents further comprises a terminal, chiral modification occurring at the first, second and third internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In one embodiment, at least one of the dsRNA agents further comprises a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the third internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In another embodiment, at least one of the dsRNA agents further comprises a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration, a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration, and a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In one embodiment, at least one of the dsRNA agents further comprises a phosphate or phosphate mimic at the 5'-end of the antisense strand.

In one embodiment, each of the phosphate mimic is independently a 5'-vinyl phosphonate (VP).

In one embodiment, the base pair at the 1 position of the 5'-end of the antisense strand of at least one of the duplex is independently an AU base pair.

In one embodiment, each of the sense strands independently has a total of 21 nucleotides and each of the antisense strands independently has a total of 23 nucleotides.

In one embodiment, the composition comprises a first dsRNA agent comprising the sense strand nucleotide sequence 5'-UAACAAUGUUGCUUUCAAC-3' (SEQ ID NO: 5) and an antisense strand comprising the nucleotide sequence 5'-GUUGAAAAGCAACAUUGUUAGU-3' (SEQ ID NO: 6); and a second dsRNA agent comprising the sense strand nucleotide sequence 5'-ACUGUACAGUC-55 UAAAAAUGUCA-3' (SEQ ID NO: 7) and an antisense strand comprising the nucleotide sequence 5'-UGA-CAUUUUAGACUGUACAGUGG-3' (SEQ ID NO: 8).

In one embodiment, the sense strand of the first dsRNA agent comprises the sense strand nucleotide sequence 5'-usasaca(Ahd)UfgUfUfGfcuuuucaasasa-3' (SEQ ID NO: 9) and the antisense strand of the first dsRNA agent comprises the nucleotide sequence 5'-VPUsUfsuugA-faaagcaaCfaUfuguasgu-3' (SEQ ID NO: 10); and the sense strand of the second dsRNA agent comprises the nucleotides sequence 5'-ascsgu(Ahd)CfaGfUfCfuaaaauguscsa-3' (SEQ ID NO:11) and the antisense strand of the second dsRNA agent comprises the nucleotide sequence

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5'-VPusGfsacaUfuuuagacUfgUfacagusgg-3' (SEQ ID NO: 12), wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexadecyl-adenosine-3'-phosphate; and VP is Vinyl-phosphonate.

The present invention further provides isolated cells, comprising the compositions of the invention.

In one embodiment, the compositions of the invention are pharmaceutical compositions. In another embodiment, the compositions of the invention are pharmaceutical composition comprising a lipid formulation.

In one aspect, the present invention provides a method of inhibiting expression of a coronavirus genome in a cell. The method includes contacting the cell with the dsRNA agent of the invention, the composition of the invention, or the pharmaceutical composition of the invention; and maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the coronavirus genome, thereby inhibiting expression of the coronavirus genome in the cell.

In one embodiment, the cell is contacted with two or more, e.g., 2, 3, or 4, of the dsRNA agents of the invention.

In one embodiment, the cell is within a subject.

In one embodiment, the subject is a human.

In one embodiment, the expression of the coronavirus genome is inhibited by at least 50%.

In one aspect, the present invention provides a method of inhibiting replication of a coronavirus in a cell. The method includes contacting the cell with the dsRNA agent of the invention, the composition of the invention, or the pharmaceutical composition of the invention; and maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the RNA transcript of the coronavirus genome, thereby inhibiting replication of the coronavirus in a cell.

In one embodiment, the cell is contacted with two or more, e.g., 2, 3, or 4, of the dsRNA agents of the invention.

In one embodiment, the cell is within a subject.

In one embodiment, the subject is a human.

In one embodiment, the expression of the coronavirus genome is inhibited by at least 50%.

In one aspect, the present invention provides a method of treating a subject having a coronavirus infection. The method includes administering to the subject a therapeutically effective amount of the dsRNA agent of the invention, the composition of the invention, or the pharmaceutical composition of the invention, thereby treating the subject.

In one embodiment, the subject is administered two or more, e.g., 2, 3, or 4, dsRNA agents of the invention.

In one embodiment, the subject is a human, e.g., an immunocompromised human.

In one embodiment, the subject having the coronavirus infection is infected with a severe acute respiratory syndrome (SARS) virus, a Middle East respiratory syndrome (MERS) virus, or a severe acute respiratory syndrome 2 (SARS-2) virus.

In one embodiment, treating comprises amelioration of at least one sign or symptom of the disease.

In one embodiment, the dsRNA agent is administered to the subject at a dose of about 0.01 mg/kg to about 50 mg/kg.

In one embodiment, the administration of the dsRNA is pulmonary system administration, e.g., intranasal administration, or oral inhalative administration.

In one embodiment, the double-stranded RNAi agent is administered intranasally.

By pulmonary system administration, e.g., intranasal administration or oral inhalative administration, of the double-stranded RNAi agent, the method can reduce the

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expression of a coronavirus genome in a pulmonary system tissue, e.g., a nasopharynx tissue, an oropharynx tissue, a laryngopharynx tissue, a larynx tissue, a trachea tissue, a carina tissue, a bronchi tissue, a bronchiole tissue, or an alveoli tissue.

In one embodiment, the dsRNA agent is administered to the subject subcutaneously.

In one embodiment, the method further comprises administering to the subject an additional agent or a therapy suitable for treatment or prevention of a coronavirus-associated disorder.

In one embodiment, the additional therapeutic agent is selected from the group consisting of an antiviral agent, an immune stimulator, a therapeutic vaccine, a viral entry inhibitor, and a combination of any of the foregoing.

In one aspect the present invention provides a method of treating a subject having a coronavirus infection. The method includes administering to the subject via pulmonary system administration a therapeutically effective amount of a first dsRNA agent comprising a first sense strand and a first antisense strand forming a first double stranded region, and a therapeutically effective amount of a second dsRNA agent comprising a second sense strand and a second antisense strand forming a second double stranded region, wherein the first sense strand comprises the nucleotide sequence 5'-UAACAAUGUJUGCUUUCAAAC-3' (SEQ ID NO: 5) and the first antisense strand comprises the nucleotide sequence 5'-GUUUGAAAAGCAACAUJGUUAGU-3' (SEQ ID NO: 6); and the second sense strand comprises the nucleotide sequence 5'-ACUGUACAGUCUAAAAUGUCA-3' (SEQ ID NO: 7) and the second antisense strand comprises the nucleotide sequence 5'-UGACAUUUAGACUGUACAGUGG-3' (SEQ ID NO: 8).

In another aspect, the present invention provides a method of treating a subject having a coronavirus infection. The method includes administering to the subject via pulmonary system administration a therapeutically effective amount of a composition for inhibiting expression of a coronavirus genome in a cell, said composition comprising: a first dsRNA agent comprising a first sense strand comprising the nucleotide sequence 5'-UAACAAUGUJUGCUUUCAAAC-3' (SEQ ID NO: 5) and a first antisense strand comprising the nucleotide sequence 5'-GUUUGAAAAGCAACAUJGUUAGU-3' (SEQ ID NO: 6), and a second dsRNA agent comprising a second sense strand comprising the nucleotide sequence 5'-ACUGUACAGUCUAAAAUGUCA-3' (SEQ ID NO: 7) and a second antisense strand comprising the nucleotide sequence 5'-UGACAUUUAGACUGUACAGUGG-3' (SEQ ID NO: 8), thereby treating the subject.

In one embodiment, the first and second dsRNA agents are present in a composition.

In one embodiment, the first and second dsRNA agents are present in separate compositions.

In another embodiment, the first and second dsRNA agents are present in the same composition.

In one embodiment, the compositions are administered to the subject at the same time.

In another embodiment, the compositions are administered to the subject at different times.

In one embodiment, the composition is a pharmaceutical composition.

In one embodiment, the first sense strand comprises the nucleotide sequence 5'-usasaca(Ahd)UfgUfJGfcuuuuucaasasa-3' (SEQ ID NO: 9) and the first antisense strand comprises the nucleotide sequence 5'-VPusUfsuugA-faaagcaaCfaUfuguuasgsu-3' (SEQ ID NO: 10); and the

second sense strand comprises the nucleotides sequence 5'-ascsgu(Ahd)CfaGfUUCfuuaauguscsa-3' (SEQ ID NO: 11) and the second antisense strand comprises the nucleotide sequence 5'-VPUsGfsacaUfuuuagacUfgUfacagusgsg-3' (SEQ ID NO: 12), wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexadecyl-adenosine-3'-phosphate; and VP is Vinyl-phosphonate.

In one embodiment, the subject is a human.

In one embodiment, the subject having the coronavirus infection is infected with a severe acute respiratory syndrome (SARS) virus, a Middle East respiratory syndrome (MERS) virus, or a severe acute respiratory syndrome 2 (SARS-2)-CoV-2 virus.

In one embodiment, treating comprises amelioration of at least one sign or symptom of the disease.

In one embodiment, the first and second dsRNA agents are independently administered to the subject at a dose of about 0.01 mg/kg to about 50 mg/kg.

In one embodiment, the pulmonary system administration is via inhalation or intranasally.

In one embodiment, the methods further comprise administering to the subject an additional agent or a therapy suitable for treatment or prevention of a coronavirus-associated disorder.

In one embodiment, the additional therapeutic agent is selected from the group consisting of an antiviral agent, an immune stimulator, a therapeutic vaccine, a viral entry inhibitor, and a combination of any of the foregoing.

The present invention is further illustrated by the following detailed description and drawings.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 depicts the genomes and structures of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV), and the Middle East Respiratory Syndrome coronavirus (MERS-CoV).

FIG. 2 schematically depicts the concatemers and the assay used for the single dose screens of the dsRNA agents of the invention.

FIG. 3 are graphs depicting the effect of the indicated siRNAs on extracellular SARS-CoV-2 genomes determined by RT-qPCR (top graph) and the effect on of the indicated siRNAs on intracellular viral nucleocapsid protein determined by in-cell ELISA (bottom graph).

FIG. 4 depicts the effect of the indicated siRNAs on resistance selected cells infected with SARS-CoV-2 determined by RT-qPCR.

FIG. 5 depicts the effect of the indicated siRNAs on resistance selected cells infected with SARS-CoV-2 determined in a focus-forming assay.

FIG. 6 are images of an immunofluorescence assay depicting SARS-CoV-2 nucleocapsid protein staining in a focus-forming assay in the presence of 10 nM of the indicated siRNAs.

FIG. 7 is a graph depicting the effect of intranasal administration of a combination of AD-1184150 and AD-1184137 on the body weight of hamsters challenged with SARS-CoV-2.

FIG. 8 is a graph depicting the effect of intranasal administration as compared to subcutaneous administration of a combination of AD-1184150 and AD-1184137 on the body weight of hamsters challenged with SARS-CoV-2.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention provides iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA genomes and RNA transcripts of coronavirus genes, e.g., a SARS-CoV-2 gene. The iRNAs of the invention have been designed to target a human coronavirus genome, e.g., a Severe Acute Respiratory Syndrome 2 (SARS-CoV-2) genome, including portions of a coronavirus genome, e.g., a Severe Acute Respiratory Syndrome 2 (SARS-CoV-2) genome, that are cross-reactive with a Severe Acute Respiratory Syndrome (SARS-CoV) gene, and/or Middle East Respiratory Syndrome (MERS-CoV) gene. The coronavirus genome may be within a cell, e.g., a cell within a subject, such as a human. The use of these iRNAs enables the targeted degradation of mRNAs of the corresponding genome (a coronavirus genome) in mammals. The present disclosure also provides methods of using the RNAi compositions of the disclosure, e.g., compositions comprising one or more, e.g., 2, 3, or 4, dsRNA agents of the invention, for inhibiting the expression of coronavirus genes or genome for treating a subject having a disorder that would benefit from inhibiting or reducing the expression of a coronavirus genome, e.g., a coronavirus-associated disorder, e.g., a subject having a coronavirus infection, e.g., a subject having Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or Middle East Respiratory Syndrome (MERS-CoV).

The iRNAs of the invention include an RNA strand (the antisense strand) having a region which is up to about 30 nucleotides or less in length, e.g., 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length, which region is substantially complementary to at least part of an mRNA transcript of a coronavirus genome. In certain embodiments, the RNAi agents of the disclosure include an RNA strand (the antisense strand) having a region which is about 21-23 nucleotides in length, which region is substantially complementary to at least part of an mRNA transcript of a coronavirus genome (either of a positive-sense genomic RNA or a negative-sense genomic RNA of a coronavirus).

In certain embodiments, one or both of the strands of the double stranded RNAi agents of the invention is up to 66 nucleotides in length, e.g., 36-66, 26-36, 25-36, 31-60, 22-43, 27-53 nucleotides in length, with a region of at least 19 contiguous nucleotides that is substantially complementary to at least a part of an mRNA of a coronavirus genome (either of a positive-sense genomic RNA or a negative-sense genomic RNA of a coronavirus). In some embodiments, such iRNA agents having longer length antisense strands preferably may include a second RNA strand (the sense strand) of 20-60 nucleotides in length wherein the sense and antisense strands form a duplex of 18-30 contiguous nucleotides.

The use of iRNAs of the invention enables the targeted degradation of mRNAs or RNA genomes of the corresponding viral genes (coronavirus gene) in mammals. Thus, methods and compositions including these iRNAs are useful for treating a subject having a coronavirus-associated disorder, e.g., a subject having a coronavirus infection, e.g., a subject having Severe Acute Respiratory Syndrome 2 (SARS-CoV-

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2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or Middle East Respiratory Syndrome (MERS-CoV).

In certain embodiments, the administration of the dsRNA to a subject results in an improvement of lung function, or a stoppage or reduction of the rate of loss of lung function, reduction of fever, reduction of cough.

The following detailed description discloses how to make and use compositions containing iRNAs to inhibit the expression of a coronavirus genomes as well as compositions, uses, and methods for treating subjects that would benefit from inhibition and/or reduction of the expression of a coronavirus genome, e.g., subjects susceptible to or diagnosed with a coronavirus-associated disorder.

### I. Definitions

In order that the present invention may be more readily understood, certain terms are first defined. In addition, it should be noted that whenever a value or range of values of a parameter are recited, it is intended that values and ranges intermediate to the recited values are also intended to be part of this invention.

The articles “a” and “an” are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element, e.g., a plurality of elements.

The term “including” is used herein to mean, and is used interchangeably with, the phrase “including but not limited to”.

The term “or” is used herein to mean, and is used interchangeably with, the term “and/or,” unless context clearly indicates otherwise.

The term “about” is used herein to mean within the typical ranges of tolerances in the art. For example, “about” can be understood as about 2 standard deviations from the mean. In certain embodiments, about means $\pm 10\%$ . In certain embodiments, about means $\pm 5\%$ . When about is present before a series of numbers or a range, it is understood that “about” can modify each of the numbers in the series or range.

The term “at least” prior to a number or series of numbers is understood to include the number adjacent to the term “at least”, and all subsequent numbers or integers that could logically be included, as clear from context. For example, the number of nucleotides in a nucleic acid molecule must be an integer. For example, “at least 19 nucleotides of a 21 nucleotide nucleic acid molecule” means that 19, 20, or 21 nucleotides have the indicated property. When at least is present before a series of numbers or a range, it is understood that “at least” can modify each of the numbers in the series or range.

As used herein, “no more than” or “less than” is understood as the value adjacent to the phrase and logical lower values or integers, as logical from context, to zero. For example, a duplex with an overhang of “no more than 2 nucleotides” has a 2, 1, or 0 nucleotide overhang. When “no more than” is present before a series of numbers or a range, it is understood that “no more than” can modify each of the numbers in the series or range. As used herein, ranges include both the upper and lower limit.

As used herein, methods of detection can include determination that the amount of analyte present is below the level of detection of the method.

In the event of a conflict between an indicated target site and the nucleotide sequence for a sense or antisense strand, the indicated sequence takes precedence.

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In the event of a conflict between a sequence and its indicated site on a transcript or other sequence, the nucleotide sequence recited in the specification takes precedence.

As used herein, the term “coronavirus,” (“CoV”; subfamily Coronavirinae, family Coronaviridae, order Nidovirales), refers to a group of highly diverse, enveloped, positive-sense, single-stranded RNA viruses that cause respiratory, enteric, hepatic and neurological diseases of varying severity in a broad range of animal species, including humans. 10 Coronaviruses are subdivided into four genera: Alphacoronavirus, Betacoronavirus (13CoV), Gammacoronavirus and Deltacoronavirus.

Any coronavirus that infects humans and animals is encompassed by the term “coronavirus” as used herein.

15 Exemplary coronaviruses encompassed by the term include the coronaviruses that cause a common cold-like respiratory illness, e.g., human coronavirus 229E (HCoV-229E), human coronavirus NL63 (HCoV-NL63), human coronavirus OC43 (HCoV-OC43), and human coronavirus HKU1 (HCoV-HKU1); the coronavirus that causes avian infectious bronchitis virus (IBV); the coronavirus that causes murine hepatitis virus (MHV); the coronavirus that causes porcine transmissible gastroenteritis virus PRCoV; the coronavirus that causes porcine respiratory coronavirus and bovine coronavirus; the coronavirus that causes Severe Acute Respiratory Syndrome (SARS), the coronavirus that causes the Middle East respiratory syndrome (MERS), and the coronavirus that causes Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19).

20 The coronavirus (CoV) genome is a single-stranded, non-segmented RNA genome, which is approximately 26-32 kb. It contains 5'-methylated caps and 3'-polyadenylated tails and is arranged in the order of 5', replicase genes, genes encoding structural proteins (spike glycoprotein (S), envelope protein (E), membrane protein (M) and nucleocapsid protein (N)), polyadenylated tail and then the 3' end. The partially overlapping 5'-terminal open reading frame 1a/b (ORF1a/b) is within the 5' two-thirds of the CoV genome and encodes the large replicase polyprotein 1a (pp1a) and 25 pp1ab. These polyproteins are cleaved by papain-like cysteine protease (PLpro) and 3C-like serine protease (3CLpro) to produce non-structural proteins, including RNA-dependent RNA polymerase (RdRp) and helicase (Hel), which are important enzymes involved in the transcription and replication of CoVs. The 3' one-third of the CoV genome encodes the structural proteins (S, E, M and N), which are essential for virus-cell-receptor binding and virion assembly, and other non-structural proteins and accessory proteins that may have immunomodulatory effects. (Peiris J S., et al., 2003, *Nat. Med.* 10 (Suppl. 12): 88-97).

30 As a coronavirus is a positive-sense, single-stranded RNA virus having a 5' methylated cap and a 3' polyadenylated tail, once the virus enters the cell and is uncoated, the viral RNA genome attaches to the host cell's ribosome for direct translation. The host ribosome translates the initial overlapping open reading frame of the virus genome and forms a long polyprotein. The polyprotein has its own proteases which cleave the polyprotein into multiple nonstructural proteins.

35 A number of the nonstructural proteins coalesce to form a multi-protein replicase-transcriptase complex (RTC). The main replicase-transcriptase protein is the RNA-dependent RNA polymerase (RdRp). It is directly involved in the replication and transcription of RNA from an RNA strand. 40 The other nonstructural proteins in the complex assist in the replication and transcription process. The exoribonuclease non-structural protein for instance provides extra fidelity to

replication by providing a proofreading function which the RNA-dependent RNA polymerase lacks.

One of the main functions of the complex is to replicate the viral genome. RdRp directly mediates the synthesis of negative-sense genomic RNA from the positive-sense genomic RNA. This is followed by the replication of positive-sense genomic RNA from the negative-sense genomic RNA. The other important function of the complex is to transcribe the viral genome. RdRp directly mediates the synthesis of negative-sense subgenomic RNA molecules from the positive-sense genomic RNA. This is followed by the transcription of these negative-sense subgenomic RNA molecules to their corresponding positive-sense mRNAs.

The replicated positive-sense genomic RNA becomes the genome of the progeny viruses.

As used herein, the term “severe acute respiratory syndrome coronavirus” or “SARS-CoV”, refers to a coronavirus that was first discovered in 2003, which causes severe acute respiratory syndrome (SARS). SARS-CoV represents the prototype of a new lineage of coronaviruses capable of causing outbreaks of clinically significant and frequently fatal human disease. The complete genome of SARS-CoV has been identified, as well as common variants thereof. The genome of SARS-CoV is a 29,727-nucleotide polyadenylated RNA, has 11 open reading frames, and 41% of the residues are G or C (see, e.g., FIG. 1). The genomic organization is typical of coronaviruses, with the characteristic gene order (5'-replicase (rep), spike (S), envelope (E), membrane (M), nucleocapsid (N)-3' and short untranslated regions at both termini. The SARS-CoV rep gene, which comprises about two-thirds of the genome, is predicted to encode two polyproteins that undergo co-translational proteolytic processing. There are four open reading frames (ORFs) downstream of rep that are predicted to encode the structural proteins, S, E, M and N. The hemagglutinin-esterase gene, which is present between ORF1b and S in group 2 and some group 3 coronaviruses was not found.

The amino acid and complete coding sequences of the SARS-CoV genomes are known may be found in for example, GenBank Accession Nos. AY502923.1; AP006559.1; AP006558.1; AY313906.1; AY345986.1; AY502931.1; AY282752.2; AY559097.1; AY559081.1; DQ182595.1; AY291451.1; AY568539.1; AY613947.1; and AY390556.1, the entire contents of each of which are incorporated herein by reference.

The term “SARS-CoV,” as used herein, also refers to naturally occurring RNA sequence variations of the SARS-CoV genome.

As used herein, the term “the Middle East respiratory syndrome coronavirus” or “MERS-CoV”, refers to a coronavirus that causes the Middle East respiratory syndrome (MERS), which was first identified in 2012. MERS-CoV is closely related to severe acute respiratory syndrome (SARS) coronavirus (SARS-CoV). Clinically similar to SARS, MERS-CoV infection leads to severe respiratory illness with renal failure. The genomic structure of MERS-CoV is shown in FIG. 1.

The amino acid and complete coding sequences of the MERS-CoV genomes are known and may be found in for example, GenBank Accession Nos. MK462243.1; MK462244.1; MK462245.1; MK462246.1; MK462247.1; MK462248.1; MK462249.1; MK462250.1; MK462251.1; MK462252.1; MK462253.1; MK462254.1; MK462255.1; MK462256.1; MK483839.1; and MH822886.1, the entire contents of each of which are incorporated herein by reference.

The term “MERS-CoV,” as used herein, also refers to naturally occurring RNA sequence variations of the MERS-CoV genome.

As used herein, the terms “severe acute respiratory syndrome coronavirus 2,” “SARS-CoV-2,” “2019-nCoV,” refer to the novel coronavirus that caused a pneumonia outbreak first reported in Wuhan, China in December 2019 (“COVID-19”). Phylogenetic analysis of the complete viral genome (29,903 nucleotides) revealed that SARS-CoV-2 was most closely related (89.1% nucleotide similarity) to SARS-CoV.

The amino acid and complete coding sequences of the SARS-CoV-2 genomes are known and may be found in for example, the GISAID EpiCoV™ Database (db.cngb.org/gisaid/), including Accession nos. EPI\_ISL\_402119; EPI\_ISL\_402120; EPI\_ISL\_402121; EPI\_ISL\_402123; EPI\_ISL\_402124; EPI\_ISL\_402125; EPI\_ISL\_402127; EPI\_ISL\_402128; EPI\_ISL\_402129; EPI\_ISL\_402130; EPI\_ISL\_402132; EPI\_ISL\_403928; EPI\_ISL\_403929; EPI\_ISL\_403930; EPI\_ISL\_403931; EPI\_ISL\_403932; EPI\_ISL\_403933; EPI\_ISL\_403934; EPI\_ISL\_403935; EPI\_ISL\_403936; EPI\_ISL\_403937; EPI\_ISL\_403962; EPI\_ISL\_404228; EPI\_ISL\_404253; and EPI\_ISL\_404895, the entire contents of which are incorporated herein by reference.

The term “SARS-CoV-2,” as used herein, also refers to naturally occurring RNA sequence variations of the SARS-CoV-2 genome.

Additional examples of coronavirus genome and mRNA sequences are readily available using publicly available databases, e.g., GenBank, UniProt, and OMIM.

As used herein, “target sequence” refers to a contiguous portion of the nucleotide sequence of an RNA molecule, such as a coronavirus positive-sense RNA molecule or a coronavirus negative-sense RNA molecule, including mRNA that is a product of RNA processing of a primary transcription product. The target portion of the sequence will be at least long enough to serve as a substrate for iRNA-directed cleavage at or near that portion of the nucleotide sequence of an RNA molecule, such as a coronavirus positive-sense RNA molecule or a coronavirus negative-sense RNA molecule. In one embodiment, the target sequence is within the protein coding region of a coronavirus genome.

The target sequence may be from about 19-36 nucleotides in length, e.g., preferably about 19-30 nucleotides in length. For example, the target sequence can be about 19-30 nucleotides, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length. In some embodiments, the target sequence is about 19 to about 30 nucleotides in length. In other embodiments, the target sequence is about 19 to about 25 nucleotides in length. In still other embodiments, the target sequence is about 19 to about 23 nucleotides in length. In some embodiments, the target sequence is about 21 to about 23 nucleotides in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the invention.

As used herein, the term “strand comprising a sequence” refers to an oligonucleotide comprising a chain of nucleotides that is described by the sequence referred to using the standard nucleotide nomenclature.

“G,” “C,” “A,” “T,” and “U” each generally stand for a nucleotide that contains guanine, cytosine, adenine, thymidine, and uracil as a base, respectively. However, it will be

understood that the term "ribonucleotide" or "nucleotide" can also refer to a modified nucleotide, as further detailed below, or a surrogate replacement moiety (see, e.g., Table 1). The skilled person is well aware that guanine, cytosine, adenine, and uracil can be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base can base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine can be replaced in the nucleotide sequences of dsRNA featured in the invention by a nucleotide containing, for example, inosine. In another example, adenine and cytosine anywhere in the oligonucleotide can be replaced with guanine and uracil, respectively to form G-U Wobble base pairing with the target mRNA. Sequences containing such replacement moieties are suitable for the compositions and methods featured in the invention.

The terms "iRNA", "RNAi agent," "iRNA agent," "RNA interference agent" as used interchangeably herein, refer to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript via an RNA-induced silencing complex (RISC) pathway. RNA interference (RNAi) is a process that directs the sequence-specific degradation of mRNA. RNAi modulates, e.g., inhibits, the expression of a coronavirus genome in a cell, e.g., a cell within a subject, such as a mammalian subject.

In one embodiment, an RNAi agent of the disclosure includes a single stranded RNAi that interacts with a target RNA sequence, e.g., a coronavirus target mRNA sequence, either a coronavirus positive-sense RNA molecule or a coronavirus negative-sense RNA molecule, to direct the cleavage of the target RNA. Without wishing to be bound by theory it is believed that long double stranded RNA introduced into cells is broken down into double-stranded short interfering RNAs (siRNAs) comprising a sense strand and an antisense strand by a Type III endonuclease known as Dicer (Sharp et al. (2001) *Genes Dev.* 15:485). Dicer, a ribonuclease-III-like enzyme, processes these dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, et al., (2001) *Nature* 409:363). These siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, et al., (2001) *Cell* 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce silencing (El-bashir, et al., (2001) *Genes Dev.* 15:188). Thus, in one aspect the disclosure relates to a single stranded RNA (ssRNA) (the antisense strand of a siRNA duplex) generated within a cell and which promotes the formation of a RISC complex to effect silencing of the target genome, i.e., a coronavirus genome or gene. Accordingly, the term "siRNA" is also used herein to refer to an RNAi as described above.

In another embodiment, the RNAi agent may be a single-stranded RNA that is introduced into a cell or organism to inhibit a target mRNA. Single-stranded RNAi agents bind to the RISC endonuclease, Argonaute 2, which then cleaves the target mRNA. The single-stranded siRNAs are generally 15-30 nucleotides and are chemically modified. The design and testing of single-stranded RNAs are described in U.S. Pat. No. 8,101,348 and in Lima et al., (2012) *Cell* 150:883-894, the entire contents of each of which are hereby incorporated herein by reference. Any of the antisense nucleotide

sequences described herein may be used as a single-stranded siRNA as described herein or as chemically modified by the methods described in Lima et al., (2012) *Cell* 150:883-894.

In another embodiment, a "RNAi agent" for use in the compositions and methods of the disclosure is a double stranded RNA and is referred to herein as a "double stranded RNAi agent," "double stranded RNA (dsRNA) molecule," "dsRNA agent," or "dsRNA". The term "dsRNA" refers to a complex of ribonucleic acid molecules, having a duplex structure comprising two anti-parallel and substantially complementary nucleic acid strands, referred to as having "sense" and "antisense" orientations with respect to a target RNA, i.e., either a coronavirus positive-sense RNA molecule or a coronavirus negative-sense RNA molecule. In some embodiments of the disclosure, a double stranded RNA (dsRNA) triggers the degradation of a target RNA, e.g., an mRNA, through a post-transcriptional gene-silencing mechanism referred to herein as RNA interference or RNAi.

In general, a dsRNA molecule can include ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, e.g., a deoxyribonucleotide, a modified nucleotide. In addition, as used in this specification, an "RNAi agent" may include ribonucleotides with chemical modifications; an RNAi agent may include substantial modifications at multiple nucleotides.

As used herein, the term "modified nucleotide" refers to a nucleotide having, independently, a modified sugar moiety, a modified internucleotide linkage, or a modified nucleobase. Thus, the term modified nucleotide encompasses substitutions, additions or removal of, e.g., a functional group or atom, to internucleoside linkages, sugar moieties, or nucleobases. The modifications suitable for use in the agents of the disclosure include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a siRNA type molecule, are encompassed by "RNAi agent" for the purposes of this specification and claims.

In certain embodiments of the instant disclosure, inclusion of a deoxy-nucleotide—which is acknowledged as a naturally occurring form of nucleotide—if present within a RNAi agent can be considered to constitute a modified nucleotide.

The duplex region may be of any length that permits specific degradation of a desired target RNA through a RISC pathway, and may range from about 9 to 36 base pairs in length, e.g., about 15-30 base pairs in length, for example, about 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 base pairs in length, such as about 15-30, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the invention.

The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting RNA chain is referred

to as a "hairpin loop." A hairpin loop can comprise at least one unpaired nucleotide. In some embodiments, the hairpin loop can comprise at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 20, at least 23 or more unpaired nucleotides or nucleotides not directed to the target site of the dsRNA. In some embodiments, the hairpin loop can be 10 or fewer nucleotides. In some embodiments, the hairpin loop can be 8 or fewer unpaired nucleotides. In some embodiments, the hairpin loop can be 4-10 unpaired nucleotides. In some embodiments, the hairpin loop can be 4-8 nucleotides.

In certain embodiment, the two strands of double-stranded oligomeric compound can be linked together. The two strands can be linked to each other at both ends, or at one end only. By linking at one end is meant that 5'-end of first strand is linked to the 3'-end of the second strand or 3'-end of first strand is linked to 5'-end of the second strand. When the two strands are linked to each other at both ends, 5'-end of first strand is linked to 3'-end of second strand and 3'-end of first strand is linked to 5'-end of second strand. The two strands can be linked together by an oligonucleotide linker including, but not limited to, (N)n; wherein N is independently a modified or unmodified nucleotide and n is 3-23. In some embodiments, n is 3-10, e.g., 3, 4, 5, 6, 7, 8, 9, or 10. In some embodiments, the oligonucleotide linker is selected from the group consisting of GNRA, (G)4, (U)4, and (dT)4, wherein N is a modified or unmodified nucleotide and R is a modified or unmodified purine nucleotide. Some of the nucleotides in the linker can be involved in base-pair interactions with other nucleotides in the linker. The two strands can also be linked together by a non-nucleoside linker, e.g. a linker described herein. It will be appreciated by one of skill in the art that any oligonucleotide chemical modifications or variations describe herein can be used in the oligonucleotide linker.

Hairpin and dumbbell type oligomeric compounds will have a duplex region equal to or at least 14, 15, 15, 16, 17, 18, 19, 29, 21, 22, 23, 24, or 25 nucleotide pairs. The duplex region can be equal to or less than 200, 100, or 50, in length. In some embodiments, ranges for the duplex region are 15-30, 17 to 23, 19 to 23, and 19 to 21 nucleotides pairs in length.

The hairpin oligomeric compounds can have a single strand overhang or terminal unpaired region, in some embodiments at the 3', and in some embodiments on the antisense side of the hairpin. In some embodiments, the overhangs are 1-4, more generally 2-3 nucleotides in length. The hairpin oligomeric compounds that can induce RNA interference are also referred to as "shRNA" herein.

Where the two substantially complementary strands of a dsRNA are comprised by separate RNA molecules, those molecules need not, but can be covalently connected. Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting structure is referred to as a "linker." The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the dsRNA minus any overhangs that are present in the duplex. In addition to the duplex structure, an RNAi may comprise one or more nucleotide overhangs.

In one embodiment, an RNAi agent of the invention is a dsRNA, each strand of which is 24-30 nucleotides in length, that interacts with a target RNA sequence, e.g., a coronavirus target RNA sequence, to direct the cleavage of the target RNA. Without wishing to be bound by theory, long double

stranded RNA introduced into cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp et al. (2001) *Genes Dev.* 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, et al., (2001) *Nature* 409:363). The siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, et al., (2001) *Cell* 107: 309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce silencing (Elbashir, et al., (2001) *Genes Dev.* 15:188).

In one embodiment, an RNAi agent of the invention is a dsRNA agent, each strand of which comprises 19-23 nucleotides that interacts with a coronavirus RNA sequence to direct the cleavage of the target RNA. Without wishing to be bound by theory, long double stranded RNA introduced into cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp et al. (2001) *Genes Dev.* 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, et al., (2001) *Nature* 409:363). The siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, et al., (2001) *Cell* 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce silencing (Elbashir, et al., (2001) *Genes Dev.* 15:188). In one embodiment, an RNAi agent of the invention is a dsRNA of 24-30 nucleotides that interacts with a coronavirus RNA sequence to direct the cleavage of the target RNA.

As used herein, the term "nucleotide overhang" refers to at least one unpaired nucleotide that protrudes from the duplex structure of a RNAi agent, e.g., a dsRNA. For example, when a 3'-end of one strand of a dsRNA extends beyond the 5'-end of the other strand, or vice versa, there is a nucleotide overhang. A dsRNA can comprise an overhang of at least one nucleotide; alternatively, the overhang can comprise at least two nucleotides, at least three nucleotides, at least four nucleotides, at least five nucleotides or more. A 45 nucleotide overhang can comprise or consist of a nucleotide/nucleoside analog, including a deoxynucleotide/nucleoside. The overhang(s) can be on the sense strand, the antisense strand or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5'-end, 3'-end or both ends of either an antisense or sense strand of a dsRNA.

In one embodiment of the dsRNA, at least one strand comprises a 3' overhang of at least 1 nucleotide. In another embodiment, at least one strand comprises a 3' overhang of at least 2 nucleotides, e.g., 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, or 15 nucleotides. In other embodiments, at least one strand of the RNAi agent comprises a 5' overhang of at least 1 nucleotide. In certain embodiments, at least one strand comprises a 5' overhang of at least 2 nucleotides, e.g., 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, or 15 nucleotides. In still other embodiments, both the 3' and the 5' end of one strand of the RNAi agent comprise an overhang of at least 1 nucleotide.

In one embodiment, the antisense strand of a dsRNA has a 1-10 nucleotide, e.g., 0-3, 1-3, 2-4, 2-5, 4-10, 5-10, e.g., a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In one embodiment, the sense strand of a dsRNA has a 1-10 nucleotide, e.g., a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end or the 5'-end. In

another embodiment, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

In certain embodiments, the overhang on the sense strand or the antisense strand, or both, can include extended lengths longer than 10 nucleotides, e.g., 1-30 nucleotides, 2-30 nucleotides, 10-30 nucleotides, or 10-15 nucleotides in length. In certain embodiments, an extended overhang is on the sense strand of the duplex. In certain embodiments, an extended overhang is present on the 3'end of the sense strand of the duplex. In certain embodiments, an extended overhang is present on the 5'end of the sense strand of the duplex. In certain embodiments, an extended overhang is on the antisense strand of the duplex. In certain embodiments, an extended overhang is present on the 3'end of the antisense strand of the duplex. In certain embodiments, an extended overhang is present on the 5'end of the antisense strand of the duplex. In certain embodiments, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate. In certain embodiments, the overhang includes a self-complementary portion such that the overhang is capable of forming a hairpin structure that is stable under physiological conditions.

The terms “blunt” or “blunt ended” as used herein in reference to a dsRNA mean that there are no unpaired nucleotides or nucleotide analogs at a given terminal end of a dsRNA, i.e., no nucleotide overhang. One or both ends of a dsRNA can be blunt. Where both ends of a dsRNA are blunt, the dsRNA is said to be blunt ended. To be clear, a “blunt ended” dsRNA is a dsRNA that is blunt at both ends, i.e., no nucleotide overhang at either end of the molecule. Most often such a molecule will be double stranded over its entire length.

The term “antisense strand” or “guide strand” refers to the strand of an iRNA, e.g., a dsRNA, which includes a region that is substantially complementary to a target sequence, e.g., a coronavirus RNA, i.e., either of a coronavirus positive-sense RNA or a coronavirus negative-sense RNA.

As used herein, the term “region of complementarity” refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, e.g., a coronavirus nucleotide sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches can be in the internal or terminal regions of the molecule. Generally, the most tolerated mismatches are in the terminal regions, e.g., within 5, 4, 3, or 2 nucleotides of the 5'- or 3'-terminus of the RNAi agent.

In some embodiments, a double stranded RNA agent of the invention includes a nucleotide mismatch in the antisense strand. In some embodiments, the antisense strand of the double stranded RNA agent of the invention includes no more than 4 mismatches with the target mRNA, e.g., the antisense strand includes 4, 3, 2, 1, or 0 mismatches with the target mRNA. In some embodiments, the antisense strand double stranded RNA agent of the invention includes no more than 4 mismatches with the sense strand, e.g., the antisense strand includes 4, 3, 2, 1, or 0 mismatches with the sense strand. In some embodiments, a double stranded RNA agent of the invention includes a nucleotide mismatch in the sense strand. In some embodiments, the sense strand of the double stranded RNA agent of the invention includes no more than 4 mismatches with the antisense strand, e.g., the sense strand includes 4, 3, 2, 1, or 0 mismatches with the antisense strand. In some embodiments, the nucleotide mismatch is, for example, within 5, 4, 3 nucleotides from the 3'-end of the iRNA. In another embodiment, the nucleotide

mismatch is, for example, in the 3'-terminal nucleotide of the iRNA agent. In some embodiments, the mismatch(s) is not in the seed region.

Thus, an RNAi agent as described herein can contain one or more mismatches to the target sequence. In one embodiment, a RNAi agent as described herein contains no more than 3 mismatches (i.e., 3, 2, 1, or 0 mismatches). In one embodiment, an RNAi agent as described herein contains no more than 2 mismatches. In one embodiment, an RNAi agent as described herein contains no more than 1 mismatch. In one embodiment, an RNAi agent as described herein contains 0 mismatches. In certain embodiments, if the antisense strand of the RNAi agent contains mismatches to the target sequence, the mismatch can optionally be restricted to be within the last 5 nucleotides from either the 5'- or 3'-end of the region of complementarity. For example, in such embodiments, for a 23 nucleotide RNAi agent, the strand which is complementary to a region of a coronavirus genome, generally does not contain any mismatch within the central 13 nucleotides. The methods described herein or methods known in the art can be used to determine whether an RNAi agent containing a mismatch to a target sequence is effective in inhibiting the expression of a coronavirus genome or gene. Consideration of the efficacy of RNAi agents with mismatches in inhibiting expression of a coronavirus genome is important, especially if the particular region of complementarity in a coronavirus genome is known to mutate.

The term “sense strand” or “passenger strand” as used herein, refers to the strand of a RNAi agent that includes a region that is substantially complementary to a region of the antisense strand as that term is defined herein.

As used herein, “substantially all of the nucleotides are modified” are largely but not wholly modified and can include not more than 5, 4, 3, 2, or 1 unmodified nucleotides.

As used herein, the term “cleavage region” refers to a region that is located immediately adjacent to the cleavage site. The cleavage site is the site on the target at which cleavage occurs. In some embodiments, the cleavage region comprises three bases on either end of, and immediately adjacent to, the cleavage site. In some embodiments, the cleavage region comprises two bases on either end of, and immediately adjacent to, the cleavage site. In some embodiments, the cleavage site specifically occurs at the site bound by nucleotides 10 and 11 of the antisense strand, and the cleavage region comprises nucleotides 11, 12 and 13.

As used herein, and unless otherwise indicated, the term “complementary,” when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Conditions, such as physiologically relevant conditions as can be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

Complementary sequences within a RNAi agent, e.g., within a dsRNA as described herein, include base-pairing of the oligonucleotide or polynucleotide comprising a first nucleotide sequence to an oligonucleotide or polynucleotide comprising a second nucleotide sequence over the entire length of one or both nucleotide sequences. Such sequences can be referred to as “fully complementary” with respect to

each other herein. However, where a first sequence is referred to as "substantially complementary" with respect to a second sequence herein, the two sequences can be fully complementary, or they can form one or more, but generally not more than 5, 4, 3, or 2 mismatched base pairs upon hybridization for a duplex up to 30 base pairs, while retaining the ability to hybridize under the conditions most relevant to their ultimate application, e.g., inhibition of gene expression via a RISC pathway. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide 21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, can yet be referred to as "fully complementary" for the purposes described herein.

"Complementary" sequences, as used herein, can also include, or be formed entirely from, non-Watson-Crick base pairs or base pairs formed from non-natural and modified nucleotides, in so far as the above requirements with respect to their ability to hybridize are fulfilled. Such non-Watson-Crick base pairs include, but are not limited to, G:U Wobble or Hoogstein base pairing.

The terms "complementary," "fully complementary" and "substantially complementary" herein can be used with respect to the base matching between the sense strand and the antisense strand of a dsRNA, or between the antisense strand of a RNAi agent and a target sequence, as will be understood from the context of their use.

As used herein, a polynucleotide that is "substantially complementary to at least part of" a messenger RNA (mRNA) or target sequence refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest or target sequence (e.g., a coronavirus target sequence, either of a coronavirus positive-sense RNA or a coronavirus negative-sense RNA). For example, a polynucleotide is complementary to at least a part of a coronavirus RNA if the sequence is substantially complementary to a non-interrupted portion of a coronavirus RNA.

Accordingly, in some embodiments, the antisense strand polynucleotides disclosed herein are fully complementary to the target coronavirus sequence, either of a coronavirus positive-sense RNA or a coronavirus negative-sense RNA.

In other embodiments, the antisense strand polynucleotides disclosed herein are substantially complementary to the target coronavirus sequence and comprise a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NO: 1, or a fragment of SEQ ID NO: 1, such as about 85%, about 90%, or about 95% complementary.

In other embodiments, the antisense strand polynucleotides disclosed herein are substantially complementary to the target coronavirus sequence and comprise a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NO: 2, or a fragment of SEQ ID NO: 2, such as about 85%, about 90%, or about 95% complementary.

In other embodiments, the antisense polynucleotides disclosed herein are substantially complementary to the target coronavirus sequence and comprise a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to any one of the sense strand nucleotide

sequences in any one of Tables 2-5, or a fragment of any one of the sense strand nucleotide sequences in any one of Tables 2-5, such as about 85%, about 90%, or about 95% complementary.

5 In one embodiment, an RNAi agent of the disclosure includes a sense strand that is substantially complementary to an antisense polynucleotide which, in turn, is the same as a target coronavirus sequence, and wherein the sense strand polynucleotide comprises a contiguous nucleotide sequence 10 which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NO: 2, or a fragment of any one of SEQ ID NO: 2, such as about 85%, about 90%, or about 95% complementary.

15 In another embodiment, an RNAi agent of the disclosure includes a sense strand that is substantially complementary to an antisense polynucleotide which, in turn, is the same as a target coronavirus sequence, and wherein the sense strand polynucleotide comprises a contiguous nucleotide sequence 20 which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NO: 1, or a fragment of any one of SEQ ID NO: 1, such as about 85%, about 90%, or about 95% complementary.

25 In some embodiments, an iRNA of the invention includes a sense strand that is substantially complementary to an antisense polynucleotide which, in turn, is complementary to a target coronavirus sequence, and wherein the sense strand polynucleotide comprises a contiguous nucleotide sequence 30 which is at least about 80% complementary over its entire length to any one of the antisense strand nucleotide sequences in any one of any one of Tables 2-5, or a fragment of any one of the antisense strand nucleotide sequences in any one of Tables 2-5, such as about 85%, about 90%, or about 95% complementary.

35 In some embodiments, the double-stranded region of a double-stranded iRNA agent is equal to or at least, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 23, 24, 25, 26, 27, 28, 29, 30 or more nucleotide pairs in length.

40 In some embodiments, the antisense strand of a double-stranded iRNA agent is equal to or at least 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length.

45 In some embodiments, the sense strand of a double-stranded iRNA agent is equal to or at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length.

50 In one embodiment, the sense and antisense strands of the double-stranded iRNA agent are each independently 15 to 30 nucleotides in length.

In one embodiment, the sense and antisense strands of the double-stranded iRNA agent are each independently 19 to 25 nucleotides in length.

55 In one embodiment, the sense and antisense strands of the double-stranded iRNA agent are each independently 21 to 23 nucleotides in length.

In one embodiment, the sense strand of the iRNA agent is 21-nucleotides in length, and the antisense strand is 23-nucleotides in length, wherein the strands form a double-stranded region of 21 consecutive base pairs having a 2-nucleotide long single stranded overhangs at the 3-end.

60 In one aspect of the invention, an agent for use in the methods and compositions of the invention is a single-stranded antisense nucleic acid molecule that inhibits a target mRNA via an antisense inhibition mechanism. The single-stranded antisense RNA molecule is complementary to a sequence within the target mRNA. The single-stranded

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antisense oligonucleotides can inhibit translation in a stoichiometric manner by base pairing to the mRNA and physically obstructing the translation machinery, see Dias, N. et al., (2002) *Mol Cancer Ther* 1:347-355. The single-stranded antisense RNA molecule may be about 15 to about 30 nucleotides in length and have a sequence that is complementary to a target sequence. For example, the single-stranded antisense RNA molecule may comprise a sequence that is at least about 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from any one of the antisense sequences described herein.

In one embodiment, at least partial suppression of the expression of a coronavirus genome, is assessed by a reduction of the amount of coronavirus genome which can be isolated from or detected in a first cell or group of cells in which a coronavirus genome is transcribed and which has or have been treated such that the expression of a coronavirus genome is inhibited, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has or have not been so treated (control cells). The degree of inhibition may be expressed in terms of:

$$\frac{(\text{genome in control cells}) - (\text{genome in treated cells})}{(\text{genome in control cells})} \times 100\%$$

In one embodiment, inhibition of expression is determined by the dual luciferase method in Example 1 wherein the RNAi agent is present at 10 nM.

The phrase "contacting a cell with an RNAi agent," such as a dsRNA, as used herein, includes contacting a cell by any possible means. Contacting a cell with an RNAi agent includes contacting a cell in vitro with the RNAi agent or contacting a cell in vivo with the RNAi agent. The contacting may be done directly or indirectly. Thus, for example, the RNAi agent may be put into physical contact with the cell by the individual performing the method, or alternatively, the RNAi agent may be put into a situation that will permit or cause it to subsequently come into contact with the cell.

Contacting a cell in vitro may be done, for example, by incubating the cell with the RNAi agent. Contacting a cell in vivo may be done, for example, via inhalation, intranasal administration, or intratracheal administration, by injecting the RNAi agent into or near the tissue where the cell is located, e.g., a pulmonary system cell, or by injecting the RNAi agent into another area, or to the bloodstream or the subcutaneous space, such that the agent will subsequently reach the tissue where the cell to be contacted is located. For example, the RNAi agent may contain or be coupled to a ligand, e.g., a lipophilic moiety or moieties as described below and further detailed, e.g., in PCT Publication No. WO 2019/217459, which is incorporated herein by reference, that directs or otherwise stabilizes the RNAi agent at a site of interest, e.g., the pulmonary system. In some embodiments, the RNAi agent may contain or be coupled to a ligand, e.g., one or more GalNAc derivatives as described below, that directs or otherwise stabilizes the RNAi agent at a site of interest, e.g., the liver. In other embodiments, the RNAi agent may contain or be coupled to a lipophilic moiety or moieties and one or more GalNAc derivatives. Combinations of in vitro and in vivo methods of contacting are also possible. For example, a cell may also be contacted in vitro with an RNAi agent and subsequently transplanted into a subject.

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In one embodiment, contacting a cell with an RNAi agent includes "introducing" or "delivering the RNAi agent into the cell" by facilitating or effecting uptake or absorption into the cell. Absorption or uptake of a RNAi agent can occur through unaided diffusive or active cellular processes, or by auxiliary agents or devices. Introducing a RNAi agent into a cell may be in vitro or in vivo. For example, for in vivo introduction, a RNAi agent can be injected into a tissue site or administered systemically. In vitro introduction into a cell includes methods known in the art such as electroporation and lipofection. Further approaches are described herein below or are known in the art.

The term "lipophile" or "lipophilic moiety" broadly refers to any compound or chemical moiety having an affinity for lipids. One way to characterize the lipophilicity of the lipophilic moiety is by the octanol-water partition coefficient,  $\log K_{ow}$ , where  $K_{ow}$  is the ratio of a chemical's concentration in the octanol-phase to its concentration in the aqueous phase of a two-phase system at equilibrium. The octanol-water partition coefficient is a laboratory-measured property of a substance. However, it may also be predicted by using coefficients attributed to the structural components of a chemical which are calculated using first-principle or empirical methods (see, for example, Tetko et al., *J. Chem. Inf Comput. Sci.* 41:1407-21 (2001), which is incorporated herein by reference in its entirety). It provides a thermodynamic measure of the tendency of the substance to prefer a non-aqueous or oily milieu rather than water (i.e. its hydrophilic/lipophilic balance). In principle, a chemical substance is lipophilic in character when its  $\log K_{ow}$  exceeds 0. Typically, the lipophilic moiety possesses a  $\log K_{ow}$  exceeding 1, exceeding 1.5, exceeding 2, exceeding 3, exceeding 4, exceeding 5, or exceeding 10. For instance, the  $\log K_{ow}$  of 6-amino hexanol, for instance, is predicted to be approximately 0.7. Using the same method, the  $\log K_{ow}$  of cholesteryl N-(hexan-6-ol) carbamate is predicted to be 10.7.

The lipophilicity of a molecule can change with respect to the functional group it carries. For instance, adding a hydroxyl group or amine group to the end of a lipophilic moiety can increase or decrease the partition coefficient (e.g.,  $\log K_{ow}$ ) value of the lipophilic moiety.

Alternatively, the hydrophobicity of the double-stranded RNAi agent, conjugated to one or more lipophilic moieties, can be measured by its protein binding characteristics. For instance, in certain embodiments, the unbound fraction in the plasma protein binding assay of the double-stranded RNAi agent could be determined to positively correlate to the relative hydrophobicity of the double-stranded RNAi agent, which could then positively correlate to the silencing activity of the double-stranded RNAi agent.

In one embodiment, the plasma protein binding assay determined is an electrophoretic mobility shift assay (EMSA) using human serum albumin protein. An exemplary protocol of this binding assay is illustrated in detail in, e.g., PCT Publication No. WO 2019/217459. The hydrophobicity of the double-stranded RNAi agent, measured by fraction of unbound siRNA in the binding assay, exceeds 0.15, exceeds 0.2, exceeds 0.25, exceeds 0.3, exceeds 0.35, exceeds 0.4, exceeds 0.45, or exceeds 0.5 for an enhanced in vivo delivery of siRNA.

Accordingly, conjugating the lipophilic moieties to the internal position(s) of the double-stranded RNAi agent provides optimal hydrophobicity for the enhanced in vivo delivery of siRNA.

The term "lipid nanoparticle" or "LNP" is a vesicle comprising a lipid layer encapsulating a pharmaceutically active molecule, such as a nucleic acid molecule, e.g., a

rNAi agent or a plasmid from which a RNAi agent is transcribed. LNPs are described in, for example, U.S. Pat. Nos. 6,858,225, 6,815,432, 8,158,601, and 8,058,069, the entire contents of which are hereby incorporated herein by reference.

As used herein, a “subject” is an animal, such as a mammal, including a primate (such as a human, a non-human primate, e.g., a monkey, and a chimpanzee), or a non-primate (such as a cow, a pig, a horse, a goat, a rabbit, a sheep, a hamster, a guinea pig, a cat, a dog, a rat, or a mouse), or a bird that expresses the target gene, either endogenously or heterologously. In a preferred embodiment, the subject is a human, such as a human being treated or assessed for a disease, disorder, or condition that would benefit from reduction in coronavirus genome expression; a human at risk for a disease, disorder, or condition that would benefit from reduction in coronavirus genome expression; a human having a disease, disorder, or condition that would benefit from reduction in coronavirus genome expression; or a human being treated for a disease, disorder, or condition that would benefit from reduction in coronavirus genome expression as described herein. In some embodiments, the subject is a female human. In other embodiments, the subject is a male human. In one embodiment, the subject is an adult subject. In another embodiment, the subject is a pediatric subject.

As used herein, the terms “treating” or “treatment” refer to a beneficial or desired result including, but not limited to, alleviation or amelioration of one or more signs or symptoms associated with coronavirus genome expression or coronavirus protein production, e.g., a coronavirus-associated disease, e.g., viral replication. Treatment also includes a reduction of one or more sign or symptoms associated with unwanted coronavirus genome expression; diminishing the extent of unwanted coronavirus genome activation or stabilization; amelioration or palliation of unwanted coronavirus genome activation or stabilization. “Treatment” can also mean prolonging survival as compared to expected survival in the absence of treatment.

The term “lower” in the context of the level of a coronavirus genome in a subject or a disease marker or symptom refers to a statistically significant decrease in such level. The decrease can be, for example, at least 10%, 15%, 20%, 25%, 30%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more. In certain embodiments, a decrease is at least 20%. In certain embodiments, the decrease is at least 50% in a disease marker, e.g., protein or gene expression level. “Lower” in the context of the level of a coronavirus genome in a subject is preferably down to a level accepted as within the range of normal for an individual without such disorder. In certain embodiments, the expression of the target is normalized, i.e., decreased towards or to a level accepted as within the range of normal for an individual without such disorder, e.g., viral load, blood oxygen level, white blood cell count, kidney function, liver function. As used here, “lower” in a subject can refer to lowering of gene expression or protein production in a cell in a subject does not require lowering of expression in all cells or tissues of a subject. For example, as used herein, lowering in a subject can include lowering of gene expression or protein production or viral replication in a subject.

The term “lower” can also be used in association with normalizing a symptom of a disease or condition, i.e. decreasing the difference between a level in a subject suffering from a coronavirus-associated disease towards or to a level in a normal subject not suffering from a coronavirus-associated disease. As used herein, if a disease is

associated with an elevated value for a symptom, “normal” is considered to be the upper limit of normal. If a disease is associated with a decreased value for a symptom, “normal” is considered to be the lower limit of normal.

As used herein, “prevention” or “preventing,” when used in reference to a disease, disorder, or condition thereof, that would benefit from a reduction in expression of a coronavirus genome or production of a coronavirus protein, refers to a reduction in the likelihood that a subject will develop a symptom associated with such a disease, disorder, or condition, e.g., a symptom of a coronavirus-associated disease. The failure to develop a disease, disorder, or condition, or the reduction in the development of a symptom associated with such a disease, disorder, or condition, e.g., pneumonia (e.g., by at least about 10% on a clinically accepted scale for that disease or disorder), or the exhibition of delayed symptoms delayed (e.g., by days, weeks, months or years) is considered effective prevention.

As used herein, the term “coronavirus-associated disease,” is a disease or disorder that is caused by, or associated with a coronavirus infection, coronavirus genome expression or coronavirus protein production. The term “coronavirus-associated disease” includes a disease, disorder or condition that would benefit from a decrease in coronavirus genome expression, replication, or protein activity. Non-limiting examples of coronavirus-associated diseases include, for example, disease or disorders caused by infection with human coronavirus 229E (HCoV-229E), human coronavirus NL63 (HCoV-NL63), human coronavirus OC43 (HCoV-OC43), human coronavirus HKU1 (HCoV-HKU1), severe acute respiratory syndrome coronavirus (SARS), the Middle East respiratory syndrome coronavirus (MERS), and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2 or COVID-19). The symptoms for a coronavirus-associated disease depend on the type of coronavirus and how serious the infection is. Patients with a mild to moderate upper-respiratory infection may develop symptoms such as runny nose, sneezing, headache, cough, sore throat, fever, or short of breath. In more severe cases, coronavirus infection can cause pneumonia, severe acute respiratory syndrome, kidney failure and even death. Further details regarding signs and symptoms of the various diseases or conditions are provided herein and are well known in the art.

“Therapeutically effective amount,” as used herein, is intended to include the amount of an RNAi agent that, when administered to a subject having a coronavirus-associated disease, is sufficient to effect treatment of the disease (e.g., by diminishing, ameliorating, or maintaining the existing disease or one or more symptoms of disease). The “therapeutically effective amount” may vary depending on the RNAi agent, how the agent is administered, the disease and its severity and the history, age, weight, family history, genetic makeup, the types of preceding or concomitant treatments, if any, and other individual characteristics of the subject to be treated.

“Prophylactically effective amount,” as used herein, is intended to include the amount of a RNAi agent that, when administered to a subject having a coronavirus-associated disorder, is sufficient to prevent or ameliorate the disease or one or more symptoms of the disease. Ameliorating the disease includes slowing the course of the disease or reducing the severity of later-developing disease. The “prophylactically effective amount” may vary depending on the RNAi agent, how the agent is administered, the degree of risk of disease, and the history, age, weight, family history,

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genetic makeup, the types of preceding or concomitant treatments, if any, and other individual characteristics of the patient to be treated.

A "therapeutically-effective amount" or "prophylactically effective amount" also includes an amount of a RNAi agent that produces some desired local or systemic effect at a reasonable benefit/risk ratio applicable to any treatment. A RNAi agent employed in the methods of the present disclosure may be administered in a sufficient amount to produce a reasonable benefit/risk ratio applicable to such treatment.

The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human subjects and animal subjects without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

The phrase "pharmaceutically-acceptable carrier" as used herein means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, manufacturing aid (e.g., lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the subject compound from one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the subject being treated. Some examples of materials which can serve as pharmaceutically-acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) lubricating agents, such as magnesium state, sodium lauryl sulfate and talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates or polyanhidrides; (22) bulking agents, such as polypeptides and amino acids (23) serum component, such as serum albumin, HDL and LDL; and (22) other non-toxic compatible substances employed in pharmaceutical formulations.

The term "sample," as used herein, includes a collection of similar fluids, cells, or tissues isolated from a subject, as well as fluids, cells, or tissues present within a subject. Examples of biological fluids include blood, serum and serosal fluids, plasma, bronchial fluids, sputum, cerebrospinal fluid, ocular fluids, lymph, urine, saliva, and the like. Tissue samples may include samples from tissues, organs or localized regions. For example, samples may be derived from particular organs, parts of organs, or fluids or cells within those organs. In certain embodiments, samples may be derived from a nasal swab. In certain embodiments, samples may be derived from a throat swab. In certain embodiments, samples may be derived from the lung, or certain types of cells in the lung. In some embodiments, the samples may be derived from the bronchioles. In some embodiments, the samples may be derived from the bronchus. In some embodiments, the samples may be derived

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from the alveoli. In other embodiments, a "sample derived from a subject" refers to liver tissue (or subcomponents thereof) derived from the subject. In some embodiments, a "sample derived from a subject" refers to blood drawn from the subject or plasma or serum derived therefrom. In further embodiments, a "sample derived from a subject" refers to pulmonary system tissue (or subcomponents thereof) derived from the subject.

## II. RNAi Agents of the Disclosure

Described herein are RNAi agents which inhibit the expression of a coronavirus genome. In one embodiment, the RNAi agent includes double stranded ribonucleic acid (dsRNA) molecules for inhibiting the expression of a coronavirus genome in a cell, such as a cell within a subject, e.g., a mammal, such as a human, e.g., a subject having a coronavirus-associated disorder, e.g., a subject having a coronavirus infection, e.g., a subject having Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or Middle East Respiratory Syndrome (MERS-CoV). The dsRNA includes an antisense strand having a region of complementarity which is complementary to at least a part of a target coronavirus RNA, e.g., an mRNA formed in the expression of a coronavirus genome. The region of complementarity is about 15-30 nucleotides or less in length. Upon contact with a cell expressing the coronavirus genome, the RNAi agent inhibits the expression of the coronavirus genome (e.g., a human gene, a primate gene, a non-primate gene) by at least 50% as assayed by, for example, a PCR or branched DNA (bDNA)-based method, or by a protein-based method, such as by immunofluorescence analysis, using, for example, western blotting or flowcytometric techniques. In preferred embodiments, inhibition of expression is by at least 50% as assayed by the Dual-Glo luciferase assay in Example a where the siRNA is at a 10 nM concentration.

A dsRNA includes two RNA strands that are complementary and hybridize to form a duplex structure under conditions in which the dsRNA will be used. One strand of a dsRNA (the antisense strand) includes a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence. For example, the target sequence can be derived from the sequence of an mRNA formed during the expression of a coronavirus genome. The other strand (the sense strand) includes a region that is complementary to the antisense strand, such that the two strands hybridize and form a duplex structure when combined under suitable conditions. As described elsewhere herein and as known in the art, the complementary sequences of a dsRNA can also be contained as self-complementary regions of a single nucleic acid molecule, as opposed to being on separate oligonucleotides.

Generally, the duplex structure is 15 to 30 base pairs in length, e.g., 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs in length. In certain preferred embodiments, the duplex structure is 18 to 25 base pairs in length, e.g., 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-25, 20-24, 20-23, 20-22, 20-21, 21-25, 21-24, 21-23, 21-22, 22-25, 22-24, 22-23, 23-25,

23-24 or 24-25 base pairs in length, for example, 19-21 basepairs in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the disclosure.

Similarly, the region of complementarity to the target sequence is 15 to 30 nucleotides in length, e.g., 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length, for example 19-23 nucleotides in length or 21-23 nucleotides in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the disclosure.

In some embodiments, the dsRNA is 15 to 23 nucleotides in length, or 25 to 30 nucleotides in length. In general, the dsRNA is long enough to serve as a substrate for the Dicer enzyme. For example, it is well known in the art that dsRNAs longer than about 21-23 nucleotides can serve as substrates for Dicer. As the ordinarily skilled person will also recognize, the region of an RNA targeted for cleavage will most often be part of a larger RNA molecule, often an mRNA molecule. Where relevant, a "part" of an mRNA target is a contiguous sequence of an mRNA target of sufficient length to allow it to be a substrate for RNAi-directed cleavage (i.e., cleavage through a RISC pathway).

One of skill in the art will also recognize that the duplex region is a primary functional portion of a dsRNA, e.g., a duplex region of about 15 to 36 base pairs, e.g., 15-36, 15-35, 15-34, 15-33, 15-32, 15-31, 15-30, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24, 20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs, for example, 19-21 base pairs. Thus, in one embodiment, to the extent that it becomes processed to a functional duplex, of e.g., 15-30 base pairs, that targets a desired RNA for cleavage, an RNA molecule or complex of RNA molecules having a duplex region greater than 30 base pairs is a dsRNA. Thus, an ordinarily skilled artisan will recognize that in one embodiment, a miRNA is a dsRNA. In another embodiment, a dsRNA is not a naturally occurring miRNA. In another embodiment, a RNAi agent useful to target coronavirus expression is not generated in the target cell by cleavage of a larger dsRNA.

A dsRNA as described herein can further include one or more single-stranded nucleotide overhangs e.g., 1, 2, 3, or 4 nucleotides. A nucleotide overhang can comprise or consist of a nucleotide/nucleoside analog, including a deoxynucleotide/nucleoside. The overhang(s) can be on the sense strand, the antisense strand or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5'-end, 3'-end or both ends of either an antisense or sense strand of a dsRNA. In certain embodiments, longer, extended overhangs are possible.

A dsRNA can be synthesized by standard methods known in the art as further discussed below, e.g., by use of an automated DNA synthesizer, such as are commercially available from, for example, Biosearch, Applied Biosystems, Inc.

iRNA compounds of the invention may be prepared using a two-step procedure. First, the individual strands of the

double stranded RNA molecule are prepared separately. Then, the component strands are annealed. The individual strands of the siRNA compound can be prepared using solution-phase or solid-phase organic synthesis or both. Organic synthesis offers the advantage that the oligonucleotide strands comprising unnatural or modified nucleotides can be easily prepared. Single-stranded oligonucleotides of the invention can be prepared using solution-phase or solid-phase organic synthesis or both.

An siRNA can be produced, e.g., in bulk, by a variety of methods. Exemplary methods include: organic synthesis and RNA cleavage, e.g., in vitro cleavage.

An siRNA can be made by separately synthesizing a single stranded RNA molecule, or each respective strand of a double-stranded RNA molecule, after which the component strands can then be annealed.

A large bioreactor, e.g., the OligoPilot II from Pharmacia Biotec AB (Uppsala Sweden), can be used to produce a large amount of a particular RNA strand for a given siRNA. The OligoPilotII reactor can efficiently couple a nucleotide using only a 1.5 molar excess of a phosphoramidite nucleotide. To make an RNA strand, ribonucleotides amidites are used. Standard cycles of monomer addition can be used to synthesize the 21 to 23 nucleotide strand for the siRNA. Typically, the two complementary strands are produced separately and then annealed, e.g., after release from the solid support and deprotection.

Organic synthesis can be used to produce a discrete siRNA species. The complementary of the species to a coronavirus genome can be precisely specified. For example, the species may be complementary to a region that includes a polymorphism, e.g., a single nucleotide polymorphism. Further the location of the polymorphism can be precisely defined. In some embodiments, the polymorphism is located in an internal region, e.g., at least 4, 5, 7, or 9 nucleotides from one or both of the termini.

In one embodiment, RNA generated is carefully purified to remove endsiRNA is cleaved in vitro into siRNAs, for example, using a Dicer or comparable RNase III-based activity. For example, the dsiRNA can be incubated in an in vitro extract from *Drosophila* or using purified components, e.g., a purified RNase or RISC complex (RNA-induced silencing complex). See, e.g., Ketting et al. *Genes Dev* 2001 Oct. 15; 15(20):2654-9 and Hammond *Science* 2001 Aug. 10; 293(5532):1146-50.

dsiRNA cleavage generally produces a plurality of siRNA species, each being a particular 21 to 23 nucleotide fragment of a source dsiRNA molecule. For example, siRNAs that include sequences complementary to overlapping regions and adjacent regions of a source dsiRNA molecule may be present.

Regardless of the method of synthesis, the siRNA preparation can be prepared in a solution (e.g., an aqueous or organic solution) that is appropriate for formulation. For example, the siRNA preparation can be precipitated and redissolved in pure double-distilled water, and lyophilized. The dried siRNA can then be resuspended in a solution appropriate for the intended formulation process.

In one aspect, a dsRNA of the disclosure includes at least two nucleotide sequences, a sense sequence and an antisense sequence. The sense strand sequence for coronavirus may be selected from the group of sequences provided in any one of Tables 2-5, and the corresponding nucleotide sequence of the antisense strand of the sense strand may be selected from the group of sequences of any one of Tables 2-5. In this aspect, one of the two sequences is complementary to the other of the two sequences, with one of the sequences being

substantially complementary to a sequence of a target coronavirus RNA, e.g., an mRNA generated in the expression of a coronavirus genome. As such, in this aspect, a dsRNA will include two oligonucleotides, where one oligonucleotide is described as the sense strand (passenger strand) in any one of Tables 2-5, and the second oligonucleotide is described as the corresponding antisense strand (guide strand) of the sense strand in any one of Tables 2-5 for coronavirus.

In certain embodiments of the invention, the sense strand or the antisense strand of the dsRNA agent is selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1184210, AD-1184270, AD-1184233, AD-1184271, AD-1184212, AD-1184228, AD-1184223, AD-1231490, AD-1231513, AD-1231485, AD-1231507, AD-1231471, AD-1231494, AD-1231496, and AD-1231497. In another embodiment, the sense strand or the antisense strand of the dsRNA agent is selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1231490, AD-1231513, AD-1231485, AD-1231471, AD-1231496, and AD-1231497. In another embodiment, the sense strand or the antisense strand of the dsRNA agent is selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137 and AD-1184150. In one embodiment, the sense strand or the antisense strand of the dsRNA agent is the sense strand or antisense strand of duplex AD-1184137. In another embodiment, the sense strand or the antisense strand of the dsRNA agent is the sense strand or antisense strand of duplex AD-1184150.

In one embodiment, the substantially complementary sequences of the dsRNA are contained on separate oligonucleotides. In another embodiment, the substantially complementary sequences of the dsRNA are contained on a single oligonucleotide.

It will be understood that, although the sequences provided herein are described as modified or conjugated sequences, the RNA of the RNAi agent of the disclosure e.g., a dsRNA of the disclosure, may comprise any one of the sequences set forth in any one of Tables 2-5 that is unmodified, un-conjugated, or modified or conjugated differently than described therein. One or more lipophilic ligands or one or more GalNAc ligands can be included in any of the positions of the RNAi agents provided in the instant application.

The skilled person is well aware that dsRNAs having a duplex structure of about 20 to 23 base pairs, e.g., 21, base pairs have been hailed as particularly effective in inducing RNA interference (Elbashir et al., (2001) *EMBO J.*, 20:6877-6888). However, others have found that shorter or longer RNA duplex structures can also be effective (Chu and Rana (2007) *RNA* 14:1714-1719; Kim et al. (2005) *Nat Biotech* 23:222-226). In the embodiments described above, by virtue of the nature of the oligonucleotide sequences provided herein, dsRNAs described herein can include at least one strand of a length of minimally 21 nucleotides. It can be reasonably expected that shorter duplexes minus only a few nucleotides on one or both ends can be similarly effective as compared to the dsRNAs described above. Hence, dsRNAs having a sequence of at least 15, 16, 17, 18, 19, 20, or more contiguous nucleotides derived from one of the sequences provided herein, and differing in their ability to inhibit the expression of a coronavirus genome by not more than 10, 15, 20, 25, or 30% inhibition from a dsRNA comprising the full sequence using the in vitro assay with Cos7 and a 10 nM concentration of the RNA agent and the

PCR assay as provided in the examples herein, are contemplated to be within the scope of the present disclosure.

In addition, the RNAs described herein identify a site(s) in a coronavirus transcript that is susceptible to RISC-mediated cleavage. As such, the present disclosure further features RNAi agents that target within this site(s). As used herein, a RNAi agent is said to target within a particular site of an RNA transcript if the RNAi agent promotes cleavage of the transcript anywhere within that particular site. Such a RNAi agent will generally include at least about 15 contiguous nucleotides, preferably at least 19 nucleotides, from one of the sequences provided herein coupled to additional nucleotide sequences taken from the region contiguous to the selected sequence in a coronavirus genome.

An RNAi agent as described herein can contain one or more mismatches to the target sequence. In one embodiment, an RNAi agent as described herein contains no more than 3 mismatches (i.e., 3, 2, 1, or 0 mismatches). In one embodiment, an RNAi agent as described herein contains no more than 2 mismatches. In one embodiment, an RNAi agent as described herein contains no more than 1 mismatch. In one embodiment, an RNAi agent as described herein contains 0 mismatches. In certain embodiments, if the antisense strand of the RNAi agent contains mismatches to the target sequence, the mismatch can optionally be restricted to be within the last 5 nucleotides from either the 5'- or 3'-end of the region of complementarity. For example, in such embodiments, for a 23 nucleotide RNAi agent, the strand which is complementary to a region of a coronavirus genome generally does not contain any mismatch within the central 13 nucleotides. The methods described herein or methods known in the art can be used to determine whether an RNAi agent containing a mismatch to a target sequence is effective in inhibiting the expression of a coronavirus genome. Consideration of the efficacy of RNAi agents with mismatches in inhibiting expression of a coronavirus genome is important, especially if the particular region of complementarity in a coronavirus genome is known to mutate.

### III. Modified RNAi Agents of the Disclosure

In one embodiment, the RNA of the RNAi agent of the disclosure e.g., a dsRNA, is un-modified, and does not comprise, e.g., chemical modifications or conjugations known in the art and described herein. In preferred embodiments, the RNA of an RNAi agent of the disclosure, e.g., a dsRNA, is chemically modified to enhance stability or other beneficial characteristics. In certain embodiments of the disclosure, substantially all of the nucleotides of an RNAi agent of the disclosure are modified. In other embodiments of the disclosure, all of the nucleotides of an RNAi agent of the disclosure are modified. RNAi agents of the disclosure in which "substantially all of the nucleotides are modified" are largely but not wholly modified and can include not more than 5, 4, 3, 2, or 1 unmodified nucleotides. In still other embodiments of the disclosure, RNAi agents of the disclosure can include not more than 5, 4, 3, 2 or 1 modified nucleotides.

The nucleic acids featured in the disclosure can be synthesized or modified by methods well established in the art, such as those described in "Current protocols in nucleic acid chemistry," Beaucage, S. L. et al. (Edrs.), John Wiley & Sons, Inc., New York, NY, USA, which is hereby incorporated herein by reference. Modifications include, for example, end modifications, e.g., 5'-end modifications (phosphorylation, conjugation, inverted linkages) or 3'-end

modifications (conjugation, DNA nucleotides, inverted linkages, etc.); base modifications, e.g., replacement with stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, removal of bases (abasic nucleotides), or conjugated bases; sugar modifications (e.g., at the 2'-position or 4'-position) or replacement of the sugar; or backbone modifications, including modification or replacement of the phosphodiester linkages. Specific examples of RNAi agents useful in the embodiments described herein include, but are not limited to, RNAs containing modified backbones or no natural internucleoside linkages. RNAs having modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In some embodiments, a modified RNAi agent will have a phosphorus atom in its internucleoside backbone.

Modified RNA backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5'-linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, e.g., sodium salts, mixed salts and free acid forms are also included.

Representative U.S. patents that teach the preparation of the above phosphorus-containing linkages include, but are not limited to, U.S. Pat. Nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,195; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,316; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,625,050; 6,028,188; 6,124,445; 6,160,109; 6,169,170; 6,172,209; 6,239,265; 6,277,603; 6,326,199; 6,346,614; 6,444,423; 6,531,590; 6,534,639; 6,608,035; 6,683,167; 6,858,715; 6,867,294; 6,878,805; 7,015,315; 7,041,816; 7,273,933; 7,321,029; and U.S. Pat. RE39464, the entire contents of each of which are hereby incorporated herein by reference.

Modified RNA backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatoms and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH<sub>2</sub> component parts.

Representative U.S. patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Pat. Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,64,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437;

and, 5,677,439, the entire contents of each of which are hereby incorporated herein by reference.

In other embodiments, suitable RNA mimetics are contemplated for use in RNAi agents, in which both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an RNA mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar backbone of an RNA is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly toaza nitrogen atoms of the amide portion of the backbone. Representative U.S. patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Pat. Nos. 5,539,082; 5,714,331; and 5,719,262, the entire contents of each of which are hereby incorporated herein by reference. Additional PNA compounds suitable for use in the RNAi agents of the disclosure are described in, for example, in Nielsen et al., *Science*, 1991, 254, 1497-1500.

Some embodiments featured in the disclosure include 25 RNAs with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular —CH<sub>2</sub>—NH—CH<sub>2</sub>—, —CH<sub>2</sub>—N(CH<sub>3</sub>)—O—CH<sub>2</sub>— [known as a methylene (methyleneimino) or MMI backbone], —CH<sub>2</sub>—O—N(CH<sub>3</sub>)—CH<sub>2</sub>—, —CH<sub>2</sub>—N(CH<sub>3</sub>)—N(CH<sub>3</sub>)—CH<sub>2</sub>— and 30 —N(CH<sub>3</sub>)—CH<sub>2</sub>—CH<sub>2</sub>— [wherein the native phosphodiester backbone is represented as —O—P—O—CH<sub>2</sub>—] of the above-referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above-referenced U.S. Pat. No. 5,602,240. In some embodiments, the RNAs featured herein have morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified RNAs can also contain one or more substituted sugar moieties. The RNAi agents, e.g., dsRNAs, featured herein can include one of the following at the 2'-position: 40 OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkyne can be substituted or unsubstituted C<sub>1</sub> to C<sub>10</sub> alkyl or C<sub>2</sub> to C<sub>10</sub> alkenyl and alkyne. Exemplary suitable modifications include O[(CH<sub>2</sub>)<sub>n</sub>O]<sub>m</sub>CH<sub>3</sub>, O(CH<sub>2</sub>)<sub>n</sub>OCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>n</sub>NH<sub>2</sub>, O(CH<sub>2</sub>)<sub>n</sub>CH<sub>3</sub>, O(CH<sub>2</sub>)<sub>n</sub>ONH<sub>2</sub>, and O(CH<sub>2</sub>)<sub>n</sub>ON[(CH<sub>2</sub>)<sub>n</sub>CH<sub>3</sub>]<sub>2</sub>, where n and m are from 1 to about 10. In other embodiments, dsRNAs include one of the following 45 at the 2' position: C<sub>1</sub> to C<sub>10</sub> lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH<sub>3</sub>, OCN, Cl, Br, CN, CF<sub>3</sub>, OCF<sub>3</sub>, SOCH<sub>3</sub>, SO<sub>2</sub>CH<sub>3</sub>, ONO<sub>2</sub>, NO<sub>2</sub>, N<sub>3</sub>, NH<sub>2</sub>, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA 50 cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of a RNAi agent, or a group for improving the pharmacodynamic properties of a RNAi agent, and other substituents having similar properties. In some embodiments, the modification includes a 2'-methoxyethoxy (2'-O—CH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub>, also known as 55 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin et al., *Helv. Chim. Acta*, 1995, 78:486-504) i.e., an alkoxy-alkoxy group. Another exemplary modification is 2'-dimethylaminoxyethoxy, i.e., a O(CH<sub>2</sub>)<sub>2</sub>ON(CH<sub>3</sub>)<sub>2</sub> group, also known as 2'-DMAOE, as described in examples herein below, and 2'-dimethylaminoethoxyethoxy (also known in the art as 60 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O—CH<sub>2</sub>—O—CH<sub>2</sub>—N(CH<sub>3</sub>)<sub>2</sub>. Further exemplary modifications include: 5'-Me-2'-F nucleotides, 5'-Me-2'-

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OMe nucleotides, 5'-Me-2'-deoxynucleotides, (both R and S isomers in these three families); 2'-alkoxyalkyl; and 2'-NMA (N-methylacetamide).

Other modifications include 2'-methoxy (2'-OCH<sub>3</sub>), 2'-aminopropoxy (2'-OCH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>NH<sub>2</sub>), 2'-O-hexadecyl, and 2'-fluoro (2'-F). Similar modifications can also be made at other positions on the RNA of a RNAi agent, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked dsRNAs and the 5' position of 5' terminal nucleotide. RNAi agents can also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative U.S. patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, certain of which are commonly owned with the instant application. The entire contents of each of the foregoing are hereby incorporated herein by reference.

An RNAi agent of the disclosure can also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiacytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo, particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-daazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in Modified Nucleosides in Biochemistry, Biotechnology and Medicine, Herdewijn, P. ed. Wiley-VCH, 2008; those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. L. ed. John Wiley & Sons, 1990, these disclosed by Englisch et al., (1991) *Angewandte Chemie, International Edition*, 30:613, and those disclosed by Sanghvi, Y.S., Chapter 15, dsRNA Research and Applications, pages 289-302, Crooke, S. T. and Lebleu, B., Ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds featured in the disclosure. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2° C. (Sanghvi, Y. S., Crooke, S. T. and Lebleu, B., Eds., dsRNA Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are exemplary base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative U.S. patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. Pat. Nos. 3,687,808, 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187;

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5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121; 5,596,091; 5,614,617; 5,681,941; 5,750,692; 6,015,886; 6,147,200; 6,166,197; 6,222,025; 6,235,887; 6,380,368; 6,528,640; 6,639,062; 6,617,438; 7,045,610; 7,427,672; and 7,495,088, the entire contents of each of which are hereby incorporated herein by reference.

An RNAi agent of the disclosure can also be modified to include one or more locked nucleic acids (LNA). A locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting the 2' and 4' carbons. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. et al., (2005) *Nucleic Acids Research* 33(1):439-447; Mook, O R. et al., (2007) *Mol Canc Ther* 6(3):833-843; Grunweller, A. et al., (2003) *Nucleic Acids Research* 31(12):3185-3193).

An RNAi agent of the disclosure can also be modified to include one or more bicyclic sugar moieties. A "bicyclic sugar" is a furanosyl ring modified by the bridging of two atoms. A "bicyclic nucleoside" ("BNA") is a nucleoside having a sugar moiety comprising a bridge connecting two carbon atoms of the sugar ring, thereby forming a bicyclic ring system. In certain embodiments, the bridge connects the 4'-carbon and the 2'-carbon of the sugar ring. Thus, in some embodiments an agent of the disclosure may include one or more locked nucleic acids (LNA). A locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting the 2' and 4' carbons. In other words, an LNA is a nucleotide comprising a bicyclic sugar moiety comprising a 4'-CH<sub>2</sub>-O-2' bridge. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. et al., (2005) *Nucleic Acids Research* 33(1):439-447; Mook, O R. et al., (2007) *Mol Canc Ther* 6(3):833-843; Grunweller, A. et al., (2003) *Nucleic Acids Research* 31(12):3185-3193). Examples of bicyclic nucleosides for use in the polynucleotides of the disclosure include without limitation nucleosides comprising a bridge between the 4' and the 2' ribosyl ring atoms. In certain embodiments, the antisense polynucleotide agents of the disclosure include one or more bicyclic nucleosides comprising a 4' to 2' bridge. Examples of such 4' to 2' bridged bicyclic nucleosides, include but are not limited to 4'-(CH<sub>2</sub>)<sub>2</sub>-O-2' (LNA); 4'-(CH<sub>2</sub>)<sub>2</sub>-S-2'; 4'-(CH<sub>2</sub>)<sub>2</sub>-O-2' (ENA); 4'-CH(CH<sub>3</sub>)-O-2' (also referred to as "constrained ethyl" or "cEt") and 4'-CH(CH<sub>2</sub>OCH<sub>3</sub>)-O-2' (and analogs thereof; see, e.g., U.S. Pat. No. 7,399,845); 4'-C(CH<sub>3</sub>)(CH<sub>3</sub>)-O-2' (and analogs thereof; see e.g., U.S. Pat. No. 8,278,283); 4'-CH<sub>2</sub>-N(OCH<sub>3</sub>)-2' (and analogs thereof; see e.g., U.S. Pat. No. 8,278,425); 4'-CH<sub>2</sub>-O-N(CH<sub>3</sub>)-2' (see, e.g., U.S. Patent Publication No. 2004/0171570); 4'-CH<sub>2</sub>-N(R)-O-2', wherein R is H, C<sub>1</sub>-C<sub>12</sub> alkyl, or a protecting group (see, e.g., U.S. Pat. No. 7,427,672); 4'-CH<sub>2</sub>-C(H)(CH<sub>3</sub>)-2' (see, e.g., Chattopadhyaya et al., *J. Org. Chem.*, 2009, 74, 118-134); and 4'-CH<sub>2</sub>-C(=CH<sub>2</sub>)-2' (and analogs thereof; see, e.g., U.S. Pat. No. 8,278,426). The entire contents of each of the foregoing are hereby incorporated herein by reference.

Additional representative US Patents and US Patent Publications that teach the preparation of locked nucleic acid nucleotides include, but are not limited to, the following:

U.S. Pat. Nos. 6,268,490; 6,525,191; 6,670,461; 6,770,748; 6,794,499; 6,998,484; 7,053,207; 7,034,133; 7,084,125; 7,399,845; 7,427,672; 7,569,686; 7,741,457; 8,022,193;

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8,030,467; 8,278,425; 8,278,426; 8,278,283; US 2008/0039618; and US 2009/0012281, the entire contents of each of which are hereby incorporated herein by reference.

Any of the foregoing bicyclic nucleosides can be prepared having one or more stereochemical sugar configurations including for example  $\alpha$ -L-ribofuranose and  $\beta$ -D-ribofuranose (see WO 99/14226).

An RNAi agent of the disclosure can also be modified to include one or more constrained ethyl nucleotides. As used herein, a “constrained ethyl nucleotide” or “cEt” is a locked nucleic acid comprising a bicyclic sugar moiety comprising a 4'-CH(CH<sub>3</sub>)-O-2' bridge. In one embodiment, a constrained ethyl nucleotide is in the S conformation referred to herein as “S-cEt.”

An RNAi agent of the disclosure may also include one or more “conformationally restricted nucleotides” (“CRN”). CRN are nucleotide analogs with a linker connecting the C2' and C4' carbons of ribose or the -C3' and -C5' carbons of ribose. CRN lock the ribose ring into a stable conformation and increase the hybridization affinity to mRNA. The linker is of sufficient length to place the oxygen in an optimal position for stability and affinity resulting in less ribose ring puckering.

Representative publications that teach the preparation of certain of the above noted CRN include, but are not limited to, US 2013/0190383; and WO 2013/036868, the entire contents of each of which are hereby incorporated herein by reference.

In some embodiments, a RNAi agent of the disclosure comprises one or more monomers that are UNA (unlocked nucleic acid) nucleotides. UNA is unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked “sugar” residue. In one example, UNA also encompasses monomer with bonds between C1'-C4' have been removed (i.e. the covalent carbon-oxygen-carbon bond between the C1' and C4' carbons). In another example, the C2'-C3' bond (i.e. the covalent carbon-carbon bond between the C2' and C3' carbons) of the sugar has been removed (see *Nuc. Acids Symp. Series*, 52, 133-134 (2008) and Fluitert et al., *Mol. Biosyst.*, 2009, 10, 1039 hereby incorporated by reference).

Representative U.S. publications that teach the preparation of UNA include, but are not limited to, U.S. Pat. No. 8,314,227; and US Patent Publication Nos. 2013/0096289; 2013/0011922; and 2011/0313020, the entire contents of each of which are hereby incorporated herein by reference.

Potentially stabilizing modifications to the ends of RNA molecules can include N-(acetylaminocaproyl)-4-hydroxyprolinol (Hyp-C6-NHAc), N-(caproyl)-4-hydroxyprolinol (Hyp-C6), N-(acetyl)-4-hydroxyprolinol (Hyp-NHAc), thymidine-2'-O-deoxythymidine (ether), N-(aminocaproyl)-4-hydroxyprolinol (Hyp-C6-amino), 2-docosanoyl-uridine-3"-phosphate, inverted base dT(idT) and others. Disclosure of this modification can be found in WO 2011/005861.

Other modifications of a RNAi agent of the disclosure include a 5' phosphate or 5' phosphate mimic, e.g., a 5'-terminal phosphate or phosphate mimic on the antisense strand of a RNAi agent. Suitable phosphate mimics are disclosed in, for example US 2012/0157511, the entire contents of which are incorporated herein by reference.

A. Modified RNAi agents Comprising Motifs of the Disclosure

In certain aspects of the disclosure, the double-stranded RNAi agents of the disclosure include agents with chemical modifications as disclosed, for example, in WO 2013/075035, the entire contents of which are incorporated herein by reference. As shown herein and in WO 2013/075035, a

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superior result may be obtained by introducing one or more motifs of three identical modifications on three consecutive nucleotides into a sense strand or antisense strand of an RNAi agent, particularly at or near the cleavage site. In some embodiments, the sense strand and antisense strand of the RNAi agent may otherwise be completely modified. The introduction of these motifs interrupts the modification pattern, if present, of the sense or antisense strand. The RNAi agent may be optionally conjugated with a lipophilic ligand, e.g., a C16 ligand, for instance on the sense strand. The RNAi agent may be optionally modified with a (S)-glycol nucleic acid (GNA) modification, for instance on one or more residues of the antisense strand. The resulting RNAi agents present superior gene silencing activity.

Accordingly, the disclosure provides double stranded RNAi agents capable of inhibiting the expression of a target genome or gene (i.e., a coronavirus genome or gene) in vivo. The RNAi agent comprises a sense strand and an antisense strand. Each strand of the RNAi agent may be 15-30 nucleotides in length. For example, each strand may be 16-30 nucleotides in length, 17-30 nucleotides in length, 25-30 nucleotides in length, 27-30 nucleotides in length, 17-23 nucleotides in length, 17-21 nucleotides in length, 17-19 nucleotides in length, 19-25 nucleotides in length, 19-23 nucleotides in length, 19-21 nucleotides in length, 21-25 nucleotides in length, or 21-23 nucleotides in length. In certain embodiments, each strand is 19-23 nucleotides in length.

The sense strand and antisense strand typically form a duplex double stranded RNA (“dsRNA”), also referred to herein as an “RNAi agent.” The duplex region of an RNAi agent may be 15-30 nucleotide pairs in length. For example, the duplex region can be 16-30 nucleotide pairs in length, 17-30 nucleotide pairs in length, 27-30 nucleotide pairs in length, 17-23 nucleotide pairs in length, 17-19 nucleotide pairs in length, 19-25 nucleotide pairs in length, 19-23 nucleotide pairs in length, 19-21 nucleotide pairs in length, 21-25 nucleotide pairs in length, or 21-23 nucleotide pairs in length. In another example, the duplex region is selected from 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 nucleotides in length. In preferred embodiments, the duplex region is 19-21 nucleotide pairs in length.

In one embodiment, the RNAi agent may contain one or more overhang regions or capping groups at the 3'-end, 5'-end, or both ends of one or both strands. The overhang can be 1-6 nucleotides in length, for instance 2-6 nucleotides in length, 1-5 nucleotides in length, 2-5 nucleotides in length, 1-4 nucleotides in length, 2-4 nucleotides in length, 1-3 nucleotides in length, 2-3 nucleotides in length, or 1-2 nucleotides in length. In preferred embodiments, the nucleotide overhang region is 2 nucleotides in length. The overhangs can be the result of one strand being longer than the other, or the result of two strands of the same length being staggered. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence. The first and second strands can also be joined, e.g., by additional bases to form a hairpin, or by other non-base linkers.

In one embodiment, the nucleotides in the overhang region of the RNAi agent can each independently be a modified or unmodified nucleotide including, but no limited to 2'-sugar modified, such as, 2-F, 2'-O-methyl, thymidine (T), and any combinations thereof.

For example, TT can be an overhang sequence for either end on either strand. The overhang can form a mismatch

with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence.

The 5'- or 3'-overhangs at the sense strand, antisense strand or both strands of the RNAi agent may be phosphorylated. In some embodiments, the overhang region(s) contains two nucleotides having a phosphorothioate between the two nucleotides, where the two nucleotides can be the same or different. In one embodiment, the overhang is present at the 3'-end of the sense strand, antisense strand, or both strands. In one embodiment, this 3'-overhang is present in the antisense strand. In one embodiment, this 3'-overhang is present in the sense strand.

The RNAi agent may contain only a single overhang, which can strengthen the interference activity of the RNAi, without affecting its overall stability. For example, the single-stranded overhang may be located at the 3-terminal end of the sense strand or, alternatively, at the 3-terminal end of the antisense strand. The RNAi may also have a blunt end, located at the 5'-end of the antisense strand (or the 3'-end of the sense strand) or vice versa. Generally, the antisense strand of the RNAi has a nucleotide overhang at the 3'-end, and the 5'-end is blunt. While not wishing to be bound by theory, the asymmetric blunt end at the 5'-end of the antisense strand and 3'-end overhang of the antisense strand favor the guide strand loading into RISC process.

In one embodiment, the RNAi agent is a double ended bluntmer of 19 nucleotides in length, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 7, 8, 9 from the 5'end. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, 13 from the 5'end.

In another embodiment, the RNAi agent is a double ended bluntmer of 20 nucleotides in length, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 8, 9, 10 from the 5'end. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, 13 from the 5'end.

In yet another embodiment, the RNAi agent is a double ended bluntmer of 21 nucleotides in length, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 9, 10, 11 from the 5'end. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, 13 from the 5'end.

In one embodiment, the RNAi agent comprises a 21 nucleotide sense strand and a 23 nucleotide antisense strand, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 9, 10, 11 from the 5'end; the antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, 13 from the 5'end, wherein one end of the RNAi agent is blunt, while the other end comprises a 2 nucleotide overhang. Preferably, the 2 nucleotide overhang is at the 3'-end of the antisense strand. When the 2 nucleotide overhang is at the 3'-end of the antisense strand, there may be two phosphorothioate internucleotide linkages between the terminal three nucleotides, wherein two of the three nucleotides are the overhang nucleotides, and the third nucleotide is a paired nucleotide next to the overhang nucleotide. In one embodiment, the RNAi agent additionally has two phosphorothioate internucleotide linkages between the terminal three nucleotides at both the 5'-end of the sense strand and at the 5'-end of the antisense strand. In one embodiment, every nucleotide in the sense strand and the antisense strand of the RNAi agent,

including the nucleotides that are part of the motifs are modified nucleotides. In one embodiment each residue is independently modified with a 2'-O-methyl or 3'-fluoro, e.g., in an alternating motif. Optionally, the RNAi agent further comprises a ligand (e.g., a lipophilic ligand, optionally a C16 ligand).

In one embodiment, the RNAi agent comprises a sense and an antisense strand, wherein the sense strand is 25-30 nucleotide residues in length, wherein starting from the 5' terminal nucleotide (position 1) positions 1 to 23 of the first strand comprise at least 8 ribonucleotides; the antisense strand is 36-66 nucleotide residues in length and, starting from the 3' terminal nucleotide, comprises at least 8 ribonucleotides in the positions paired with positions 1-23 of sense strand to form a duplex; wherein at least the 3' terminal nucleotide of antisense strand is unpaired with sense strand, and up to 6 consecutive 3' terminal nucleotides are unpaired with sense strand, thereby forming a 3' single stranded overhang of 1-6 nucleotides; wherein the 5' terminus of antisense strand comprises from 10-30 consecutive nucleotides which are unpaired with sense strand, thereby forming a 10-30 nucleotide single stranded 5' overhang; wherein at least the sense strand 5' terminal and 3' terminal nucleotides are base paired with nucleotides of antisense strand when sense and antisense strands are aligned for maximum complementarity, thereby forming a substantially duplexed region between sense and antisense strands; and antisense strand is sufficiently complementary to a target RNA along at least 19 ribonucleotides of antisense strand length to reduce target gene expression when the double stranded nucleic acid is introduced into a mammalian cell; and wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides, where at least one of the motifs occurs at or near the cleavage site. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at or near the cleavage site.

In one embodiment, the RNAi agent comprises sense and antisense strands, wherein the RNAi agent comprises a first strand having a length which is at least 25 and at most 29 nucleotides and a second strand having a length which is at most 30 nucleotides with at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at position 11, 12, 13 from the 5' end; wherein the 3' end of the first strand and the 5' end of the second strand form a blunt end and the second strand is 1-4 nucleotides longer at its 3' end than the first strand, wherein the duplex region which is at least 25 nucleotides in length, and the second strand is sufficiently complementary to a target mRNA along at least 19 nucleotide of the second strand length to reduce target gene expression when the RNAi agent is introduced into a mammalian cell, and wherein dicer cleavage of the RNAi agent preferentially results in an siRNA comprising the 3' end of the second strand, thereby reducing expression of the target gene in the mammal. Optionally, the RNAi agent further comprises a ligand.

In one embodiment, the sense strand of the RNAi agent contains at least one motif of three identical modifications on three consecutive nucleotides, where one of the motifs occurs at the cleavage site in the sense strand.

In one embodiment, the antisense strand of the RNAi agent can also contain at least one motif of three identical modifications on three consecutive nucleotides, where one of the motifs occurs at or near the cleavage site in the antisense strand.

For an RNAi agent having a duplex region of 17-23 nucleotide in length, the cleavage site of the antisense strand

is typically around the 10, 11 and 12 positions from the 5'-end. Thus the motifs of three identical modifications may occur at the 9, 10, 11 positions; 10, 11, 12 positions; 11, 12, 13 positions; 12, 13, 14 positions; or 13, 14, 15 positions of the antisense strand, the count starting from the 1<sup>st</sup> nucleotide from the 5'-end of the antisense strand, or, the count starting from the 1<sup>st</sup> paired nucleotide within the duplex region from the 5'-end of the antisense strand. The cleavage site in the antisense strand may also change according to the length of the duplex region of the RNAi from the 5'-end.

The sense strand of the RNAi agent may contain at least one motif of three identical modifications on three consecutive nucleotides at the cleavage site of the strand; and the antisense strand may have at least one motif of three identical modifications on three consecutive nucleotides at or near the cleavage site of the strand. When the sense strand and the antisense strand form a dsRNA duplex, the sense strand and the antisense strand can be so aligned that one motif of the three nucleotides on the sense strand and one motif of the three nucleotides on the antisense strand have at least one nucleotide overlap, i.e., at least one of the three nucleotides of the motif in the sense strand forms a base pair with at least one of the three nucleotides of the motif in the antisense strand. Alternatively, at least two nucleotides may overlap, or all three nucleotides may overlap.

In one embodiment, the sense strand of the RNAi agent may contain more than one motif of three identical modifications on three consecutive nucleotides. The first motif may occur at or near the cleavage site of the strand and the other motifs may be a wing modification. The term "wing modification" herein refers to a motif occurring at another portion of the strand that is separated from the motif at or near the cleavage site of the same strand. The wing modification is either adjacent to the first motif or is separated by at least one or more nucleotides. When the motifs are immediately adjacent to each other then the chemistry of the motifs are distinct from each other and when the motifs are separated by one or more nucleotide than the chemistries can be the same or different. Two or more wing modifications may be present. For instance, when two wing modifications are present, each wing modification may occur at one end relative to the first motif which is at or near cleavage site or on either side of the lead motif.

Like the sense strand, the antisense strand of the RNAi agent may contain more than one motif of three identical modifications on three consecutive nucleotides, with at least one of the motifs occurring at or near the cleavage site of the strand. This antisense strand may also contain one or more wing modifications in an alignment similar to the wing modifications that may be present on the sense strand.

In one embodiment, the wing modification on the sense strand or antisense strand of the RNAi agent typically does not include the first one or two terminal nucleotides at the 3'-end, 5'-end or both ends of the strand.

In another embodiment, the wing modification on the sense strand or antisense strand of the RNAi agent typically does not include the first one or two paired nucleotides within the duplex region at the 3<sup>1</sup>-end, 5<sup>1</sup>-end or both ends of the strand.

When the sense strand and the antisense strand of the RNAi agent each contain at least one wing modification, the wing modifications may fall on the same end of the duplex region, and have an overlap of one, two or three nucleotides.

When the sense strand and the antisense strand of the RNAi agent each contain at least two wing modifications, the sense strand and the antisense strand can be so aligned that two modifications each from one strand fall on one end

of the duplex region, having an overlap of one, two or three nucleotides; two modifications each from one strand fall on the other end of the duplex region, having an overlap of one, two or three nucleotides; two modifications one strand fall on each side of the lead motif, having an overlap of one, two, or three nucleotides in the duplex region.

In one embodiment, the RNAi agent comprises mismatch (es) with the target, within the duplex, or combinations thereof. The mismatch may occur in the overhang region or 10 the duplex region. The base pair may be ranked on the basis of their propensity to promote dissociation or melting (e.g., on the free energy of association or dissociation of a particular pairing, the simplest approach is to examine the pairs on an individual pair basis, though next neighbor or 15 similar analysis can also be used). In terms of promoting dissociation: A:U is preferred over G:C; G:U is preferred over G:C; and I:C is preferred over G:C (I=inosine). Mismatches, e.g., non-canonical or other than canonical pairings 20 (as described elsewhere herein) are preferred over canonical (A:T, A:U, G:C) pairings; and pairings which include a universal base are preferred over canonical pairings.

In one embodiment, the RNAi agent comprises at least one of the first 1, 2, 3, 4, or 5 base pairs within the duplex regions from the 5'-end of the antisense strand independently 25 selected from the group of: A:U, G:U, I:C, and mismatched pairs, e.g., non-canonical or other than canonical pairings or pairings which include a universal base, to promote the dissociation of the antisense strand at the 5'-end of the duplex.

30 In one embodiment, the nucleotide at the 1 position within the duplex region from the 5'-end in the antisense strand is selected from the group consisting of A, dA, dU, U, and dT. Alternatively, at least one of the first 1, 2 or 3 base pair within the duplex region from the 5'-end of the antisense strand is an AU base pair. For example, the first base pair within the duplex region from the 5'-end of the antisense strand is an AU base pair.

In another embodiment, the nucleotide at the 3'-end of the sense strand is deoxy-thymine (dT). In another embodiment, 40 the nucleotide at the 3'-end of the antisense strand is deoxy-thymine (dT). In one embodiment, there is a short sequence of deoxy-thymine nucleotides, for example, two dT nucleotides on the 3'-end of the sense or antisense strand.

In one embodiment, the sense strand sequence may be 45 represented by formula (I):



wherein:

i and j are each independently 0 or 1;

p and q are each independently 0-6;

each  $N_a$  independently represents an oligonucleotide sequence comprising 0-25 modified nucleotides, each sequence comprising at least two differently modified nucleotides;

each  $N_b$  independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides; each  $n_p$  and  $n_q$  independently represent an overhang nucleotide;

wherein Nb and Y do not have the same modification; and XXX, YYY and ZZZ each independently represent one motif of three identical modifications on three consecutive nucleotides. Preferably YYY is all 2'-F modified nucleotides.

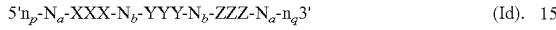
In one embodiment, the  $N_a$  or  $N_b$  comprise modifications of alternating pattern.

In one embodiment, the YYY motif occurs at or near the cleavage site of the sense strand. For example, when the

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RNAi agent has a duplex region of 17-23 nucleotides in length, the YYY motif can occur at or the vicinity of the cleavage site (e.g.: can occur at positions 6, 7, 8, 7, 8, 9, 8, 9, 10, 9, 10, 11, 10, 11, 12 or 11, 12, 13) of—the sense strand, the count starting from the 1<sup>st</sup> nucleotide, from the 5'-end; or optionally, the count starting at the 1<sup>st</sup> paired nucleotide within the duplex region, from the 5'-end. Preferably, the Y'Y'Y' motif occurs at positions 11, 12, 13.

In one embodiment, i is 1 and j is 0, or i is 0 and j is 1, or both i and j are 1. The sense strand can therefore be represented by the following formulas:



When the sense strand is represented by formula (Ib), N<sub>b</sub> represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides.

Each N<sub>a</sub> independently can represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the sense strand is represented as formula (Ic), N<sub>b</sub> represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N<sub>a</sub> can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the sense strand is represented as formula (Id), each N<sub>b</sub> independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Preferably, N<sub>b</sub> is 0, 1, 2, 3, 4, 5 or 6. Each N<sub>a</sub> can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

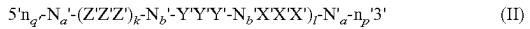
Each of X, Y and Z may be the same or different from each other.

In other embodiments, i is 0 and j is 0, and the sense strand may be represented by the formula:



When the sense strand is represented by formula (Ia), each N<sub>a</sub> independently can represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

In one embodiment, the antisense strand sequence of the RNAi may be represented by formula (II):



wherein:

k and l are each independently 0 or 1;

p' and q' are each independently 0-6;

each N<sub>a</sub>' independently represents an oligonucleotide sequence comprising 0-25 modified nucleotides, each sequence comprising at least two differently modified nucleotides;

each N<sub>b</sub>' independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

each n<sub>p</sub>' and n<sub>q</sub>' independently represent an overhang nucleotide;

wherein N<sub>b</sub>' and Y' do not have the same modification; and X'X'X, Y'Y'Y' and Z'Z'Z' each independently represent one motif of three identical modifications on three consecutive nucleotides.

In one embodiment, the N<sub>a</sub>' or N<sub>b</sub>' comprise modifications of alternating pattern.

The Y'Y'Y' motif occurs at or near the cleavage site of the antisense strand. For example, when the RNAi agent has a duplex region of 17-23 nucleotide in length, the Y'Y'Y' motif can occur at positions 9, 10, 11; 10, 11, 12; 11, 12, 13; 12, 13, 14; or 13, 14, 15 of the antisense strand, with the count

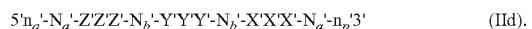
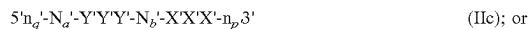
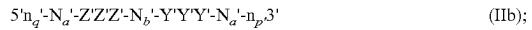
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starting from the 1<sup>st</sup> nucleotide, from the 5'-end; or optionally, the count starting at the 1<sup>st</sup> paired nucleotide within the duplex region, from the 5'-end. Preferably, the Y'Y'Y' motif occurs at positions 11, 12, 13.

In one embodiment, Y'Y'Y' motif is all 2'-OMe modified nucleotides.

In one embodiment, k is 1 and l is 0, or k is 0 and l is 1, or both k and l are 1.

The antisense strand can therefore be represented by the following formulas:



When the antisense strand is represented by formula (IIb), N<sub>b</sub>' represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N<sub>a</sub>' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the antisense strand is represented as formula (IIc), N<sub>b</sub>' represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N<sub>a</sub>' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the antisense strand is represented as formula (IID), each N<sub>b</sub>' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N<sub>a</sub>' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. Preferably, N<sub>b</sub> is 0, 1, 2, 3, 4, 5 or 6.

In other embodiments, k is 0 and l is 0 and the antisense strand may be represented by the formula:



When the antisense strand is represented as formula (IIa), each N<sub>a</sub>' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

Each of X', Y' and Z' may be the same or different from each other.

Each nucleotide of the sense strand and antisense strand may be independently modified with LNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-methyl, 2'-O-allyl, 2'-C-allyl, 2'-hydroxyl, or 2'-fluoro. For example, each nucleotide of the sense strand and antisense strand is independently modified with 2'-O-methyl or 2'-fluoro. Each X, Y, Z, X', Y' and Z', in particular, may represent a 2'-O-methyl modification or a 2'-fluoro modification.

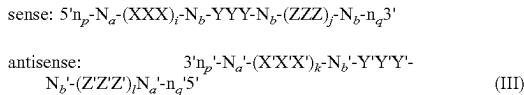
In one embodiment, the sense strand of the RNAi agent may contain YYY motif occurring at 9, 10 and 11 positions of the strand when the duplex region is 21 nt, the count starting from the 1<sup>st</sup> nucleotide from the 5'-end, or optionally, the count starting at the 1<sup>st</sup> paired nucleotide within the duplex region, from the 5'-end; and Y represents 2'-F modification. The sense strand may additionally contain XXX motif or ZZZ motifs as wing modifications at the opposite end of the duplex region; and XXX and ZZZ each independently represents a 2'-OMe modification or 2'-F modification.

In one embodiment the antisense strand may contain Y'Y'Y' motif occurring at positions 11, 12, 13 of the strand, the count starting from the 1<sup>st</sup> nucleotide from the 5'-end, or optionally, the count starting at the 1<sup>st</sup> paired nucleotide within the duplex region, from the 5'-end; and Y' represents 2'-O-methyl modification. The antisense strand may addi-

tionally contain X'X'X' motif or Z'Z'Z' motifs as wing modifications at the opposite end of the duplex region; and X'X'X' and Z'Z'Z' each independently represents a 2'-OMe modification or 2'-F modification.

The sense strand represented by any one of the above formulas (Ia), (Ib), (Ic), and (Id) forms a duplex with a antisense strand being represented by any one of formulas (IIa), (IIb), (IIc), and (IID), respectively.

Accordingly, the RNAi agents for use in the methods of the disclosure may comprise a sense strand and an antisense strand, each strand having 14 to 30 nucleotides, the RNAi duplex represented by formula (III):

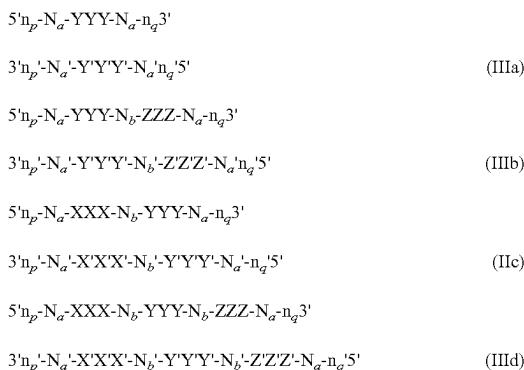


wherein:

- i, j, k, and l are each independently 0 or 1;
- p, p', q, and q' are each independently 0-6;
- each N<sub>a</sub> and N<sub>a'</sub> independently represents an oligonucleotide sequence comprising 0-25 modified nucleotides, each sequence comprising at least two differently modified nucleotides;
- each N<sub>b</sub> and N<sub>b'</sub> independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides; wherein
- each n<sub>p</sub>', n<sub>p</sub>, n<sub>q</sub>', and n<sub>q</sub>, each of which may or may not be present, independently represents an overhang nucleotide; and
- XXX, YYY, ZZZ, X'X'X', Y'Y'Y', and Z'Z'Z' each independently represent one motif of three identical modifications on three consecutive nucleotides.

In one embodiment, i is 0 and j is 0; or i is 1 and j is 1; or i is 0 and j is 1; or both i and j are 0; or both i and j are 1. In another embodiment, k is 0 and l is 0; or k is 1 and l is 0; k is 0 and l is 1; or both k and l are 0; or both k and l are 1.

Exemplary combinations of the sense strand and antisense strand forming a RNAi duplex include the formulas below:



When the RNAi agent is represented by formula (IIIa), each N<sub>a</sub> independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the RNAi agent is represented by formula (IIIb), each N<sub>b</sub> independently represents an oligonucleotide sequence comprising 1-10, 1-7, 1-5 or 1-4 modified nucleotides. Each N<sub>a</sub> independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the RNAi agent is represented as formula (IIIc), each N<sub>b</sub>, N<sub>b'</sub> independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0

modified nucleotides. Each N<sub>a</sub> independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the RNAi agent is represented as formula (IID), each N<sub>b</sub>, N<sub>b'</sub> independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N<sub>a</sub>, N<sub>a'</sub> independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. Each of N<sub>a</sub>, N<sub>a'</sub>, N<sub>b</sub> and N<sub>b'</sub> independently comprises modifications of alternating pattern.

In one embodiment, when the RNAi agent is represented by formula (IIIa), the N<sub>a</sub> modifications are 2'-O-methyl or 2'-fluoro modifications. In another embodiment, when the RNAi agent is represented by formula (IIIb), the N<sub>a</sub> modifications are 2'-O-methyl or 2'-fluoro modifications and n<sub>p</sub>'>0 and at least one n<sub>p</sub>' is linked to a neighboring nucleotide a via phosphorothioate linkage. In yet another embodiment, when the RNAi agent is represented by formula (IIIc), the N<sub>a</sub> modifications are 2'-O-methyl or 2'-fluoro modifications, n<sub>p</sub>'>0 and at least one n<sub>p</sub>' is linked to a neighboring nucleotide via phosphorothioate linkage, and the sense strand is conjugated to one or more C16 (or related) moieties attached through a bivalent or trivalent branched linker (described below). In another embodiment, when the RNAi agent is represented by formula (IID), the N<sub>a</sub> modifications are 2'-O-methyl or 2'-fluoro modifications, n<sub>p</sub>'>0 and at least one n<sub>p</sub>' is linked to a neighboring nucleotide via phosphorothioate linkage, the sense strand comprises at least one phosphorothioate linkage, and the sense strand is conjugated to one or more lipophilic, e.g., C16 (or related) moieties, optionally attached through a bivalent or trivalent branched linker.

In one embodiment, when the RNAi agent is represented by formula (IIIa), the N<sub>a</sub> modifications are 2'-O-methyl or 2'-fluoro modifications, n<sub>p</sub>'>0 and at least one n<sub>p</sub>' is linked to a neighboring nucleotide via phosphorothioate linkage, the sense strand comprises at least one phosphorothioate linkage, and the sense strand is conjugated to one or more lipophilic, e.g., C16 (or related) moieties attached through a bivalent or trivalent branched linker.

In one embodiment, the RNAi agent is a multimer containing at least two duplexes represented by formula (III), (IIIa), (IIIb), (IIIc), and (IID), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable. Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

In one embodiment, the RNAi agent is a multimer containing three, four, five, six or more duplexes represented by formula (III), (IIIa), (IIIb), (IIIc), and (IID), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable. Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

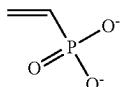
In one embodiment, two RNAi agents represented by formula (III), (IIIa), (IIIb), (IIIc), and (IID) are linked to each other at the 5' end, and one or both of the 3' ends are optionally conjugated to a ligand. Each of the agents can target the same gene or two different genes; or each of the agents can target same gene at two different target sites.

Various publications describe multimeric RNAi agents that can be used in the methods of the disclosure. Such publications include WO2007/091269, WO2010/141511, WO2007/117686, WO2009/014887, and WO2011/031520;

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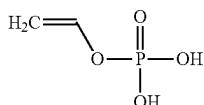
and U.S. Pat. No. 7,858,769, the entire contents of each of which are hereby incorporated herein by reference.

In certain embodiments, the compositions and methods of the disclosure include a vinyl phosphonate (VP) modification of an RNAi agent as described herein. In exemplary embodiments, a vinyl phosphonate of the disclosure has the following structure:



A vinyl phosphonate of the instant disclosure may be attached to either the antisense or the sense strand of a dsRNA of the disclosure. In certain preferred embodiments, a vinyl phosphonate of the instant disclosure is attached to the antisense strand of a dsRNA, optionally at the 5' end of the antisense strand of the dsRNA.

Vinyl phosphate modifications are also contemplated for the compositions and methods of the instant disclosure. An exemplary vinyl phosphate structure is:



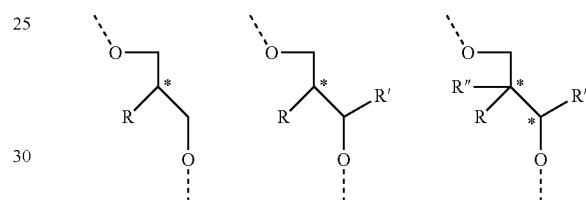
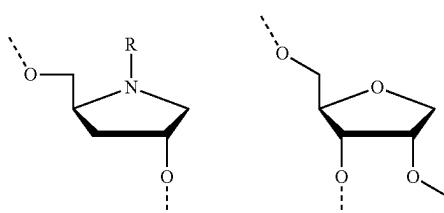
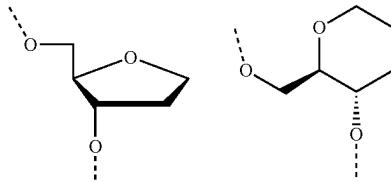
#### E. Thermally Destabilizing Modifications

In certain embodiments, a dsRNA molecule can be optimized for RNA interference by incorporating thermally destabilizing modifications in the seed region of the antisense strand (i.e., at positions 2-9 of the 5'-end of the antisense strand) to reduce or inhibit off-target gene silencing. It has been discovered that dsRNAs with an antisense strand comprising at least one thermally destabilizing modification of the duplex within the first 9 nucleotide positions, counting from the 5' end, of the antisense strand have reduced off-target gene silencing activity. Accordingly, in some embodiments, the antisense strand comprises at least one (e.g., one, two, three, four, five or more) thermally destabilizing modification of the duplex within the first 9 nucleotide positions of the 5' region of the antisense strand. In some embodiments, one or more thermally destabilizing modification(s) of the duplex is/are located in positions 2-9, or preferably positions 4-8, from the 5'-end of the antisense strand. In some further embodiments, the thermally destabilizing modification(s) of the duplex is/are located at position 6, 7 or 8 from the 5'-end of the antisense strand. In still some further embodiments, the thermally destabilizing modification of the duplex is located at position 7 from the 5'-end of the antisense strand. The term "thermally destabilizing modification(s)" includes modification(s) that would result with a dsRNA with a lower overall melting temperature (T<sub>m</sub>) (preferably a T<sub>m</sub> with one, two, three or four degrees lower than the T<sub>m</sub> of the dsRNA without having such modification(s)). In some embodiments, the thermally destabilizing modification of the duplex is located at position 2, 3, 4, 5 or 9 from the 5'-end of the antisense strand.

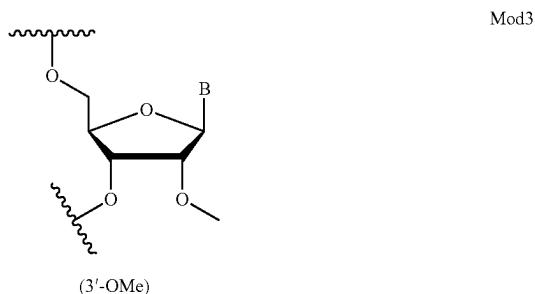
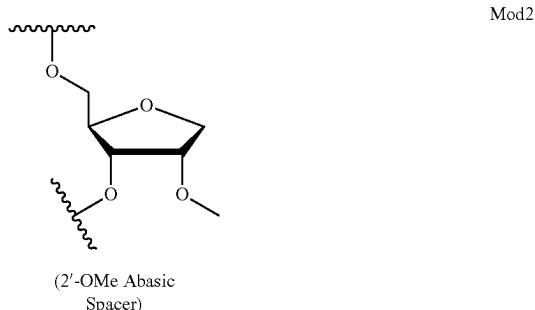
The thermally destabilizing modifications can include, but are not limited to, abasic modification; mismatch with the opposing nucleotide in the opposing strand; and sugar modification such as 2'-deoxy modification or acyclic nucleotide, e.g., unlocked nucleic acids (UNA) or glycol nucleic acid (GNA).

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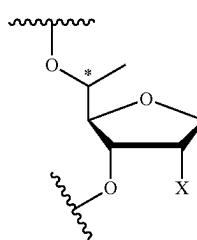
Exemplified abasic modifications include, but are not limited to the following:



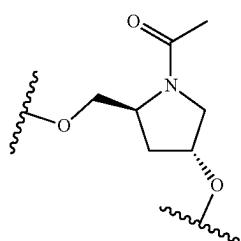
Wherein R=H, Me, Et or OMe; R' H, Me, Et or OMe; R''=H, Me, Et or OMe



**57**  
-continued



(*S*<sup>5'</sup>-Me)  
X = OMe, F



(Hyp-spacer)

Mod4

5

unlocked nucleic acid

R = H, OH, CH<sub>3</sub>, CH<sub>2</sub>CH<sub>3</sub>, O-alkyl, NH<sub>2</sub>, NHMe, NMe<sub>2</sub>

R' = H, OH, CH<sub>3</sub>, CH<sub>2</sub>CH<sub>3</sub>, O-alkyl, NH<sub>2</sub>, NHMe, NMe<sub>2</sub>

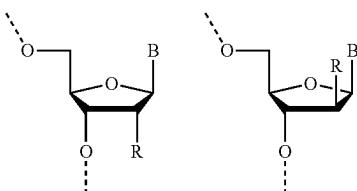
R'' = H, OH, CH<sub>3</sub>, CH<sub>2</sub>CH<sub>3</sub>, O-alkyl, NH<sub>2</sub>, NHMe, NMe<sub>2</sub>

R''' = H, OH, CH<sub>3</sub>, CH<sub>2</sub>CH<sub>3</sub>, O-alkyl, NH<sub>2</sub>, NHMe, NMe<sub>2</sub>

R''''' = H, OH, CH<sub>3</sub>, CH<sub>2</sub>CH<sub>3</sub>, O-alkyl, NH<sub>2</sub>, NHMe, NMe<sub>2</sub>

Mod5

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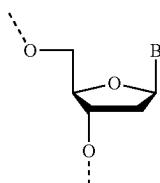
R = H, methyl, ethyl

wherein B is a modified or unmodified nucleobase.

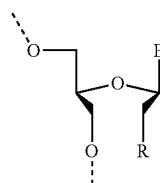
In some embodiments the thermally destabilizing modification of the duplex is selected from the group consisting of:

wherein B is a modified or unmodified nucleobase.

Exemplified sugar modifications include, but are not limited to the following:

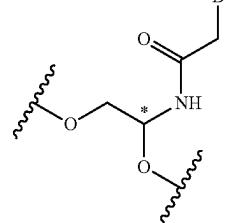
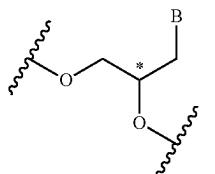


2'-deoxy



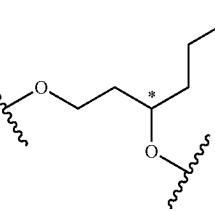
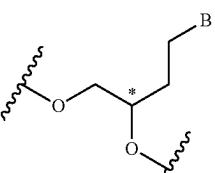
unlocked nucleic acid  
R = H, OH, O-alkyl

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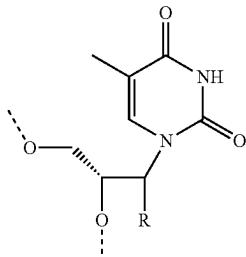
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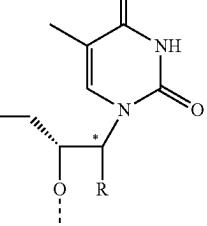
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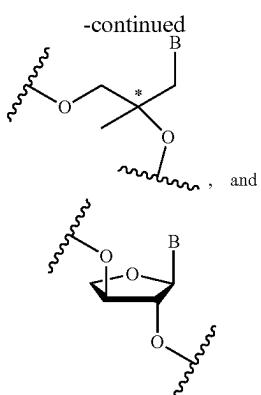


glycol nucleic acid  
R = H, OH, O-alkyl



glycol nucleic acid  
R = H, OH, O-alkyl

59



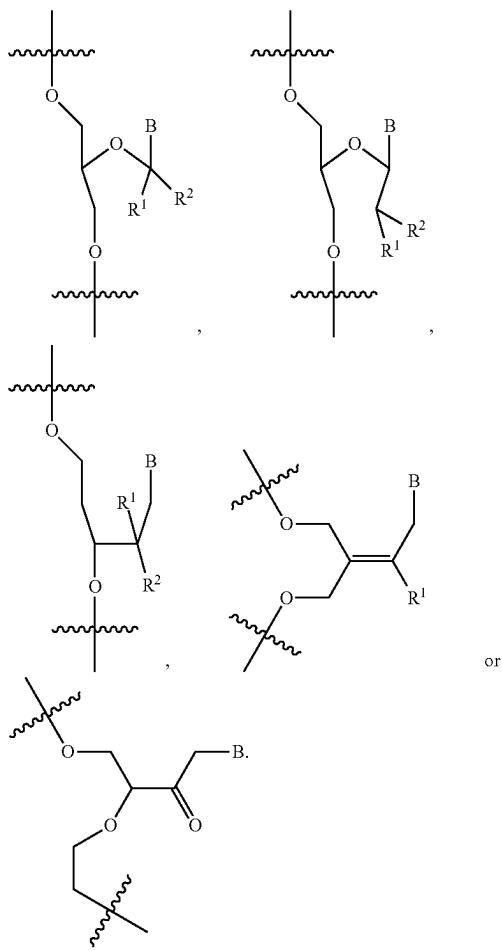
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alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or sugar). The term "UNA" refers to unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked "sugar" residue. In one example, UNA also encompasses monomers with bonds between C1'-C4' being removed (i.e. the covalent carbon-oxygen-carbon bond between the C1' and C4' carbons). In another example, the C2'-C3' bond (i.e. the covalent carbon-carbon bond between the C2' and C3' carbons) of the sugar is removed (see Mikhailov et. al., Tetrahedron Letters, 26 (17): 2059 (1985); and Fluitier et al., Mol. Biosyst., 10: 1039 (2009), which are hereby incorporated by reference in their entirety). The acyclic derivative provides greater backbone flexibility without affecting the Watson-Crick pairings. The acyclic nucleotide can be linked via 2'-5' or 3'-5' linkage.

The term 'GNA' refers to glycol nucleic acid which is a polymer similar to DNA or RNA but differing in the composition of its "backbone" in that it is composed of repeating glycerol units linked by phosphodiester bonds:

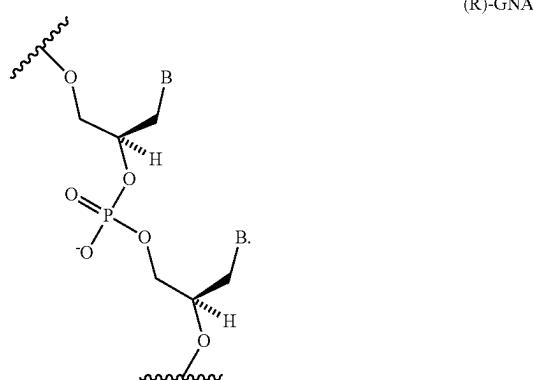
wherein B is a modified or unmodified nucleobase and the asterisk on each structure represents either R, S or racemic.

The term "acyclic nucleotide" refers to any nucleotide having an acyclic ribose sugar, for example, where any of bonds between the ribose carbons (e.g., C1'-C2', C2'-C3', C3'-C4', C4'-O4', or C1'-O4') is absent or at least one of ribose carbons or oxygen (e.g., C1', C2', C3', C4', or O4') are independently or in combination absent from the nucleotide. In some embodiments, acyclic nucleotide is



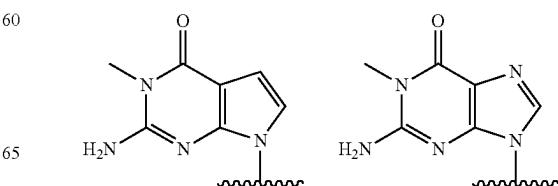
wherein B is a modified or unmodified nucleobase, R<sup>1</sup> and R<sup>2</sup> independently are H, halogen, OR<sub>3</sub>, or alkyl; and R<sub>3</sub> is H,

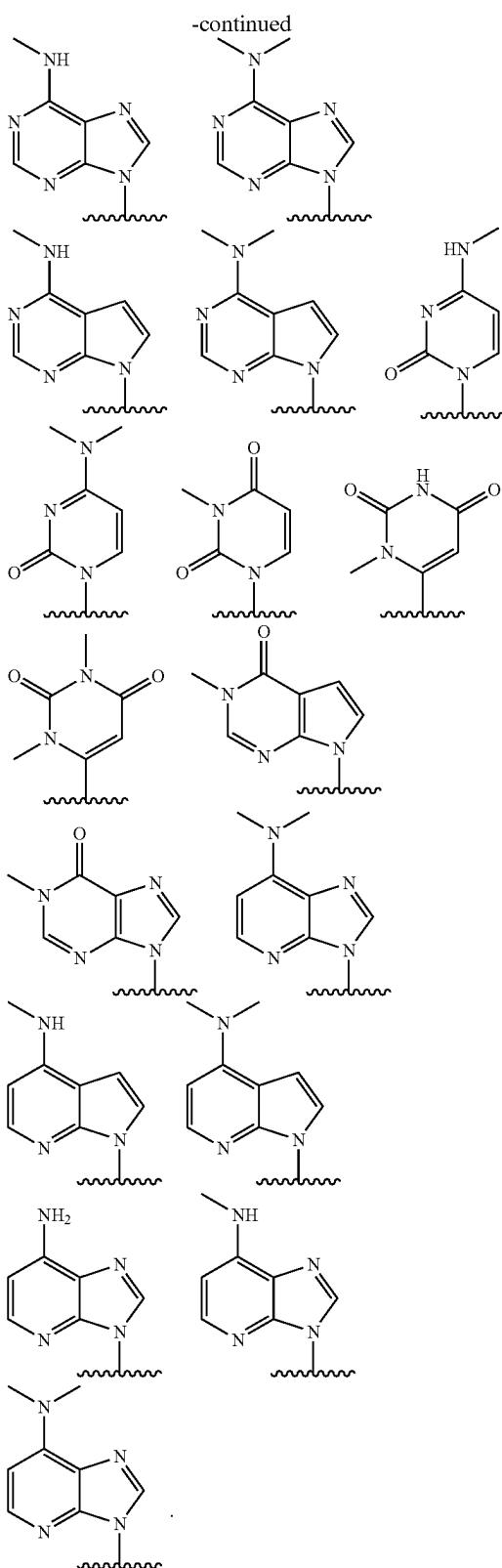
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The thermally destabilizing modification of the duplex can be mismatches (i.e., noncomplementary base pairs) between the thermally destabilizing nucleotide and the opposing nucleotide in the opposite strand within the dsRNA duplex. Exemplary mismatch base pairs include G:G, G:A, G:U, G:T, A:A, A:C, C:C, C:U, C:T, U:U, T:T, U:T, or a combination thereof. Other mismatch base pairings known in the art are also amenable to the present invention. A mismatch can occur between nucleotides that are either naturally occurring nucleotides or modified nucleotides, i.e., the mismatch base pairing can occur between the nucleobases from respective nucleotides independent of the modifications on the ribose sugars of the nucleotides. In certain embodiments, the dsRNA molecule contains at least one nucleobase in the mismatch pairing that is a 2'-deoxy nucleobase; e.g., the 2'-deoxy nucleobase is in the sense strand.

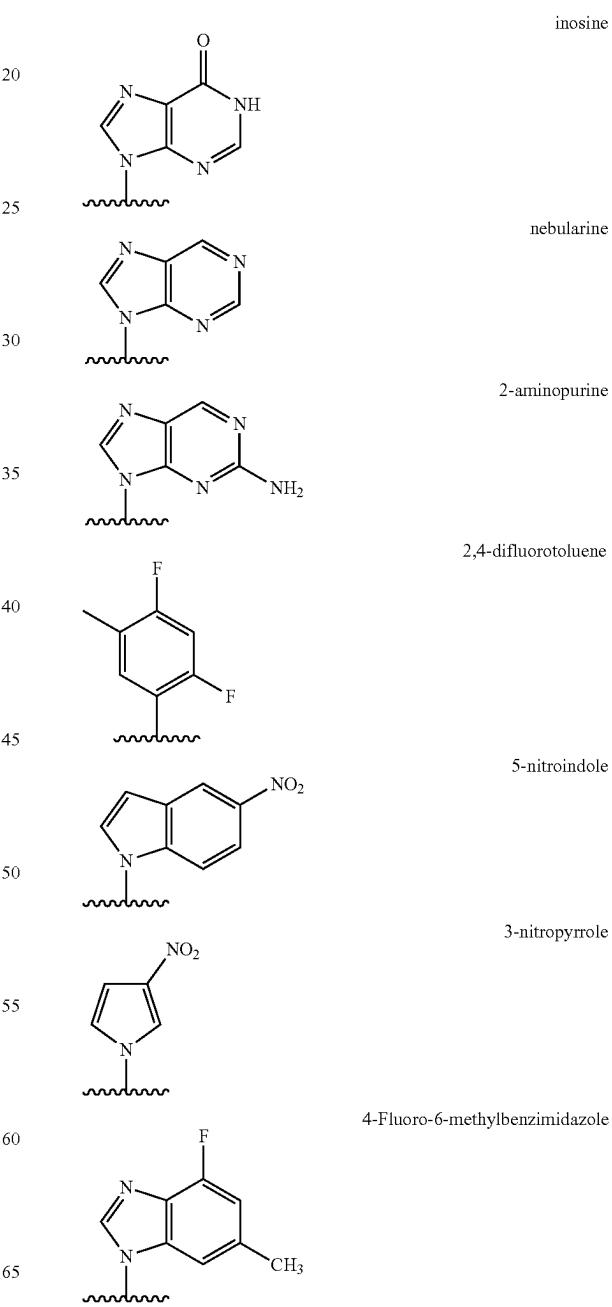
In some embodiments, the thermally destabilizing modification of the duplex in the seed region of the antisense strand includes nucleotides with impaired W—C H-bonding to complementary base on the target mRNA, such as:



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The thermally destabilizing modifications may also include universal base with reduced or abolished capability to form hydrogen bonds with the opposing bases, and phosphate modifications.

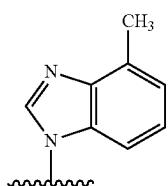
In some embodiments, the thermally destabilizing modification of the duplex includes nucleotides with non-canonical bases such as, but not limited to, nucleobase modifications with impaired or completely abolished capability to form hydrogen bonds with bases in the opposite strand. These nucleobase modifications have been evaluated for destabilization of the central region of the dsRNA duplex as described in WO 2010/0011895, which is herein incorporated by reference in its entirety. Exemplary nucleobase modifications are:



More examples of abasic nucleotide, acyclic nucleotide modifications (including UNA and GNA), and mismatch modifications have been described in detail in WO 2011/133876, which is herein incorporated by reference in its entirety.

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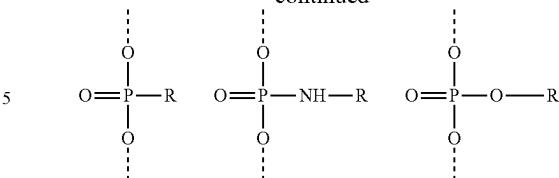
-continued



4-Methylbenzimidazole

**64**

-continued



10      R=alkyl

The alkyl for the R group can be a C<sub>1</sub>-C<sub>6</sub>alkyl. Specific alkyls for the R group include, but are not limited to methyl, ethyl, propyl, isopropyl, butyl, pentyl and hexyl.

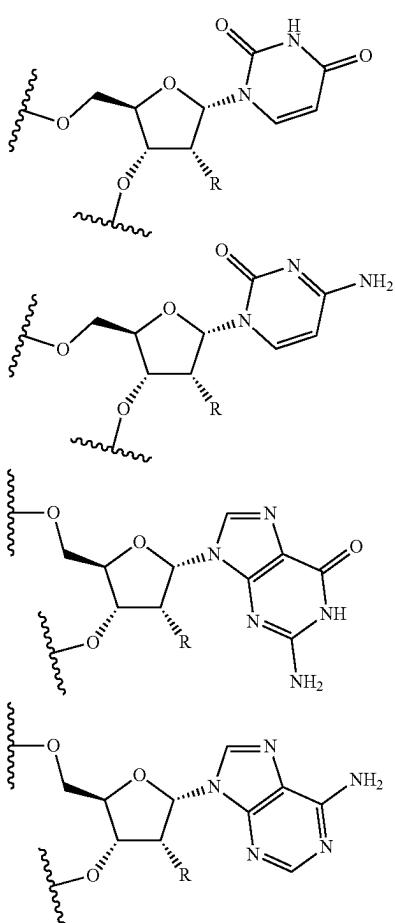
15      As the skilled artisan will recognize, in view of the functional role of nucleobases is defining specificity of a RNAi agent of the disclosure, while nucleobase modifications can be performed in the various manners as described herein, e.g., to introduce destabilizing modifications into a RNAi agent of the disclosure, e.g., for purpose of enhancing on-target effect relative to off-target effect, the range of modifications available and, in general, present upon RNAi agents of the disclosure tends to be much greater for non-nucleobase modifications, e.g., modifications to sugar 20 groups or phosphate backbones of polyribonucleotides. Such modifications are described in greater detail in other sections of the instant disclosure and are expressly contemplated for RNAi agents of the disclosure, either possessing native nucleobases or modified nucleobases as described 25 above or elsewhere herein.

30      In addition to the antisense strand comprising a thermally destabilizing modification, the dsRNA can also comprise one or more stabilizing modifications. For example, the dsRNA can comprise at least two (e.g., two, three, four, five, six, seven, eight, nine, ten or more) stabilizing modifications. Without limitations, the stabilizing modifications all 35 can be present in one strand. In some embodiments, both the sense and the antisense strands comprise at least two stabilizing modifications. The stabilizing modification can occur 40 on any nucleotide of the sense strand or antisense strand. For instance, the stabilizing modification can occur on every nucleotide on the sense strand or antisense strand; each stabilizing modification can occur in an alternating pattern on the sense strand or antisense strand; or the sense strand 45 or antisense strand comprises both stabilizing modification in an alternating pattern. The alternating pattern of the stabilizing modifications on the sense strand may be the same or different from the antisense strand, and the alternating pattern of the stabilizing modifications on the sense 50 strand can have a shift relative to the alternating pattern of the stabilizing modifications on the antisense strand.

In some embodiments, the antisense strand comprises at 55 least two (e.g., two, three, four, five, six, seven, eight, nine, ten or more) stabilizing modifications. Without limitations, a stabilizing modification in the antisense strand can be present at any positions. In some embodiments, the antisense comprises stabilizing modifications at positions 2, 6, 8, 9, 14, and 16 from the 5'-end. In some other embodiments, the antisense comprises stabilizing modifications at positions 2, 6, 14, and 16 from the 5'-end. In still some other embodiments, the antisense comprises stabilizing modifications at positions 2, 14, and 16 from the 5'-end.

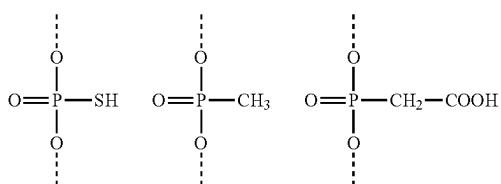
60      In some embodiments, the antisense strand comprises at least one stabilizing modification adjacent to the destabilizing modification. For example, the stabilizing modification can be the nucleotide at the 5'-end or the 3'-end of the destabilizing modification, i.e., at position -1 or +1 from the 65

In some embodiments, the thermally destabilizing modification of the duplex in the seed region of the antisense strand includes one or more α-nucleotide complementary to the base on the target mRNA, such as:



wherein R is H, OH, OCH<sub>3</sub>, F, NH<sub>2</sub>, NHMe, NMe<sub>2</sub> or O-alkyl.

Exemplary phosphate modifications known to decrease the thermal stability of dsRNA duplexes compared to natural phosphodiester linkages are:



position of the destabilizing modification. In some embodiments, the antisense strand comprises a stabilizing modification at each of the 5'-end and the 3'-end of the destabilizing modification, i.e., positions -1 and +1 from the position of the destabilizing modification.

In some embodiments, the antisense strand comprises at least two stabilizing modifications at the 3'-end of the destabilizing modification, i.e., at positions +1 and +2 from the position of the destabilizing modification.

In some embodiments, the sense strand comprises at least two (e.g., two, three, four, five, six, seven, eight, nine, ten or more) stabilizing modifications. Without limitations, a stabilizing modification in the sense strand can be present at any positions. In some embodiments, the sense strand comprises stabilizing modifications at positions 7, 10, and 11 from the 5'-end. In some other embodiments, the sense strand comprises stabilizing modifications at positions 7, 9, 10, and 11 from the 5'-end. In some embodiments, the sense strand comprises stabilizing modifications at positions opposite or complimentary to positions 11, 12, and 15 of the antisense strand, counting from the 5'-end of the antisense strand. In some other embodiments, the sense strand comprises stabilizing modifications at positions opposite or complimentary to positions 11, 12, 13, and 15 of the antisense strand, counting from the 5'-end of the antisense strand. In some embodiments, the sense strand comprises a block of two, three, or four stabilizing modifications.

In some embodiments, the sense strand does not comprise a stabilizing modification in position opposite or complimentary to the thermally destabilizing modification of the duplex in the antisense strand.

Exemplary thermally stabilizing modifications include, but are not limited to, 2'-fluoro modifications. Other thermally stabilizing modifications include, but are not limited to, LNA.

In some embodiments, the dsRNA of the disclosure comprises at least four (e.g., four, five, six, seven, eight, nine, ten, or more) 2'-fluoro nucleotides. Without limitations, the 2'-fluoro nucleotides all can be present in one strand. In some embodiments, both the sense and the antisense strands comprise at least two 2'-fluoro nucleotides. The 2'-fluoro modification can occur on any nucleotide of the sense strand or antisense strand. For instance, the 2'-fluoro modification can occur on every nucleotide on the sense strand or antisense strand; each 2'-fluoro modification can occur in an alternating pattern on the sense strand or antisense strand; or the sense strand or antisense strand comprises both 2'-fluoro modifications in an alternating pattern. The alternating pattern of the 2'-fluoro modifications on the sense strand may be the same or different from the antisense strand, and the alternating pattern of the 2'-fluoro modifications on the sense strand can have a shift relative to the alternating pattern of the 2'-fluoro modifications on the antisense strand.

In some embodiments, the antisense strand comprises at least two (e.g., two, three, four, five, six, seven, eight, nine, ten, or more) 2'-fluoro nucleotides. Without limitations, a 2'-fluoro modification in the antisense strand can be present at any positions. In some embodiments, the antisense comprises 2'-fluoro nucleotides at positions 2, 6, 8, 9, 14, and 16 from the 5'-end. In some other embodiments, the antisense comprises 2'-fluoro nucleotides at positions 2, 6, 14, and 16 from the 5'-end. In still some other embodiments, the antisense comprises 2'-fluoro nucleotides at positions 2, 14, and 16 from the 5'-end.

In some embodiments, the antisense strand comprises at least one 2'-fluoro nucleotide adjacent to the destabilizing

modification. For example, the 2'-fluoro nucleotide can be the nucleotide at the 5'-end or the 3'-end of the destabilizing modification, i.e., at position -1 or +1 from the position of the destabilizing modification. In some embodiments, the antisense strand comprises a 2'-fluoro nucleotide at each of the 5'-end and the 3'-end of the destabilizing modification, i.e., positions -1 and +1 from the position of the destabilizing modification.

In some embodiments, the antisense strand comprises at least two 2'-fluoro nucleotides at the 3'-end of the destabilizing modification, i.e., at positions +1 and +2 from the position of the destabilizing modification.

In some embodiments, the sense strand comprises at least two (e.g., two, three, four, five, six, seven, eight, nine, ten, or more) 2'-fluoro nucleotides. Without limitations, a 2'-fluoro modification in the sense strand can be present at any positions. In some embodiments, the antisense comprises 2'-fluoro nucleotides at positions 7, 10, and 11 from the 5'-end. In some other embodiments, the sense strand comprises 2'-fluoro nucleotides at positions 7, 9, 10, and 11 from the 5'-end. In some embodiments, the sense strand comprises 2'-fluoro nucleotides at positions opposite or complimentary to positions 11, 12, and 15 of the antisense strand, counting from the 5'-end of the antisense strand. In some other embodiments, the sense strand comprises 2'-fluoro nucleotides at positions opposite or complimentary to positions 11, 12, 13, and 15 of the antisense strand, counting from the 5'-end of the antisense strand. In some embodiments, the sense strand comprises a block of two, three or four 2'-fluoro nucleotides.

In some embodiments, the sense strand does not comprise a 2'-fluoro nucleotide in position opposite or complimentary to the thermally destabilizing modification of the duplex in the antisense strand.

In some embodiments, the dsRNA molecule of the disclosure comprises a 21 nucleotides (nt) sense strand and a 23 nucleotides (nt) antisense, wherein the antisense strand contains at least one thermally destabilizing nucleotide, where the at least one thermally destabilizing nucleotide occurs in the seed region of the antisense strand (i.e., at position 2-9 of the 5'-end of the antisense strand), wherein one end of the dsRNA is blunt, while the other end is comprises a 2 nt overhang, and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six or all seven) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the antisense comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (iii) the sense strand is conjugated with a ligand; (iv) the sense strand comprises 2, 3, 4, or 5 2'-fluoro modifications; (v) the sense strand comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (vi) the dsRNA comprises at least four 2'-fluoro modifications; and (vii) the dsRNA comprises a blunt end at 5'-end of the antisense strand. Preferably, the 2 nt overhang is at the 3'-end of the antisense.

In some embodiments, the dsRNA molecule of the disclosure comprising a sense and antisense strands, wherein: the sense strand is 25-30 nucleotide residues in length, wherein starting from the 5' terminal nucleotide (position 1), positions 1 to 23 of said sense strand comprise at least 8 ribonucleotides; antisense strand is 36-66 nucleotide residues in length and, starting from the 3' terminal nucleotide, at least 8 ribonucleotides in the positions paired with positions 1-23 of sense strand to form a duplex; wherein at least the 3' terminal nucleotide of antisense strand is unpaired with sense strand, and up to 6 consecutive 3' terminal nucleotides are unpaired with sense strand, thereby forming

a 3' single stranded overhang of 1-6 nucleotides; wherein the 5' terminus of antisense strand comprises from 10-30 consecutive nucleotides which are unpaired with sense strand, thereby forming a 10-30 nucleotide single stranded 5' overhang; wherein at least the sense strand 5' terminal and 3' terminal nucleotides are base paired with nucleotides of antisense strand when sense and antisense strands are aligned for maximum complementarity, thereby forming a substantially duplexed region between sense and antisense strands; and antisense strand is sufficiently complementary to a target RNA along at least 19 ribonucleotides of antisense strand length to reduce target gene expression when said double stranded nucleic acid is introduced into a mammalian cell; and wherein the antisense strand contains at least one thermally destabilizing nucleotide, where at least one thermally destabilizing nucleotide is in the seed region of the antisense strand (i.e. at position 2-9 of the 5'-end of the antisense strand). For example, the thermally destabilizing nucleotide occurs between positions opposite or complementary to positions 14-17 of the 5'-end of the sense strand, and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six or all seven) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the antisense comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (iii) the sense strand is conjugated with a ligand; (iv) the sense strand comprises 2, 3, 4, or 5 2'-fluoro modifications; (v) the sense strand comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; and (vi) the dsRNA comprises at least four 2'-fluoro modifications; and (vii) the dsRNA comprises a duplex region of 12-30 nucleotide pairs in length.

In some embodiments, the dsRNA molecule of the disclosure comprises a sense and antisense strands, wherein said dsRNA molecule comprises a sense strand having a length which is at least 25 and at most 29 nucleotides and an antisense strand having a length which is at most 30 nucleotides with the sense strand comprises a modified nucleotide that is susceptible to enzymatic degradation at position 11 from the 5' end, wherein the 3' end of said sense strand and the 5' end of said antisense strand form a blunt end and said antisense strand is 1-4 nucleotides longer at its 3' end than the sense strand, wherein the duplex region which is at least 25 nucleotides in length, and said antisense strand is sufficiently complementary to a target mRNA along at least 19 nt of said antisense strand length to reduce target gene expression when said dsRNA molecule is introduced into a mammalian cell, and wherein dicer cleavage of said dsRNA preferentially results in an siRNA comprising said 3' end of said antisense strand, thereby reducing expression of the target gene in the mammal, wherein the antisense strand contains at least one thermally destabilizing nucleotide, where the at least one thermally destabilizing nucleotide is in the seed region of the antisense strand (i.e. at position 2-9 of the 5'-end of the antisense strand), and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six or all seven) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the antisense comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (iii) the sense strand is conjugated with a ligand; (iv) the sense strand comprises 2, 3, 4, or 5 2'-fluoro modifications; (v) the sense strand comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; and (vi) the dsRNA comprises at least four 2'-fluoro modifications; and (vii) the dsRNA has a duplex region of 12-29 nucleotide pairs in length.

In some embodiments, every nucleotide in the sense strand and antisense strand of the dsRNA molecule may be

modified. Each nucleotide may be modified with the same or different modification which can include one or more alteration of one or both of the non-linking phosphate oxygens or of one or more of the linking phosphate oxygens; alteration of a constituent of the ribose sugar, e.g., of the 2' hydroxyl on the ribose sugar; wholesale replacement of the phosphate moiety with "dephospho" linkers; modification or replacement of a naturally occurring base; and replacement or modification of the ribose-phosphate backbone.

As nucleic acids are polymers of subunits, many of the modifications occur at a position which is repeated within a nucleic acid, e.g., a modification of a base, or a phosphate moiety, or a non-linking O of a phosphate moiety. In some cases, the modification will occur at all of the subject positions in the nucleic acid but in many cases it will not. By way of example, a modification may only occur at a 3' or 5' terminal position, may only occur in a terminal region, e.g., at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10 nucleotides of a strand. A modification may occur in a double strand region, a single strand region, or in both. A modification may occur only in the double strand region of an RNA or may only occur in a single strand region of an RNA. e.g., a phosphorothioate modification at a non-linking O position may only occur at one or both termini, may only occur in a terminal region, e.g., at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10 nucleotides of a strand, or may occur in double strand and single strand regions, particularly at termini. The 5' end or ends can be phosphorylated.

It may be possible, e.g., to enhance stability, to include particular bases in overhangs, or to include modified nucleotides or nucleotide surrogates, in single strand overhangs, e.g., in a 5' or 3' overhang, or in both. E.g., it can be desirable to include purine nucleotides in overhangs. In some embodiments all or some of the bases in a 3' or 5' overhang may be modified, e.g., with a modification described herein. Modifications can include, e.g., the use of modifications at the 2' position of the ribose sugar with modifications that are known in the art, e.g., the use of deoxyribonucleotides, 2'-deoxy-2'-fluoro (2'-F) or 2'-O-methyl modified instead of the ribosugar of the nucleobase, and modifications in the phosphate group, e.g., phosphorothioate modifications. Overhangs need not be homologous with the target sequence.

In some embodiments, each residue of the sense strand and antisense strand is independently modified with LNA, HNA, CeNA, 2'-methoxyethyl, 2'-O-methyl, 2'-O-allyl, 2'-C-allyl, 2'-deoxy, or 2'-fluoro. The strands can contain more than one modification. In some embodiments, each residue of the sense strand and antisense strand is independently modified with 2'-O-methyl or 2'-fluoro. It is to be understood that these modifications are in addition to the at least one thermally destabilizing modification of the duplex present in the antisense strand.

At least two different modifications are typically present on the sense strand and antisense strand. Those two modifications may be the 2'-deoxy, 2'-O-methyl or 2'-fluoro modifications, acyclic nucleotides or others. In some embodiments, the sense strand and antisense strand each comprises two differently modified nucleotides selected from 2'-O-methyl or 2'-deoxy. In some embodiments, each residue of the sense strand and antisense strand is independently modified with 2'-O-methyl nucleotide, 2'-deoxy nucleotide, 2'-deoxy-2'-fluoro nucleotide, 2'-O—N-methyl-acetamido (2'-O-NMA) nucleotide, a 2'-O-dimethylaminooxyethyl (2'-O-DMAEOE) nucleotide, 2'-O-aminopropyl (2'-O-AP) nucleotide, or 2'-ara-F nucleotide. Again, it is to

be understood that these modifications are in addition to the at least one thermally destabilizing modification of the duplex present in the antisense strand.

In some embodiments, the dsRNA molecule of the disclosure comprises modifications of an alternating pattern, particular in the B1, B2, B3, B1', B2', B3', B4' regions. The term "alternating motif" or "alternative pattern" as used herein refers to a motif having one or more modifications, each modification occurring on alternating nucleotides of one strand. The alternating nucleotide may refer to one per every other nucleotide or one per every three nucleotides, or a similar pattern. For example, if A, B and C each represent one type of modification to the nucleotide, the alternating motif can be "ABABABABABAB . . . , " "AABBAABBAABB . . . , " "AABAABAABAAB . . . , " "AAABAAA-BAAAB . . . , " "AAABBBAAAABB . . . , " or "ABCABCABCABC . . . , " etc. The type of modifications contained in the alternating motif may be the same or different. For example, if A, B, C, D each represent one type of modification on the nucleotide, the alternating pattern, i.e., modifications on every other nucleotide, may be the same, but each of the sense strand or antisense strand can be selected from several possibilities of modifications within the alternating motif such as "ABABAB . . . , " "ACACAC . . . , " "BDBBDB . . . , " or "CDCDCD . . . , " etc.

In some embodiments, the dsRNA molecule of the disclosure comprises the modification pattern for the alternating motif on the sense strand relative to the modification pattern for the alternating motif on the antisense strand is shifted. The shift may be such that the modified group of nucleotides of the sense strand corresponds to a differently modified group of nucleotides of the antisense strand and vice versa. For example, the sense strand when paired with the antisense strand in the dsRNA duplex, the alternating motif in the sense strand may start with "ABABAB" from 5'-3' of the strand and the alternating motif in the antisense strand may start with "BABABA" from 3'-5' of the strand within the duplex region. As another example, the alternating motif in the sense strand may start with "AABBAABB" from 5'-3' of the strand and the alternating motif in the antisense strand may start with "BBAABBAA" from 3'-5' of the strand within the duplex region, so that there is a complete or partial shift of the modification patterns between the sense strand and the antisense strand.

The dsRNA molecule of the disclosure may further comprise at least one phosphorothioate or methylphosphonate internucleotide linkage. The phosphorothioate or methylphosphonate internucleotide linkage modification may occur on any nucleotide of the sense strand or antisense strand or both in any position of the strand. For instance, the internucleotide linkage modification may occur on every nucleotide on the sense strand or antisense strand; each internucleotide linkage modification may occur in an alternating pattern on the sense strand or antisense strand; or the sense strand or antisense strand comprises both internucleotide linkage modifications in an alternating pattern. The alternating pattern of the internucleotide linkage modification on the sense strand may be the same or different from the antisense strand, and the alternating pattern of the internucleotide linkage modification on the sense strand may have a shift relative to the alternating pattern of the internucleotide linkage modification on the antisense strand.

In some embodiments, the dsRNA molecule comprises the phosphorothioate or methylphosphonate internucleotide linkage modification in the overhang region. For example, the overhang region comprises two nucleotides having a phosphorothioate or methylphosphonate internucleotide

linkage between the two nucleotides. Internucleotide linkage modifications also may be made to link the overhang nucleotides with the terminal paired nucleotides within duplex region. For example, at least 2, 3, 4, or all the overhang nucleotides may be linked through phosphorothioate or methylphosphonate internucleotide linkage, and optionally, there may be additional phosphorothioate or methylphosphonate internucleotide linkages linking the overhang nucleotide with a paired nucleotide that is next to the overhang nucleotide. For instance, there may be at least two phosphorothioate internucleotide linkages between the terminal three nucleotides, in which two of the three nucleotides are overhang nucleotides, and the third is a paired nucleotide next to the overhang nucleotide. Preferably, these terminal three nucleotides may be at the 3'-end of the antisense strand.

In some embodiments, the sense strand of the dsRNA molecule comprises 1-10 blocks of two to ten phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said sense strand is paired with an antisense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of two phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of three phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of four phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of five phosphorothioate or methylphosphonate internucleotide linkages separated by 1,

2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of six phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of seven phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, or 8 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of eight phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, or 6 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the antisense strand of the dsRNA molecule comprises two blocks of nine phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, or 4 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the oligonucleotide sequence and the said antisense strand is paired with a sense strand comprising any combination of phosphorothioate, methylphosphonate and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

In some embodiments, the dsRNA molecule of the disclosure further comprises one or more phosphorothioate or methylphosphonate internucleotide linkage modification within 1-10 of the termini position(s) of the sense or antisense strand. For example, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides may be linked through phosphorothioate or methylphosphonate internucleotide linkage at one end or both ends of the sense or antisense strand.

In some embodiments, the dsRNA molecule of the disclosure further comprises one or more phosphorothioate or methylphosphonate internucleotide linkage modification

within 1-10 of the internal region of the duplex of each of the sense or antisense strand. For example, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides may be linked through phosphorothioate methylphosphonate internucleotide linkage at position 8-16 of the duplex region counting from the 5'-end of the sense strand; the dsRNA molecule can optionally further comprise one or more phosphorothioate or methylphosphonate internucleotide linkage modification within 1-10 of the termini position(s).

In some embodiments, the dsRNA molecule of the disclosure further comprises one to five phosphorothioate or methylphosphonate internucleotide linkage modification(s) within position 1-5 and one to five phosphorothioate or methylphosphonate internucleotide linkage modification(s) within position 18-23 of the sense strand (counting from the 5'-end), and one to five phosphorothioate or methylphosphonate internucleotide linkage modification at positions 1 and 2 and one to five within positions 18-23 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises one phosphorothioate internucleotide linkage modification within position 1-5 and one phosphorothioate or methylphosphonate internucleotide linkage modification within position 18-23 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and 2 and two phosphorothioate or methylphosphonate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises two phosphorothioate internucleotide linkage modifications within position 1-5 and one phosphorothioate internucleotide linkage modification within position 18-23 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises two phosphorothioate internucleotide linkage modifications within position 1-5 and two phosphorothioate internucleotide linkage modifications within position 18-23 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises two phosphorothioate internucleotide linkage modifications within position 1-5 and two phosphorothioate internucleotide linkage modifications within position 18-23 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and 2 and one phosphorothioate internucleotide linkage modification within positions 18-23 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises one phosphorothioate internucleotide linkage modification within position 1-5 and one phosphorothioate internucleotide linkage modification within position 18-23 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications within positions 18-23 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises one phosphorothioate internucle-



of backbone chiral centers comprises at least 18 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 19 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 8 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 7 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 6 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 5 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 4 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 3 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 2 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 1 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 8 internucleotidic linkages which are not chiral (as a non-limiting example, a phosphodiester). In some embodiments, a common pattern of backbone chiral centers comprises no more than 7 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 6 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 5 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 4 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 3 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 2 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 1 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises at least 10 internucleotidic linkages in the Sp configuration, and no more than 8 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises at least 11 internucleotidic linkages in the Sp configuration, and no more than 7 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises at least 12 internucleotidic linkages in the Sp configuration, and no more than 6 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises at least 13 internucleotidic linkages in the Sp configuration, and no more than 6 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises at least 14 internucleotidic linkages in the Sp configuration, and no more than 5 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises at least 15 internucleotidic linkages in the Sp configuration, and no more than 4 internucleotidic linkages which are not chiral. In some embodiments, the internucleotidic linkages in the Sp configuration are optionally contiguous or not contiguous.

In some embodiments, the internucleotidic linkages in the Rp configuration are optionally contiguous or not contiguous. In some embodiments, the internucleotidic linkages which are not chiral are optionally contiguous or not contiguous.

In some embodiments, compound of the disclosure comprises a block is a stereochemistry block. In some embodiments, a block is an Rp block in that each internucleotidic linkage of the block is Rp. In some embodiments, a 5'-block is an Rp block. In some embodiments, a 3'-block is an Rp block. In some embodiments, a block is an Sp block in that each internucleotidic linkage of the block is Sp. In some embodiments, a 5'-block is an Sp block. In some embodiments, a 3'-block is an Sp block. In some embodiments, provided oligonucleotides comprise both Rp and Sp blocks. In some embodiments, provided oligonucleotides comprise one or more Rp but no Sp blocks. In some embodiments, provided oligonucleotides comprise one or more Sp but no Rp blocks. In some embodiments, provided oligonucleotides comprise one or more PO blocks wherein each internucleotidic linkage in a natural phosphate linkage.

In some embodiments, compound of the disclosure comprises a 5'-block is an Sp block wherein each sugar moiety comprises a 2'-F modification. In some embodiments, a 5'-block is an Sp block wherein each of internucleotidic linkage is a modified internucleotidic linkage and each sugar moiety comprises a 2'-F modification. In some embodiments, a 5'-block is an Sp block wherein each of internucleotidic linkage is a phosphorothioate linkage and each sugar moiety comprises a 2'-F modification. In some embodiments, a 5'-block comprises 4 or more nucleoside units. In some embodiments, a 5'-block comprises 5 or more nucleoside units. In some embodiments, a 5'-block comprises 6 or more nucleoside units. In some embodiments, a 5'-block comprises 7 or more nucleoside units. In some embodiments, a 3'-block is an Sp block wherein each sugar moiety comprises a 2'-F modification. In some embodiments, a 3'-block is an Sp block wherein each of internucleotidic linkage is a modified internucleotidic linkage and each sugar moiety comprises a 2'-F modification. In some embodiments, a 3'-block is an Sp block wherein each of internucleotidic linkage is a phosphorothioate linkage and each sugar moiety comprises a 2'-F modification. In some embodiments, a 3'-block comprises 4 or more nucleoside units. In some embodiments, a 3'-block comprises 5 or more nucleoside units. In some embodiments, a 3'-block comprises 6 or more nucleoside units. In some embodiments, a 3'-block comprises 7 or more nucleoside units.

In some embodiments, compound of the disclosure comprises a type of nucleoside in a region or an oligonucleotide is followed by a specific type of internucleotidic linkage, e.g., natural phosphate linkage, modified internucleotidic linkage, Rp chiral internucleotidic linkage, Sp chiral internucleotidic linkage, etc. In some embodiments, A is followed by Sp. In some embodiments, A is followed by Rp. In some embodiments, A is followed by natural phosphate linkage (PO). In some embodiments, U is followed by Sp. In some embodiments, U is followed by Rp. In some embodiments, U is followed by natural phosphate linkage (PO). In some embodiments, C is followed by Sp. In some embodiments, C is followed by Rp. In some embodiments, C is followed by natural phosphate linkage (PO). In some embodiments, G is followed by Sp. In some embodiments, G is followed by Rp. In some embodiments, G is followed by natural phosphate linkage (PO). In some embodiments, C and U are followed by Sp. In some embodiments, C and U are followed by Rp. In some embodiments, C and U are

followed by natural phosphate linkage (PO). In some embodiments, A and G are followed by Sp. In some embodiments, A and G are followed by Rp.

In some embodiments, the antisense strand comprises phosphorothioate internucleotide linkages between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23, wherein the antisense strand contains at least one thermally destabilizing modification of the duplex located in the seed region of the antisense strand (i.e., at position 2-9 of the 5'-end of the antisense strand), and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six, seven or all eight) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the antisense comprises 3, 4, or 5 phosphorothioate internucleotide linkages; (iii) the sense strand is conjugated with a ligand; (iv) the sense strand comprises 2, 3, 4 or 5 2'-fluoro modifications; (v) the sense strand comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (vi) the dsRNA comprises at least four 2'-fluoro modifications; (vii) the dsRNA comprises a duplex region of 12-40 nucleotide pairs in length; and (viii) the dsRNA has a blunt end at 5'-end of the antisense strand. In some embodiments, the antisense strand comprises phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide positions 21 and 22, and between nucleotide positions 22 and 23, wherein the antisense strand contains at least one thermally destabilizing modification of the duplex located in the seed region of the antisense strand (i.e., at position 2-9 of the 5'-end of the antisense strand), and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six, seven or all eight) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the sense strand is conjugated with a ligand; (iii) the sense strand comprises 2, 3, 4 or 5 2'-fluoro modifications; (iv) the sense strand comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (v) the dsRNA comprises at least four 2'-fluoro modifications; (vi) the dsRNA comprises a duplex region of 12-40 nucleotide pairs in length; (vii) the dsRNA comprises a duplex region of 12-40 nucleotide pairs in length; and (viii) the dsRNA has a blunt end at 5'-end of the antisense strand.

In some embodiments, the sense strand comprises phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3, wherein the antisense strand contains at least one thermally destabilizing modification of the duplex located in the seed region of the antisense strand (i.e., at position 2-9 of the 5'-end of the antisense strand), and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six, seven or all eight) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the antisense comprises 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages; (iii) the sense strand is conjugated with a ligand; (iv) the sense strand comprises 2, 3, 4 or 5 2'-fluoro modifications; (v) the sense strand comprises 3, 4 or 5 phosphorothioate internucleotide linkages; (vi) the dsRNA comprises at least four 2'-fluoro modifications; (vii) the dsRNA comprises a duplex region of 12-40 nucleotide pairs in length; and (viii) the dsRNA has a blunt end at 5'-end of the antisense strand.

In some embodiments, the sense strand comprises phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, and between nucleotide positions 2 and 3, the antisense strand comprises phosphorothioate internucleotide linkages between nucleotide positions 1 and 2, between nucleotide positions 2 and 3, between nucleotide

positions 21 and 22, and between nucleotide positions 22 and 23, wherein the antisense strand contains at least one thermally destabilizing modification of the duplex located in the seed region of the antisense strand (i.e., at position 2-9 of the 5'-end of the antisense strand), and wherein the dsRNA optionally further has at least one (e.g., one, two, three, four, five, six or all seven) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5 or 6 2'-fluoro modifications; (ii) the sense strand is conjugated with a ligand; (iii) the sense strand comprises 2, 3, 4 or 5 2'-fluoro modifications; (iv) the sense strand comprises 3, 4 or 5 phosphorothioate internucleotide linkages; (v) the dsRNA comprises at least four 2'-fluoro modifications; (vi) the dsRNA comprises a duplex region of 12-40 nucleotide pairs in length; and (vii) the dsRNA has a blunt end at 5'-end of the antisense strand.

In some embodiments, the dsRNA molecule of the disclosure comprises mismatch(es) with the target, within the duplex, or combinations thereof. The mismatch can occur in the overhang region or the duplex region. The base pair can be ranked on the basis of their propensity to promote dissociation or melting (e.g., on the free energy of association or dissociation of a particular pairing, the simplest approach is to examine the pairs on an individual pair basis, though next neighbor or similar analysis can also be used). In terms of promoting dissociation: A:U is preferred over G:C; G:U is preferred over G:C; and I:C is preferred over G:C (I=inosine). Mismatches, e.g., non-canonical or other than canonical pairings (as described elsewhere herein) are preferred over canonical (A:T, A:U, G:C) pairings; and pairings which include a universal base are preferred over canonical pairings.

In some embodiments, the dsRNA molecule of the disclosure comprises at least one of the first 1, 2, 3, 4, or 5 base pairs within the duplex regions from the 5'-end of the antisense strand can be chosen independently from the group of: A:U, G:U, I:C, and mismatched pairs, e.g., non-canonical or other than canonical pairings or pairings which include a universal base, to promote the dissociation of the antisense strand at the 5'-end of the duplex.

In some embodiments, the nucleotide at the 1 position within the duplex region from the 5'-end in the antisense strand is selected from the group consisting of A, dA, dU, U, and dT. Alternatively, at least one of the first 1, 2 or 3 base pair within the duplex region from the 5'-end of the antisense strand is an AU base pair. For example, the first base pair within the duplex region from the 5'-end of the antisense strand is an AU base pair.

It was found that introducing 4'-modified or 5'-modified nucleotide to the 3'-end of a phosphodiester (PO), phosphorothioate (PS), or phosphorodithioate (PS2) linkage of a dinucleotide at any position of single stranded or double stranded oligonucleotide can exert steric effect to the internucleotide linkage and, hence, protecting or stabilizing it against nucleases.

In some embodiments, 5'-modified nucleoside is introduced at the 3'-end of a dinucleotide at any position of single stranded or double stranded siRNA. For instance, a 5'-alkylated nucleoside may be introduced at the 3'-end of a dinucleotide at any position of single stranded or double stranded siRNA. The alkyl group at the 5' position of the ribose sugar can be racemic or chirally pure R or S isomer. An exemplary 5'-alkylated nucleoside is 5'-methyl nucleoside. The 5'-methyl can be either racemic or chirally pure R or S isomer.

In some embodiments, 4'-modified nucleoside is introduced at the 3'-end of a dinucleotide at any position of single

stranded or double stranded siRNA. For instance, a 4'-alkylated nucleoside may be introduced at the 3'-end of a dinucleotide at any position of single stranded or double stranded siRNA. The alkyl group at the 4' position of the ribose sugar can be racemic or chirally pure R or S isomer. An exemplary 4'-alkylated nucleoside is 4'-methyl nucleoside. The 4'-methyl can be either racemic or chirally pure R or S isomer. Alternatively, a 4'-O-alkylated nucleoside may be introduced at the 3'-end of a dinucleotide at any position of single stranded or double stranded siRNA. The 4'-O-alkyl of the ribose sugar can be racemic or chirally pure R or S isomer. An exemplary 4'-O-alkylated nucleoside is 4'-O-methyl nucleoside. The 4'-O-methyl can be either racemic or chirally pure R or S isomer.

In some embodiments, 5'-alkylated nucleoside is introduced at any position on the sense strand or antisense strand of a dsRNA, and such modification maintains or improves potency of the dsRNA. The 5'-alkyl can be either racemic or chirally pure R or S isomer. An exemplary 5'-alkylated nucleoside is 5'-methyl nucleoside. The 5'-methyl can be either racemic or chirally pure R or S isomer.

In some embodiments, 4'-alkylated nucleoside is introduced at any position on the sense strand or antisense strand of a dsRNA, and such modification maintains or improves potency of the dsRNA. The 4'-alkyl can be either racemic or chirally pure R or S isomer. An exemplary 4'-alkylated nucleoside is 4'-methyl nucleoside. The 4'-methyl can be either racemic or chirally pure R or S isomer.

In some embodiments, 4'-O-alkylated nucleoside is introduced at any position on the sense strand or antisense strand of a dsRNA, and such modification maintains or improves potency of the dsRNA. The 5'-alkyl can be either racemic or chirally pure R or S isomer. An exemplary 4'-O-alkylated nucleoside is 4'-O-methyl nucleoside. The 4'-O-methyl can be either racemic or chirally pure R or S isomer.

In some embodiments, the dsRNA molecule of the disclosure can comprise 2'-5' linkages (with 2'-H, 2'-OH and 2'-OMe and with P=O or P=S). For example, the 2'-5' linkages modifications can be used to promote nuclease resistance or to inhibit binding of the sense to the antisense strand, or can be used at the 5' end of the sense strand to avoid sense strand activation by RISC.

In another embodiment, the dsRNA molecule of the disclosure can comprise L sugars (e.g., L ribose, L-arabinose with 2'-H, 2'-OH and 2'-OMe). For example, these L sugars modifications can be used to promote nuclease resistance or to inhibit binding of the sense to the antisense strand, or can be used at the 5' end of the sense strand to avoid sense strand activation by RISC.

Various publications describe multimeric siRNA which can all be used with the dsRNA of the disclosure. Such publications include WO2007/091269, U.S. Pat. No. 7,858,769, WO2010/141511, WO2007/117686, WO2009/014887, and WO2011/031520 which are hereby incorporated by their entirety.

As described in more detail below, the RNAi agent that contains conjugations of one or more carbohydrate moieties to an RNAi agent can optimize one or more properties of the RNAi agent. In many cases, the carbohydrate moiety will be attached to a modified subunit of the RNAi agent. For example, the ribose sugar of one or more ribonucleotide subunits of a dsRNA agent can be replaced with another

moiety, e.g., a non-carbohydrate (preferably cyclic) carrier to which is attached a carbohydrate ligand. A ribonucleotide subunit in which the ribose sugar of the subunit has been so replaced is referred to herein as a ribose replacement modification subunit (RRMS). A cyclic carrier may be a carbocyclic ring system, i.e., all ring atoms are carbon atoms, or a heterocyclic ring system, i.e., one or more ring atoms may be a heteroatom, e.g., nitrogen, oxygen, sulfur. The cyclic carrier may be a monocyclic ring system, or may contain two or more rings, e.g. fused rings. The cyclic carrier may be a fully saturated ring system, or it may contain one or more double bonds.

The ligand may be attached to the polynucleotide via a carrier. The carriers include (i) at least one "backbone attachment point," preferably two "backbone attachment points" and (ii) at least one "tethering attachment point." A "backbone attachment point" as used herein refers to a functional group, e.g. a hydroxyl group, or generally, a bond available for, and that is suitable for incorporation of the carrier into the backbone, e.g., the phosphate, or modified phosphate, e.g., sulfur containing, backbone, of a ribonucleic acid. A "tethering attachment point" (TAP) in some embodiments refers to a constituent ring atom of the cyclic carrier, e.g., a carbon atom or a heteroatom (distinct from an atom which provides a backbone attachment point), that connects a selected moiety. The moiety can be, e.g., a carbohydrate, e.g. monosaccharide, disaccharide, trisaccharide, tetrasaccharide, oligosaccharide and polysaccharide. Optionally, the selected moiety is connected by an intervening tether to the cyclic carrier. Thus, the cyclic carrier will often include a functional group, e.g., an amino group, or generally, provide a bond, that is suitable for incorporation or tethering of another chemical entity, e.g., a ligand to the constituent ring.

The RNAi agents may be conjugated to a ligand via a carrier, wherein the carrier can be cyclic group or acyclic group; preferably, the cyclic group is selected from pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolane, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuryl and decalin; preferably, the acyclic group is selected from serinol backbone or diethanolamine backbone.

In certain specific embodiments, the RNAi agent for use in the methods of the disclosure is an agent selected from the group of agents listed in any one of Tables 2-5. These agents may further comprise a ligand, such as one or more lipophilic moieties, one or more GalNAc derivatives, or both of one or more lipophilic moieties and one or more GalNAc derivatives.

#### IV. iRNAs Conjugated to Ligands

Another modification of the RNA of an iRNA of the invention involves chemically linking to the iRNA one or more ligands, moieties or conjugates that enhance the activity, cellular distribution or cellular uptake of the iRNA, e.g., into a cell. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., *Proc. Natl. Acad. Sci. USA*, 1989, 86: 6553-6556), cholic acid (Manoharan et al., *Biorg. Med. Chem. Let.*, 1994, 4:1053-

1060), a thioether, e.g., beryl-S-tritylthiol (Manoharan et al., *Ann. N. Y. Acad. Sci.*, 1992, 660:306-309; Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1993, 3:2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, 20:533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., *EMBO J.*, 1991, 10:1111-1118; Kabanov et al., *FEBS Lett.*, 1990, 259:327-330; Svinarchuk et al., *Biochimie*, 1993, 75:49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-phosphonate (Manoharan et al., *Tetrahedron Lett.*, 1995, 36:3651-3654; Shea et al., *Nucl. Acids Res.*, 1990, 18:3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14:969-973), or adamantane acetic acid (Manoharan et al., *Tetrahedron Lett.*, 1995, 36:3651-3654), a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264:229-237), or an octadecylamine or hexylaminocarbonyloxycholesterol moiety (Cooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277:923-937).

In certain embodiments, a ligand alters the distribution, targeting or lifetime of an iRNA agent into which it is incorporated. In some embodiments, a ligand provides an enhanced affinity for a selected target, e.g., molecule, cell or cell type, compartment, e.g., a cellular or organ compartment, tissue, organ or region of the body, as, e.g., compared to a species absent such a ligand. Typical ligands will not take part in duplex pairing in a duplexed nucleic acid.

Ligands can include a naturally occurring substance, such as a protein (e.g., human serum albumin (HSA), low-density lipoprotein (LDL), or globulin); carbohydrate (e.g., a dextran, pullulan, chitin, chitosan, inulin, cyclodextrin or hyaluronic acid); or a lipid. The ligand may also be a recombinant or synthetic molecule, such as a synthetic polymer, e.g., a synthetic polyamino acid. Examples of polyamino acids include polyamino acid is a polylysine (PLL), poly L-aspartic acid, poly L-glutamic acid, styrene-maleic acid anhydride copolymer, poly(L-lactide-co-glycolic) copolymer, divinyl ether-maleic anhydride copolymer, N-(2-hydroxypropyl)methacrylamide copolymer (HMPA), polyethylene glycol (PEG), polyvinyl alcohol (PVA), polyurethane, poly(2-ethylacrylic acid), N-isopropylacrylamide polymers, or polyphosphazine. Example of polyamines include: polyethylenimine, polylysine (PLL), spermine, spermidine, polyamine, pseudopeptide-polyamine, peptidomimetic polyamine, dendrimer polyamine, arginine, amidine, protamine, cationic lipid, cationic porphyrin, quaternary salt of a polyamine, or an helical peptide.

Ligands can also include targeting groups, e.g., a cell or tissue targeting agent, e.g., a lectin, glycoprotein, lipid or protein, e.g., an antibody, that binds to a specified cell type such as a kidney cell. A targeting group can be a thyrotropin, melanotropin, lectin, glycoprotein, surfactant protein A, Mucin carbohydrate, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-glucosamine multivalent mannose, multivalent fucose, glycosylated polyaminoacids, multivalent galactose, transferrin, bisphosphonate, polyglutamate, polyaspartate, a lipid, cholesterol, a steroid, bile acid, folate, vitamin B12, biotin, or an RGD peptide or RGD peptide mimetic. In certain embodiments, the ligand is a multivalent galactose, e.g., an N-acetyl-galactosamine.

Other examples of ligands include dyes, intercalating agents (e.g. acridines), cross-linkers (e.g. psoralene, mitomycin C), porphyrins (TPPC4, texaphyrin, Sapphyrin), polycyclic aromatic hydrocarbons (e.g., phenazine, dihydrophenazine), artificial endonucleases (e.g. EDTA), lipophilic molecules, e.g., cholesterol, cholic acid, adamantine acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-Bis-O(hexadecyl)glycerol, geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl) lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine) and peptide conjugates (e.g., antennapedia peptide, Tat peptide), alkylating agents, phosphate, amino, mercapto, PEG (e.g., PEG-40K), MPEG, [MPEG]<sub>2</sub>, polyamino, alkyl, substituted alkyl, radiolabeled markers, enzymes, haptens (e.g. biotin), transport/absorption facilitators (e.g., aspirin, vitamin E, folic acid), synthetic ribonucleases (e.g., imidazole, bisimidazole, histamine, imidazole clusters, acridine-imidazole conjugates, Eu<sup>3+</sup> complexes of tetraazamacrocycles), dinitrophenyl, HRP, or AP.

Ligands can be proteins, e.g., glycoproteins, or peptides, e.g., molecules having a specific affinity for a co-ligand, or antibodies e.g., an antibody, that binds to a specified cell type such as a cancer cell, endothelial cell, or bone cell. Ligands may also include hormones and hormone receptors. They can also include non-peptidic species, such as lipids, lectins, carbohydrates, vitamins, cofactors, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-glucosamine multivalent mannose, or multivalent fucose. The ligand can be, for example, a lipopolysaccharide, an activator of p38 MAP kinase, or an activator of NF-κB.

The ligand can be a substance, e.g., a drug, which can increase the uptake of the iRNA agent into the cell, for example, by disrupting the cell's cytoskeleton, e.g., by disrupting the cell's microtubules, microfilaments, or intermediate filaments. The drug can be, for example, taxol, vincristine, vinblastine, cytochalasin, nocodazole, japlakinolide, latrunculin A, phalloidin, swinholide A, indanocine, or myoservin.

In some embodiments, a ligand attached to an iRNA as described herein acts as a pharmacokinetic modulator (PK modulator). PK modulators include lipophiles, bile acids, steroids, phospholipid analogues, peptides, protein binding agents, PEG, vitamins etc. Exemplary PK modulators include, but are not limited to, cholesterol, fatty acids, cholic acid, lithocholic acid, dialkylglycerides, diacylglyceride, phospholipids, sphingolipids, naproxen, ibuprofen, vitamin E, biotin etc. Oligonucleotides that comprise a number of phosphorothioate linkages are also known to bind to serum protein, thus short oligonucleotides, e.g., oligonucleotides of about 5 bases, 10 bases, 15 bases or 20 bases, comprising multiple of phosphorothioate linkages in the backbone are also amenable to the present invention as ligands (e.g. as PK modulating ligands). In addition, aptamers that bind serum components (e.g. serum proteins) are also suitable for use as PK modulating ligands in the embodiments described herein.

Ligand-conjugated iRNAs of the invention may be synthesized by the use of an oligonucleotide that bears a pendant reactive functionality, such as that derived from the

attachment of a linking molecule onto the oligonucleotide (described below). This reactive oligonucleotide may be reacted directly with commercially-available ligands, ligands that are synthesized bearing any of a variety of protecting groups, or ligands that have a linking moiety attached thereto.

The oligonucleotides used in the conjugates of the present invention may be conveniently and routinely made through the well-known technique of solid-phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems® (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is also known to use similar techniques to prepare other oligonucleotides, such as the phosphorothioates and alkylated derivatives.

In the ligand-conjugated oligonucleotides and ligand-molecule bearing sequence-specific linked nucleosides of the present invention, the oligonucleotides and oligonucleosides may be assembled on a suitable DNA synthesizer utilizing standard nucleotide or nucleoside precursors, or nucleotide or nucleoside conjugate precursors that already bear the linking moiety, ligand-nucleotide or nucleoside-conjugate precursors that already bear the ligand molecule, or non-nucleoside ligand-bearing building blocks.

When using nucleotide-conjugate precursors that already bear a linking moiety, the synthesis of the sequence-specific linked nucleosides is typically completed, and the ligand molecule is then reacted with the linking moiety to form the ligand-conjugated oligonucleotide. In some embodiments, the oligonucleotides or linked nucleosides of the present invention are synthesized by an automated synthesizer using phosphoramidites derived from ligand-nucleoside conjugates in addition to the standard phosphoramidites and non-standard phosphoramidites that are commercially available and routinely used in oligonucleotide synthesis.

#### A. Lipid Conjugates

In certain embodiments, the ligand or conjugate is a lipid or lipid-based molecule. Such a lipid or lipid-based molecule can typically bind a serum protein, such as human serum albumin (HSA). An HSA binding ligand allows for distribution of the conjugate to a target tissue, e.g., a non-kidney target tissue of the body. For example, the target tissue can be the liver, including parenchymal cells of the liver. Other molecules that can bind HSA can also be used as ligands. For example, naproxen or aspirin can be used. A lipid or lipid-based ligand can (a) increase resistance to degradation of the conjugate, (b) increase targeting or transport into a target cell or cell membrane, or (c) can be used to adjust binding to a serum protein, e.g., HSA.

A lipid-based ligand can be used to modulate, e.g., control (e.g., inhibit) the binding of the conjugate to a target tissue. For example, a lipid or lipid-based ligand that binds to HSA more strongly will be less likely to be targeted to the kidney and therefore less likely to be cleared from the body. A lipid or lipid-based ligand that binds to HSA less strongly can be used to target the conjugate to the kidney.

In certain embodiments, the lipid-based ligand binds HSA. For example, the ligand can bind HSA with a sufficient affinity such that distribution of the conjugate to a non-

kidney tissue is enhanced. However, the affinity is typically not so strong that the HSA-ligand binding cannot be reversed.

In certain embodiments, the lipid-based ligand binds HSA weakly or not at all, such that distribution of the conjugate to the kidney is enhanced. Other moieties that target to kidney cells can also be used in place of or in addition to the lipid-based ligand.

In another aspect, the ligand is a moiety, e.g., a vitamin, which is taken up by a target cell, e.g., a proliferating cell. These are particularly useful for treating disorders characterized by unwanted cell proliferation, e.g., of the malignant or non-malignant type, e.g., cancer cells. Exemplary vitamins include vitamin A, E, and K. Other exemplary vitamins include are B vitamin, e.g., folic acid, B12, riboflavin, biotin, pyridoxal or other vitamins or nutrients taken up by cancer cells. Also included are HSA and low density lipoprotein (LDL).

#### B. Cell Permeation Agents

In another aspect, the ligand is a cell-permeation agent, such as a helical cell-permeation agent. In certain embodiments, the agent is amphipathic. An exemplary agent is a peptide such as tat or antennapedia. If the agent is a peptide, it can be modified, including a peptidomimetic, inveromers, non-peptide or pseudo-peptide linkages, and use of D-amino acids. The helical agent is typically an  $\alpha$ -helical agent and can have a lipophilic and a lipophobic phase.

The ligand can be a peptide or peptidomimetic. A peptidomimetic (also referred to herein as an oligopeptidomimetic) is a molecule capable of folding into a defined three-dimensional structure similar to a natural peptide. The attachment of peptide and peptidomimetics to iRNA agents can affect pharmacokinetic distribution of the iRNA, such as by enhancing cellular recognition and absorption. The peptide or peptidomimetic moiety can be about 5-50 amino acids long, e.g., about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

A peptide or peptidomimetic can be, for example, a cell permeation peptide, cationic peptide, amphipathic peptide, or hydrophobic peptide (e.g., consisting primarily of Tyr, Trp, or Phe). The peptide moiety can be a dendrimer peptide, constrained peptide or crosslinked peptide. In another alternative, the peptide moiety can include a hydrophobic membrane translocation sequence (MTS). An exemplary hydrophobic MTS-containing peptide is RFGF having the amino acid sequence AAVALLPAVLLALLAP (SEQ ID NO:13). An RFGF analogue (e.g., amino acid sequence AALLPVL-LAAP (SEQ ID NO:14)) containing a hydrophobic MTS can also be a targeting moiety. The peptide moiety can be a "delivery" peptide, which can carry large polar molecules including peptides, oligonucleotides, and protein across cell membranes. For example, sequences from the HIV Tat protein (GRKKRRQRRPPQ (SEQ ID NO:15)) and the *Drosophila* Antennapedia protein (RQIKIWFQNRRMKWKK (SEQ ID NO:16)) have been found to be capable of functioning as delivery peptides. A peptide or peptidomimetic can be encoded by a random sequence of DNA, such as a peptide identified from a phage-display library, or one-bead-one-compound (OBOC) combinatorial library (Lam et al., *Nature*, 354:82-84, 1991).

Typically, the peptide or peptidomimetic tethered to a dsRNA agent via an incorporated monomer unit is a cell targeting peptide such as an arginine-glycine-aspartic acid

(RGD)-peptide, or RGD mimic. A peptide moiety can range in length from about 5 amino acids to about 40 amino acids. The peptide moieties can have a structural modification, such as to increase stability or direct conformational properties. Any of the structural modifications described below can be utilized.

An RGD peptide for use in the compositions and methods of the invention may be linear or cyclic, and may be modified, e.g., glycosylated or methylated, to facilitate targeting to a specific tissue(s). RGD-containing peptides and peptidomimetics may include D-amino acids, as well as synthetic RGD mimics. In addition to RGD, one can use other moieties that target the integrin ligand. Preferred conjugates of this ligand target PECAM-1 or VEGF.

An RGD peptide moiety can be used to target a particular cell type, e.g., a tumor cell, such as an endothelial tumor cell or a breast cancer tumor cell (Zitzmann et al., *Cancer Res.*, 62:5139-43, 2002). An RGD peptide can facilitate targeting of an dsRNA agent to tumors of a variety of other tissues, including the lung, kidney, spleen, or liver (Aoki et al., *Cancer Gene Therapy* 8:783-787, 2001). Typically, the RGD peptide will facilitate targeting of an iRNA agent to the kidney. The RGD peptide can be linear or cyclic, and can be modified, e.g., glycosylated or methylated to facilitate targeting to specific tissues. For example, a glycosylated RGD peptide can deliver an iRNA agent to a tumor cell expressing  $\alpha_v\beta_3$  (Haubner et al., *Jour. Nucl. Med.*, 42:326-336, 2001).

A "cell permeation peptide" is capable of permeating a cell, e.g., a microbial cell, such as a bacterial or fungal cell, or a mammalian cell, such as a human cell. A microbial cell-permeating peptide can be, for example, an  $\alpha$ -helical linear peptide (e.g., LL-37 or Ceropin P1), a disulfide bond-containing peptide (e.g.,  $\alpha$ -defensin,  $\beta$ -defensin or bactenecin), or a peptide containing only one or two dominating amino acids (e.g., PR-39 or indolicidin). A cell permeation peptide can also include a nuclear localization signal (NLS). For example, a cell permeation peptide can be a bipartite amphipathic peptide, such as MPG, which is derived from the fusion peptide domain of HIV-1 gp41 and the NLS of SV40 large T antigen (Simeoni et al., *Nucl. Acids Res.* 31:2717-2724, 2003).

#### C. Carbohydrate Conjugates

In some embodiments of the compositions and methods of the invention, an iRNA further comprises a carbohydrate. The carbohydrate conjugated iRNA are advantageous for the in vivo delivery of nucleic acids, as well as compositions suitable for in vivo therapeutic use, as described herein. As used herein, "carbohydrate" refers to a compound which is either a carbohydrate per se made up of one or more monosaccharide units having at least 6 carbon atoms (which can be linear, branched or cyclic) with an oxygen, nitrogen or sulfur atom bonded to each carbon atom; or a compound having as a part thereof a carbohydrate moiety made up of one or more monosaccharide units each having at least six carbon atoms (which can be linear, branched or cyclic), with an oxygen, nitrogen or sulfur atom bonded to each carbon atom. Representative carbohydrates include the sugars (mono-, di-, tri- and oligosaccharides containing from about 4, 5, 6, 7, 8, or 9 monosaccharide units), and polysaccharides such as starches, glycogen, cellulose and polysaccharide gums. Specific monosaccharides include C5 and above (e.g., C5, C6, C7, or C8) sugars; di- and tri-saccharides include sugars having two or three monosaccharide units (e.g., C5, C6, C7, or C8).

In certain embodiments, a carbohydrate conjugate comprises a monosaccharide.

In certain embodiments, the monosaccharide is an N-acetylgalactosamine (GalNAc). GalNAc conjugates,

which comprise one or more N-acetylgalactosamine (GalNAc) derivatives, are described, for example, in U.S. Pat. No. 8,106,022, the entire content of which is hereby incorporated herein by reference. In some embodiments, the GalNAc conjugate serves as a ligand that targets the iRNA to particular cells. In some embodiments, the GalNAc conjugate targets the iRNA to liver cells, e.g., by serving as a ligand for the asialoglycoprotein receptor of liver cells (e.g., hepatocytes).

In some embodiments, the carbohydrate conjugate comprises one or more GalNAc derivatives. The GalNAc derivatives may be attached via a linker, e.g., a bivalent or trivalent branched linker. In some embodiments the GalNAc conjugate is conjugated to the 3' end of the sense strand. In some embodiments, the GalNAc conjugate is conjugated to the iRNA agent (e.g., to the 3' end of the sense strand) via a linker, e.g., a linker as described herein. In some embodiments the GalNAc conjugate is conjugated to the 5' end of the sense strand. In some embodiments, the GalNAc conjugate is conjugated to the iRNA agent (e.g., to the 5' end of the sense strand) via a linker, e.g., a linker as described herein.

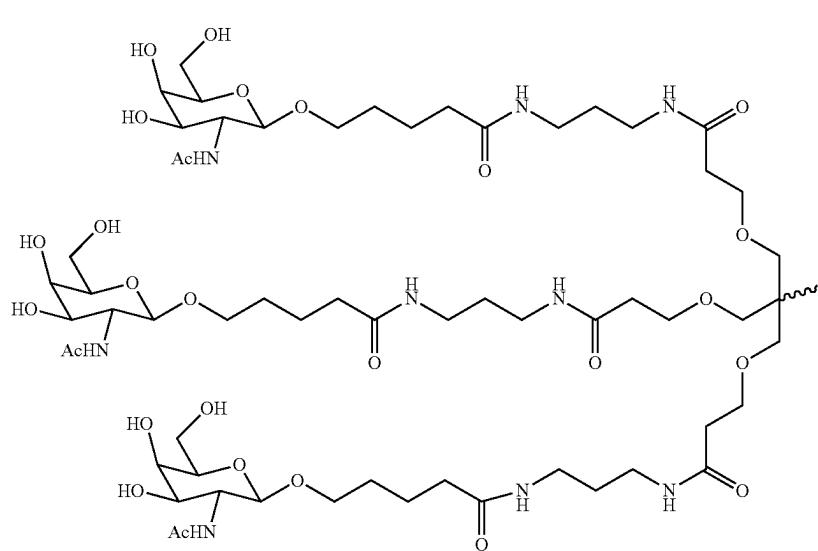
In certain embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a monovalent linker. In some embodiments, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a bivalent linker. In yet other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a trivalent linker. In other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a tetravalent linker.

In certain embodiments, the double stranded RNAi agents of the invention comprise one GalNAc or GalNAc derivative attached to the iRNA agent. In certain embodiments, the double stranded RNAi agents of the invention comprise a plurality (e.g., 2, 3, 4, 5, or 6) GalNAc or GalNAc derivatives, each independently attached to a plurality of nucleotides of the double stranded RNAi agent through a plurality of monovalent linkers.

In some embodiments, for example, when the two strands of an iRNA agent of the invention are part of one larger molecule connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming a hairpin loop comprising, a plurality of unpaired nucleotides, each unpaired nucleotide within the hairpin loop may independently comprise a GalNAc or GalNAc derivative attached via a monovalent linker. The hairpin loop may also be formed by an extended overhang in one strand of the duplex.

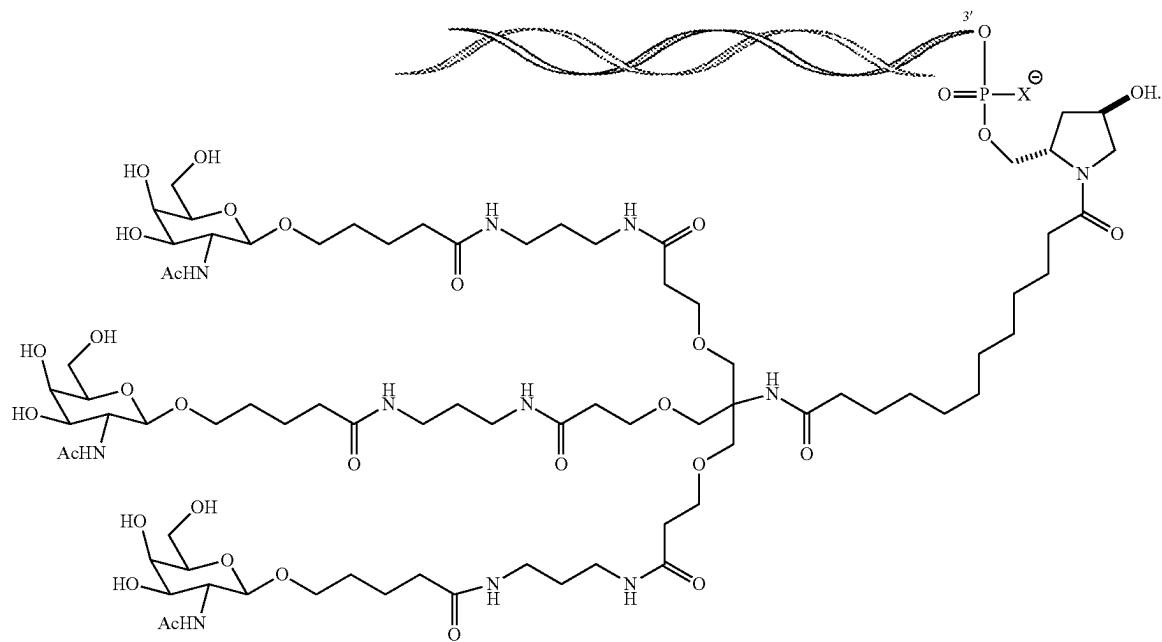
In some embodiments, for example, when the two strands of an iRNA agent of the invention are part of one larger molecule connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming a hairpin loop comprising, a plurality of unpaired nucleotides, each unpaired nucleotide within the hairpin loop may independently comprise a GalNAc or GalNAc derivative attached via a monovalent linker. The hairpin loop may also be formed by an extended overhang in one strand of the duplex.

In some embodiments, the GalNAc conjugate is

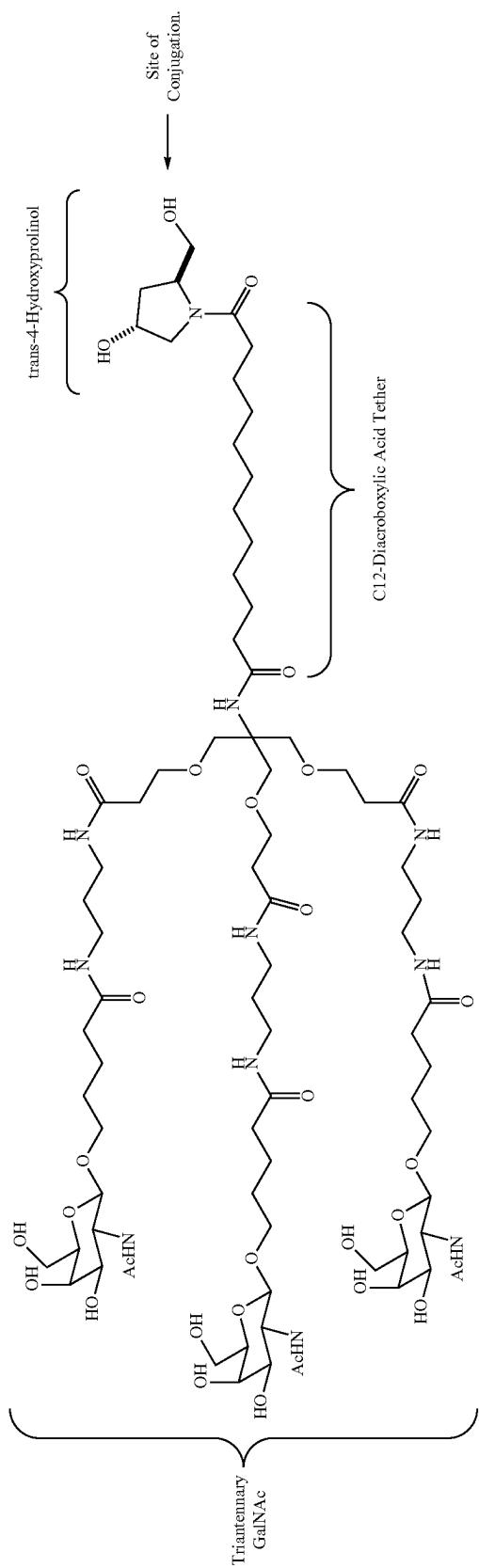


Formula II

In some embodiments, the RNAi agent is attached to the carbohydrate conjugate via a linker as shown in the following schematic, wherein X is O or S

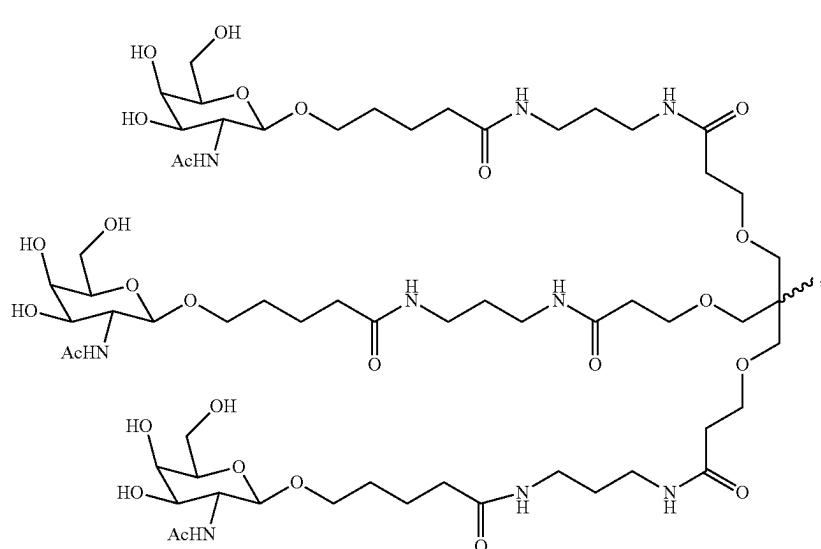


In some embodiments, the RNAi agent is conjugated to L96 as defined in Table 1 and shown below:

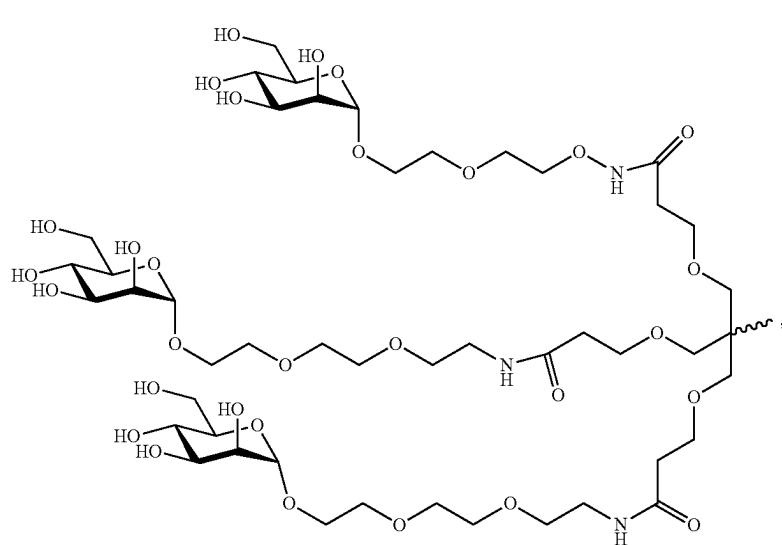


**91**

In certain embodiments, a carbohydrate conjugate for use in the compositions and methods of the invention is selected from the group consisting of:

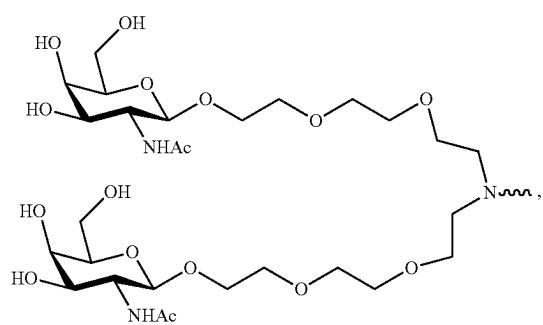


Formula II

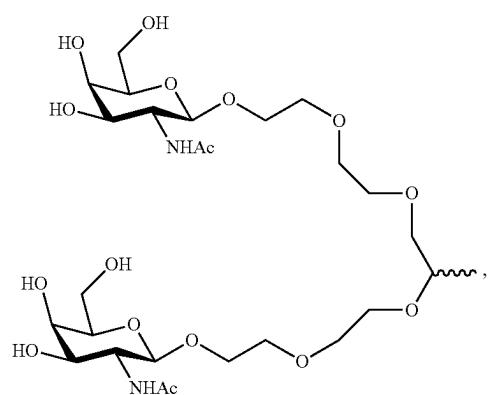
**92**

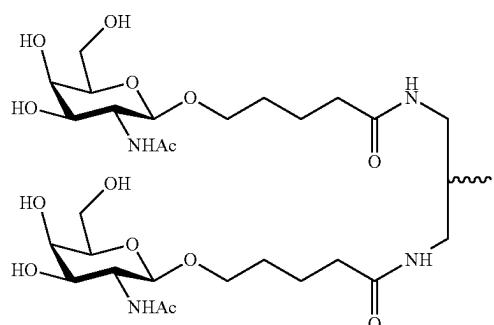
Formula III

Formula IV



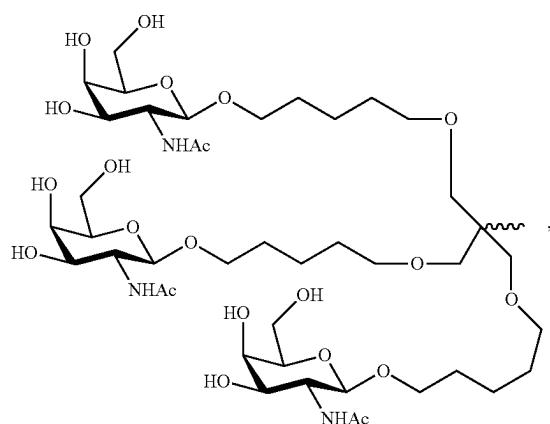
Formula V



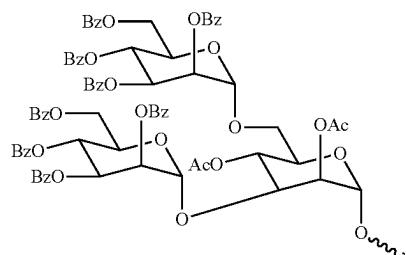
**93****94**

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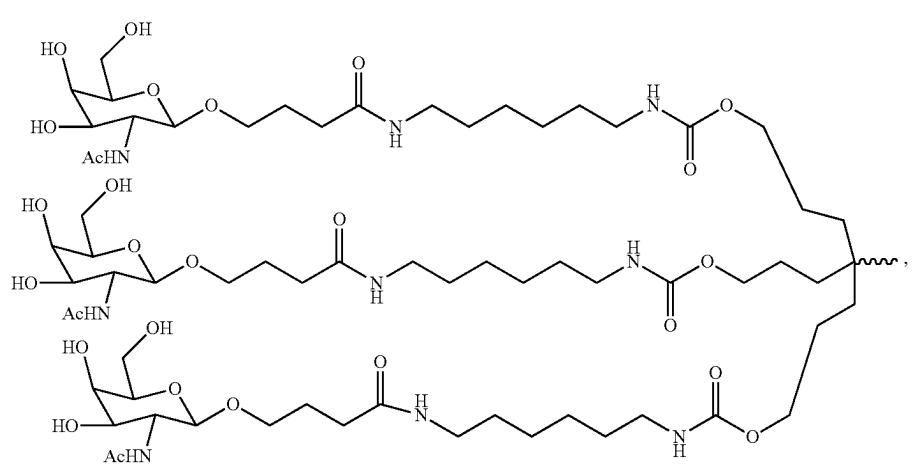
Formula VI



Formula VII



Formula VIII

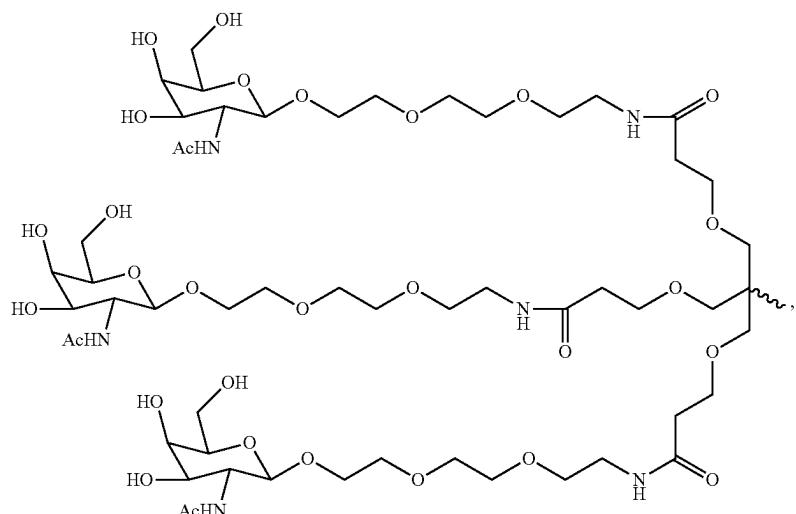


Formula IX

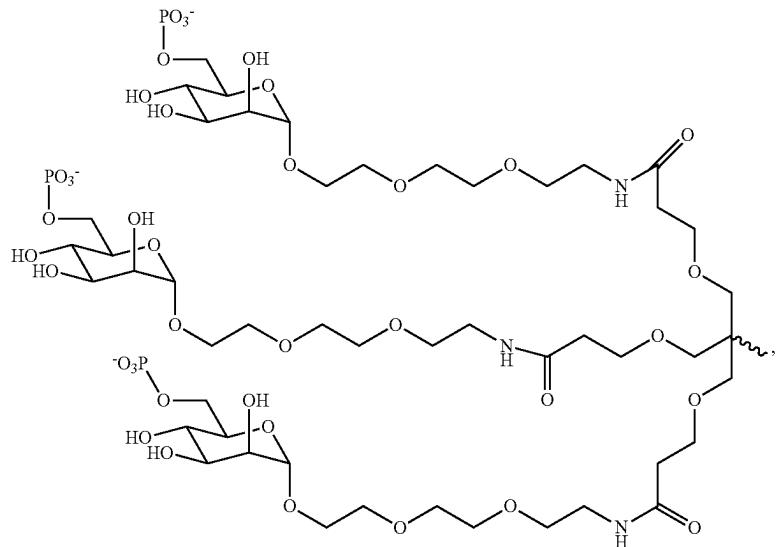
**95****96**

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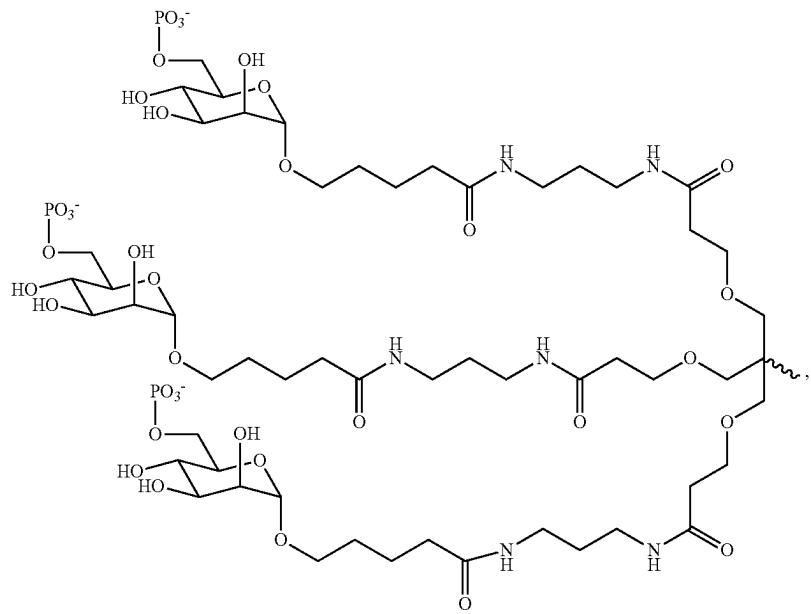
Formula X



Formula XI

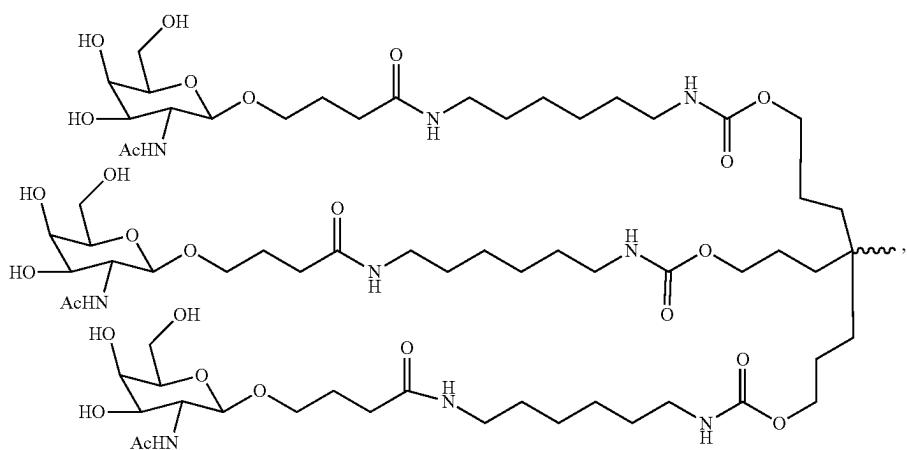


Formula XII

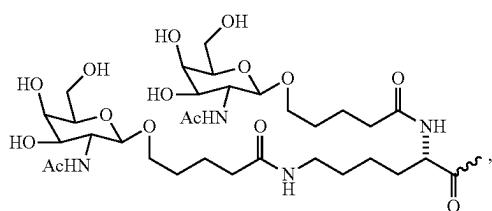


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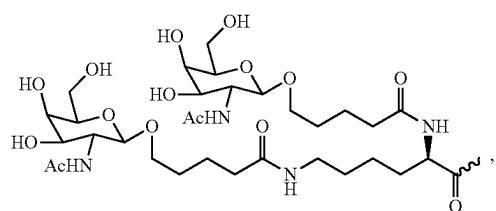
Formula XIII



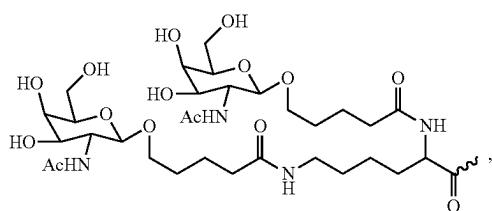
Formula XIV



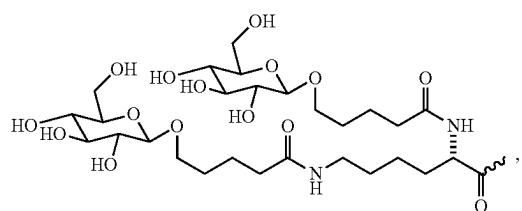
Formula XV



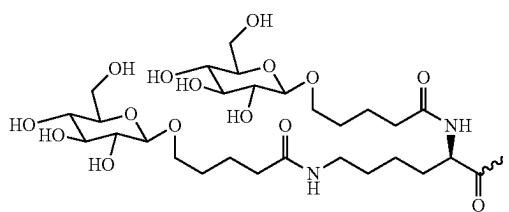
Formula XVI



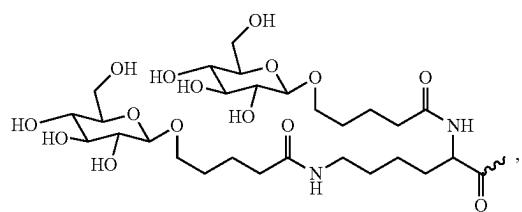
Formula XVII



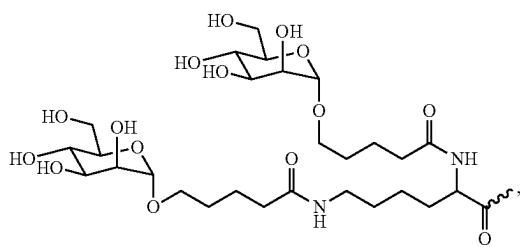
Formula XVIII



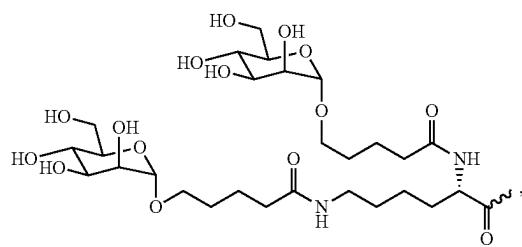
Formula XIX



Formula XX



Formula XXI

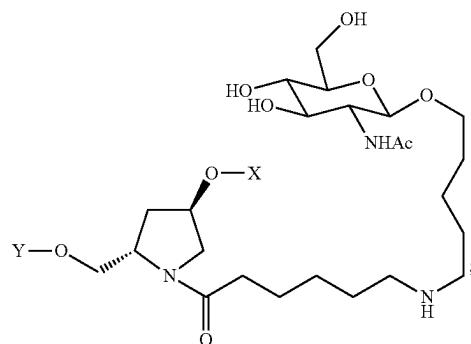
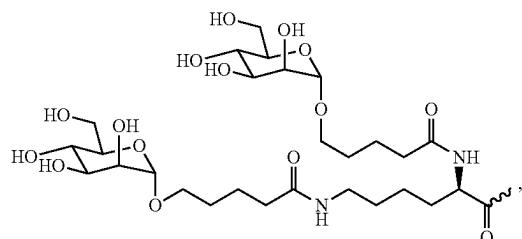


**99****100**

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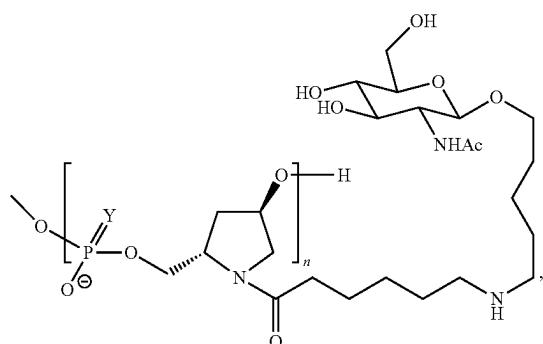
Formula XXII

Formula XXIII

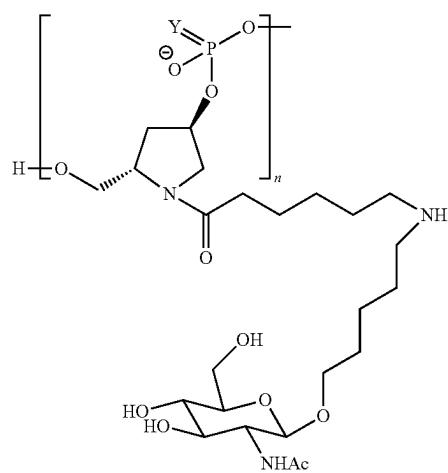


(Formula XXIV)

(Formula XXV)

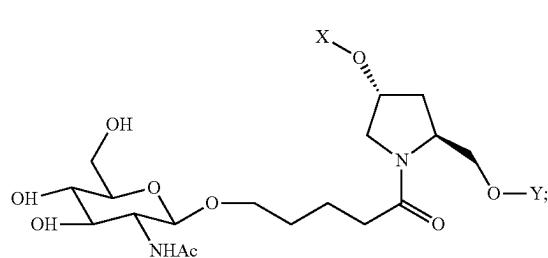


wherein Y is O or S and N is 3-6;



wherein Y is O or S and N is 3-6;

Formula XXVI



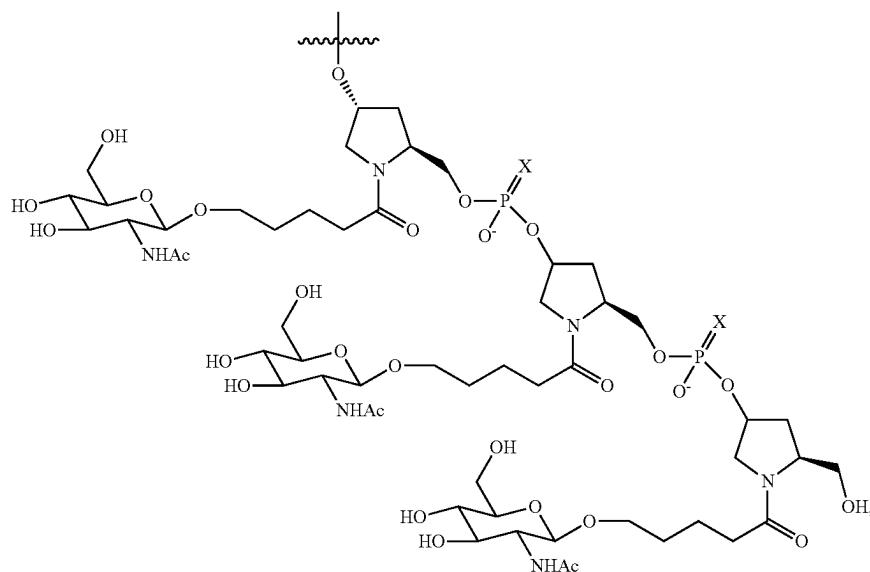
US 12,391,945 B2

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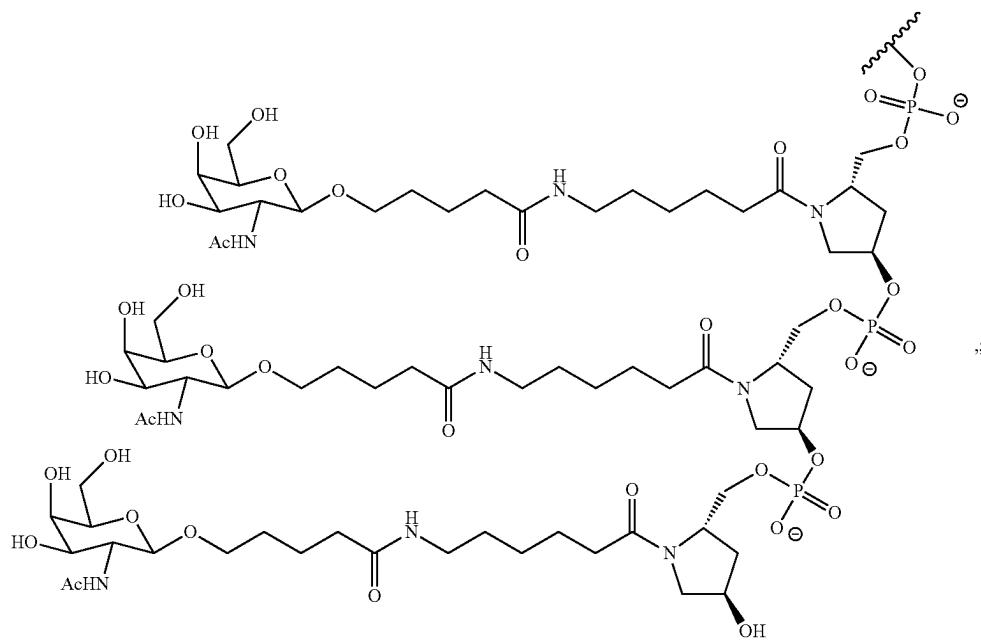
-continued

(Formula XXVII)



wherein X is O or S;

Formula XXVII



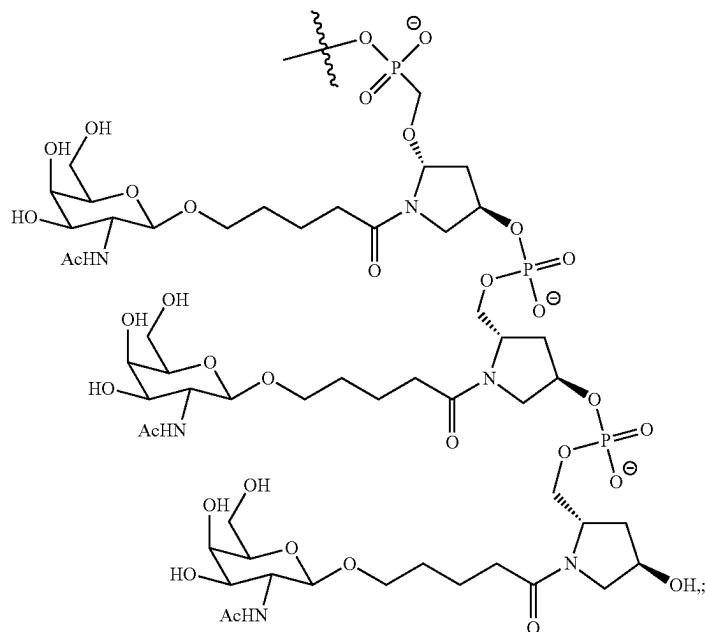
US 12,391,945 B2

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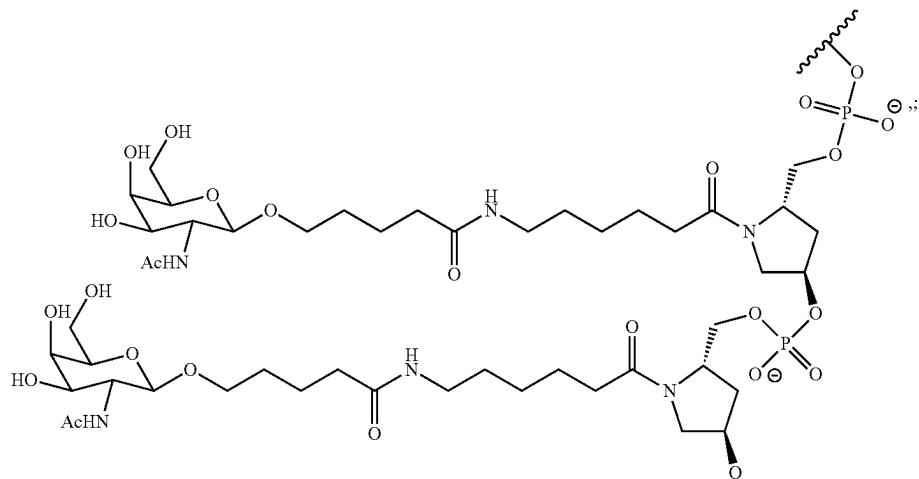
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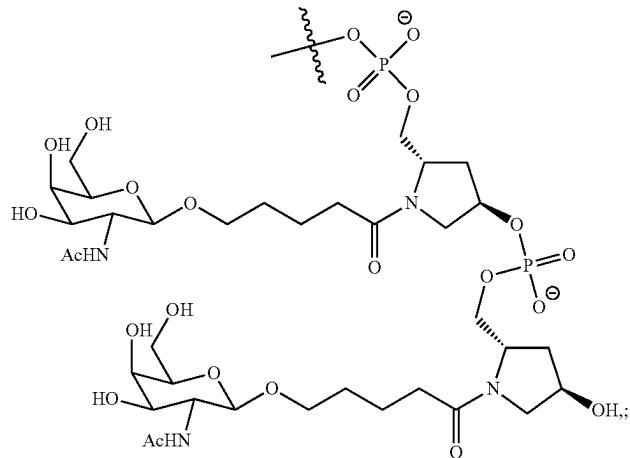
Formula XXIX



Formula XXX



Formula XXXI



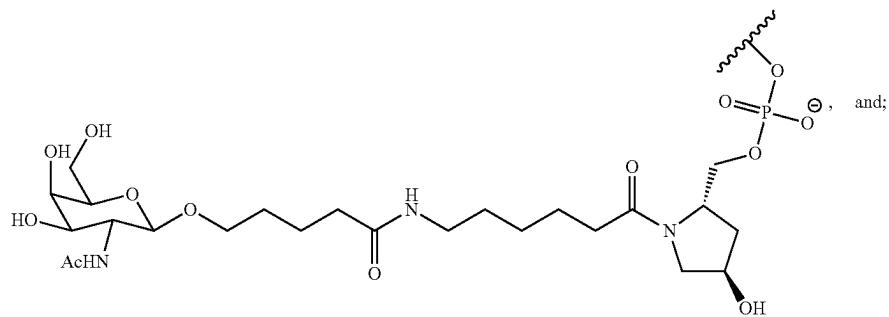
US 12,391,945 B2

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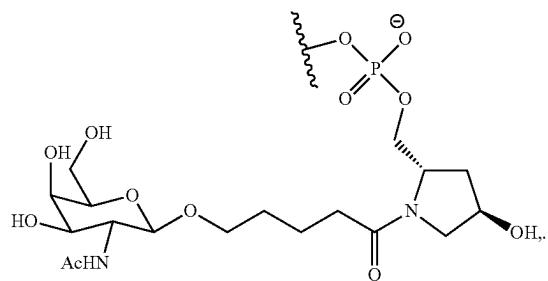
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106

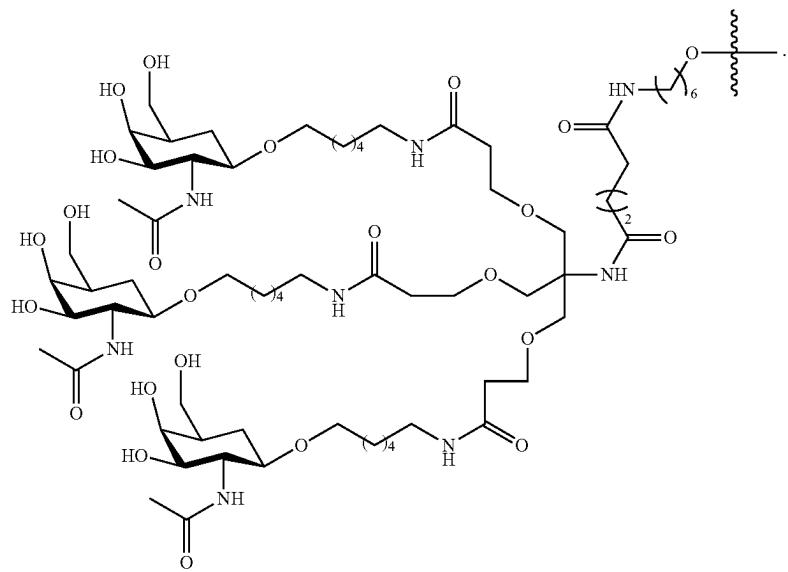
Formula XXXII



Formula XXXIII



Formula XXXIV

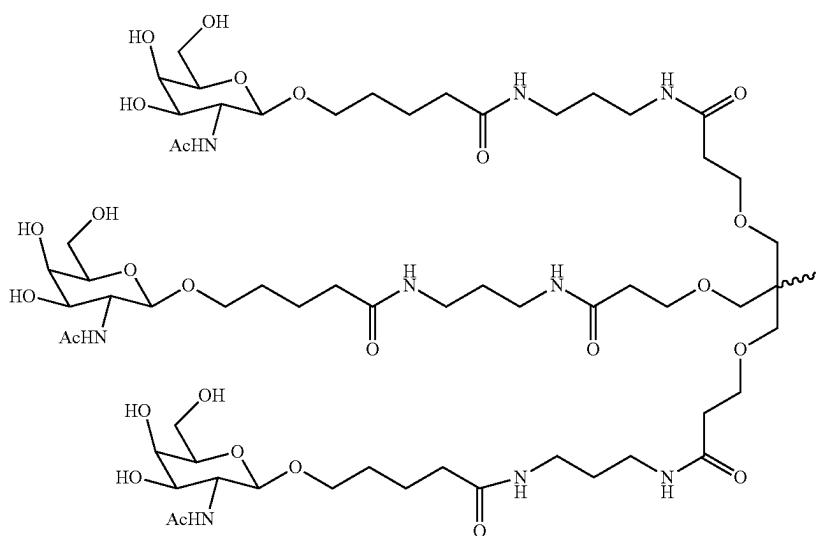


**107**

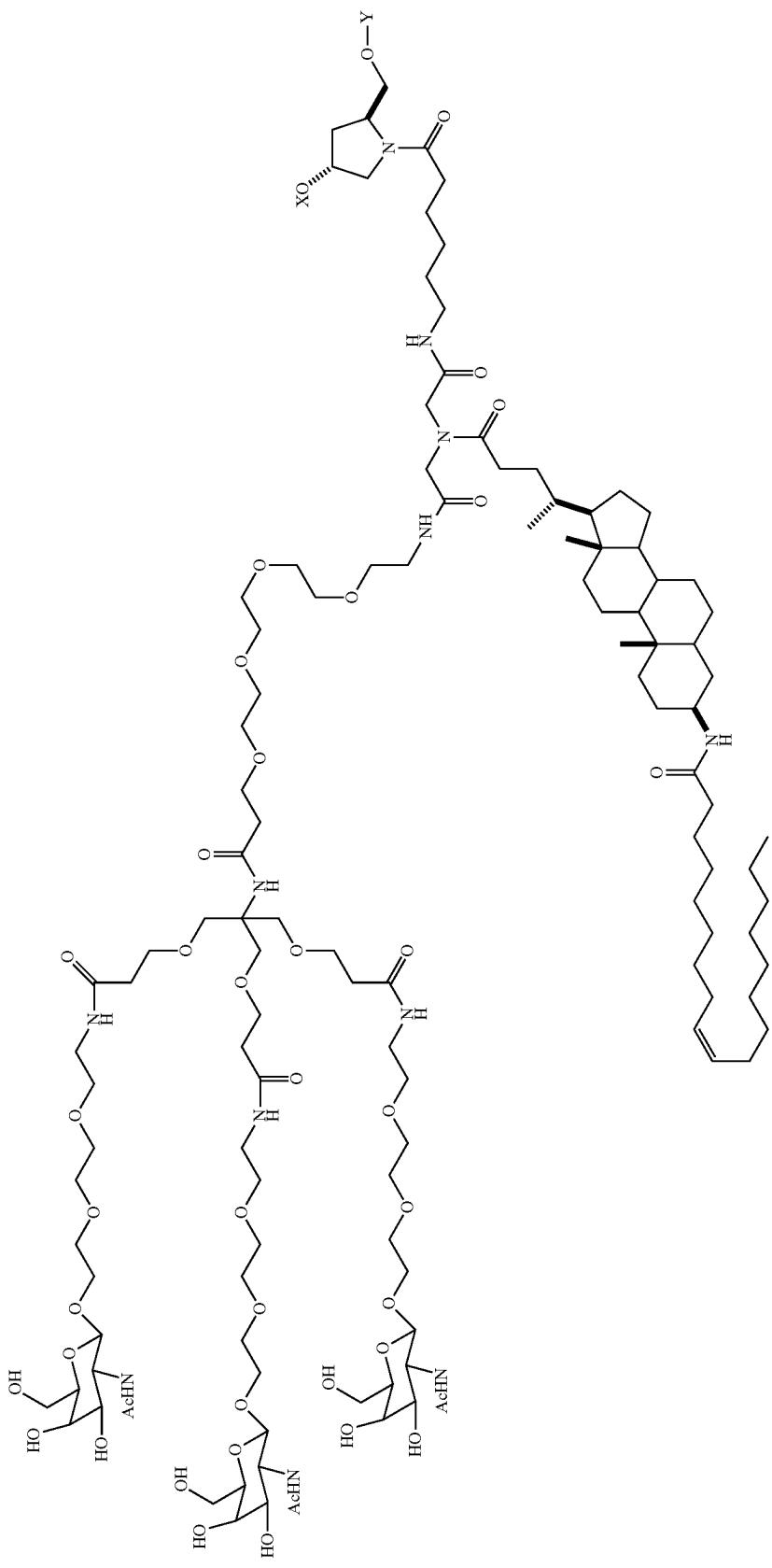
In certain embodiments, a carbohydrate conjugate for use in the compositions and methods of the invention is a monosaccharide. In certain embodiments, the monosaccharide is an N-acetylgalactosamine, such as

**108**

Formula II



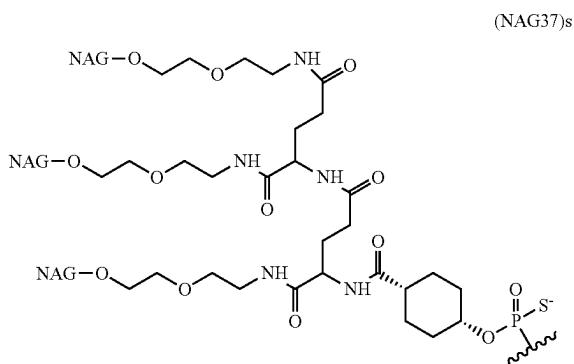
Another representative carbohydrate conjugate for use in the embodiments described herein includes, but is not limited to,



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when one of X or Y is an oligonucleotide, the other is a hydrogen.

In some embodiments, a suitable ligand is a ligand disclosed in WO 2019/055633, the entire contents of which are incorporated herein by reference. In one embodiment the ligand comprises the structure below:



In certain embodiments, the RNAi agents of the disclosure may include GalNAc ligands, even if such GalNAc ligands are currently projected to be of limited value for the preferred intrathecal/CNS delivery route(s) of the instant disclosure.

In certain embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a monovalent linker. In some embodiments, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a bivalent linker. In yet other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a trivalent linker. In other embodiments of the invention, the GalNAc or GalNAc derivative is attached to an iRNA agent of the invention via a tetravalent linker.

In certain embodiments, the double stranded RNAi agents of the invention comprise one GalNAc or GalNAc derivative attached to the iRNA agent, e.g., the 5'end of the sense strand of a dsRNA agent, or the 5' end of one or both sense strands of a dual targeting RNAi agent as described herein. In certain embodiments, the double stranded RNAi agents of the invention comprise a plurality (e.g., 2, 3, 4, 5, or 6) GalNAc or GalNAc derivatives, each independently attached to a plurality of nucleotides of the double stranded RNAi agent through a plurality of monovalent linkers.

In some embodiments, for example, when the two strands of an iRNA agent of the invention are part of one larger molecule connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming a hairpin loop comprising, a plurality of unpaired nucleotides, each unpaired nucleotide within the hairpin loop may independently comprise a GalNAc or GalNAc derivative attached via a monovalent linker.

In some embodiments, the carbohydrate conjugate further comprises one or more additional ligands as described above, such as, but not limited to, a PK modulator or a cell permeation peptide.

Additional carbohydrate conjugates and linkers suitable for use in the present invention include those described in WO 2014/179620 and WO 2014/179627, the entire contents of each of which are incorporated herein by reference.

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#### D. Linkers

In some embodiments, the conjugate or ligand described herein can be attached to an iRNA oligonucleotide with various linkers that can be cleavable or non-cleavable.

The term "linker" or "linking group" means an organic moiety that connects two parts of a compound, e.g., covalently attaches two parts of a compound. Linkers typically comprise a direct bond or an atom such as oxygen or sulfur, a unit such as NR8, C(O), C(O)NH, SO, SO<sub>2</sub>, SO<sub>2</sub>NH or a chain of atoms, such as, but not limited to, substituted or unsubstituted alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, arylalkyl, arylalkenyl, arylalkynyl, heteroarylalkyl, heteroarylalkenyl, heteroarylalkynyl, heterocyclalkyl, heterocyclalkenyl, heterocyclalkynyl, aryl, heteroaryl, heterocycl, cycloalkyl, cycloalkenyl, alkylarylkyl, alkylarylalkenyl, alkylaryllalkynyl, alkenylarylkyl, alkenylarylalkenyl, alkenylaryllalkynyl, alkynylarylkyl, alkynylarylalkenyl, alkynylaryllalkynyl, alkylheteroarylalkyl, alkylheteroarylalkenyl, alkylheteroarylalkynyl, alkenylheteroarylalkyl, alkenylheteroarylalkenyl, alkenylheteroarylalkynyl, alkynylheteroarylalkyl, alkynylheteroarylalkenyl, alkynylheteroarylalkynyl, alkynylheterocyclalkyl, alkynylheterocyclalkenyl, alkynylheterocyclalkynyl, alkylaryl, alkenylaryl, alkynylaryl, alkylheteroaryl, alkenylheteroaryl, alkynylheteroaryl, which one or more methylenes can be interrupted or terminated by O, S, S(O), SO<sub>2</sub>, N(R8), C(O), substituted or unsubstituted aryl, substituted or unsubstituted heteroaryl, substituted or unsubstituted heterocyclic; where R8 is hydrogen, acyl, aliphatic or substituted aliphatic. In certain embodiments, the linker is between about 1-24 atoms, 2-24, 3-24, 4-24, 5-24, 6-24, 6-18, 7-18, 8-18 atoms, 7-17, 8-17, 6-16, 7-16, or 8-16 atoms.

A cleavable linking group is one which is sufficiently stable outside the cell, but which upon entry into a target cell is cleaved to release the two parts the linker is holding together. In a preferred embodiment, the cleavable linking group is cleaved at least about 10 times, 20, times, 30 times, 40 times, 50 times, 60 times, 70 times, 80 times, 90 times or more, or at least about 100 times faster in a target cell or under a first reference condition (which can, e.g., be selected to mimic or represent intracellular conditions) than in the blood of a subject, or under a second reference condition (which can, e.g., be selected to mimic or represent conditions found in the blood or serum).

Cleavable linking groups are susceptible to cleavage agents, e.g., pH, redox potential or the presence of degradative molecules. Generally, cleavage agents are more prevalent or found at higher levels or activities inside cells than in serum or blood. Examples of such degradative agents include: redox agents which are selected for particular substrates or which have no substrate specificity, including, e.g., oxidative or reductive enzymes or reductive agents such as mercaptans, present in cells, that can degrade a redox cleavable linking group by reduction; esterases; endosomes or agents that can create an acidic environment, e.g., those that result in a pH of five or lower; enzymes that can hydrolyze or degrade an acid cleavable linking group by acting as a general acid, peptidases (which can be substrate specific), and phosphatases.

A cleavable linkage group, such as a disulfide bond can be susceptible to pH. The pH of human serum is 7.4, while the average intracellular pH is slightly lower, ranging from about 7.1-7.3. Endosomes have a more acidic pH, in the range of 5.5-6.0, and lysosomes have an even more acidic

pH at around 5.0. Some linkers will have a cleavable linking group that is cleaved at a preferred pH, thereby releasing a cationic lipid from the ligand inside the cell, or into the desired compartment of the cell.

A linker can include a cleavable linking group that is cleavable by a particular enzyme. The type of cleavable linking group incorporated into a linker can depend on the cell to be targeted. For example, a liver-targeting ligand can be linked to a cationic lipid through a linker that includes an ester group. Liver cells are rich in esterases, and therefore the linker will be cleaved more efficiently in liver cells than in cell types that are not esterase-rich. Other cell-types rich in esterases include cells of the lung, renal cortex, and testis.

Linkers that contain peptide bonds can be used when targeting cell types rich in peptidases, such as liver cells and synoviocytes.

In general, the suitability of a candidate cleavable linking group can be evaluated by testing the ability of a degradative agent (or condition) to cleave the candidate linking group. It will also be desirable to also test the candidate cleavable linking group for the ability to resist cleavage in the blood or when in contact with other non-target tissue. Thus, one can determine the relative susceptibility to cleavage between a first and a second condition, where the first is selected to be indicative of cleavage in a target cell and the second is selected to be indicative of cleavage in other tissues or biological fluids, e.g., blood or serum. The evaluations can be carried out in cell free systems, in cells, in cell culture, in organ or tissue culture, or in whole animals. It can be useful to make initial evaluations in cell-free or culture conditions and to confirm by further evaluations in whole animals. In preferred embodiments, useful candidate compounds are cleaved at least about 2, 4, 10, 20, 30, 40, 50, 60, 70, 80, 90, or about 100 times faster in the cell (or under in vitro conditions selected to mimic intracellular conditions) as compared to blood or serum (or under in vitro conditions selected to mimic extracellular conditions).

#### i. Redox Cleavable Linking Groups

In certain embodiments, a cleavable linking group is a redox cleavable linking group that is cleaved upon reduction or oxidation. An example of reductively cleavable linking group is a disulphide linking group ( $-S-S-$ ). To determine if a candidate cleavable linking group is a suitable “reductively cleavable linking group,” or for example is suitable for use with a particular iRNA moiety and particular targeting agent one can look to methods described herein. For example, a candidate can be evaluated by incubation with dithiothreitol (DTT), or other reducing agent using reagents known in the art, which mimic the rate of cleavage which would be observed in a cell, e.g., a target cell. The candidates can also be evaluated under conditions which are selected to mimic blood or serum conditions. In one, candidate compounds are cleaved by at most about 10% in the blood. In other embodiments, useful candidate compounds are degraded at least about 2, 4, 10, 20, 30, 40, 50, 60, 70, 80, 90, or about 100 times faster in the cell (or under in vitro conditions selected to mimic intracellular conditions) as compared to blood (or under in vitro conditions selected to mimic extracellular conditions). The rate of cleavage of candidate compounds can be determined using standard

enzyme kinetics assays under conditions chosen to mimic intracellular media and compared to conditions chosen to mimic extracellular media.

#### ii. Phosphate-Based Cleavable Linking Groups

In certain embodiments, a cleavable linker comprises a phosphate-based cleavable linking group. A phosphate-based cleavable linking group is cleaved by agents that degrade or hydrolyze the phosphate group. An example of an agent that cleaves phosphate groups in cells are enzymes such as phosphatases in cells. Examples of phosphate-based linking groups are  $-O-P(O)(ORk)-O-$ ,  $-O-P(S)(ORk)-O-$ ,  $-O-P(S)(SRk)-O-$ ,  $-S-P(O)(ORk)-O-$ ,  $-O-P(O)(ORk)-S-$ ,  $-S-P(O)(ORk)-S-$ ,  $-O-P(S)(ORk)-S-$ ,  $-S-P(S)(ORk)-O-$ ,  $-O-P(O)(Rk)-O-$ ,  $-O-P(S)(Rk)-O-$ ,  $-S-P(O)(Rk)-O-$ ,  $-S-P(S)(Rk)-O-$ ,  $-S-P(O)(Rk)-S-$ ,  $-O-P(S)(Rk)-S$ . Preferred embodiments are  $-O-P(O)(OH)-O-$ ,  $-O-P(S)(OH)-O-$ ,  $-O-P(S)(SH)-O-$ ,  $-S-P(O)(OH)-O-$ ,  $-O-P(S)(OH)-S-$ ,  $-S-P(S)(OH)-O-$ ,  $-O-P(O)(H)-O-$ ,  $-O-P(S)(H)-O-$ ,  $-S-P(O)(H)-O-$ ,  $-O-P(S)(H)-S-$ ,  $-O-P(S)(H)-S-$ . A preferred embodiment is  $-O-P(O)(OH)-O-$ . These candidates can be evaluated using methods analogous to those described above.

#### iii. Acid Cleavable Linking Groups

In certain embodiments, a cleavable linker comprises an acid cleavable linking group. An acid cleavable linking group is a linking group that is cleaved under acidic conditions. In preferred embodiments acid cleavable linking groups are cleaved in an acidic environment with a pH of about 6.5 or lower (e.g., about 6.0, 5.75, 5.5, 5.25, 5.0, or lower), or by agents such as enzymes that can act as a general acid. In a cell, specific low pH organelles, such as endosomes and lysosomes can provide a cleaving environment for acid cleavable linking groups. Examples of acid cleavable linking groups include but are not limited to hydrazones, esters, and esters of amino acids. Acid cleavable groups can have the general formula  $-C=NN-$ ,  $C(O)O$ , or  $-OC(O)$ . A preferred embodiment is when the carbon attached to the oxygen of the ester (the alkoxy group) is an aryl group, substituted alkyl group, or tertiary alkyl group such as dimethyl pentyl or t-butyl. These candidates can be evaluated using methods analogous to those described above.

#### iv. Ester-Based Cleavable Linking Groups

In certain embodiments, a cleavable linker comprises an ester-based cleavable linking group. An ester-based cleavable linking group is cleaved by enzymes such as esterases and amidases in cells. Examples of ester-based cleavable linking groups include but are not limited to esters of alkylene, alkenylene and alkynylene groups. Ester cleavable linking groups have the general formula  $-C(O)O-$ , or  $-OC(O)-$ . These candidates can be evaluated using methods analogous to those described above.

#### v. Peptide-Based Cleavable Linking Groups

In yet another embodiment, a cleavable linker comprises a peptide-based cleavable linking group. A peptide-based cleavable linking group is cleaved by enzymes such as peptidases and proteases in cells. Peptide-based cleavable linking groups are peptide bonds formed between amino acids to yield oligopeptides (e.g., dipeptides, tripeptides etc.) and polypeptides. Peptide-based cleavable groups do not include the amide group ( $-C(O)NH-$ ). The amide group can be formed between any alkylene, alkenylene or alkynylene. A peptide bond is a special type of amide bond formed

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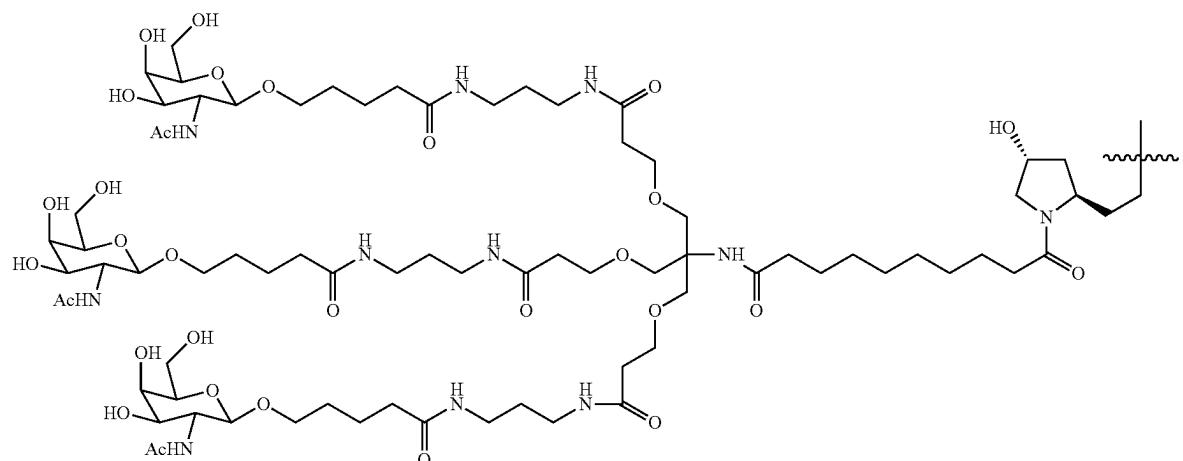
between amino acids to yield peptides and proteins. The peptide based cleavage group is generally limited to the peptide bond (i.e., the amide bond) formed between amino acids yielding peptides and proteins and does not include the entire amide functional group. Peptide-based cleavable linking groups have the general formula —NHCHRAC(O)NHCHRBC(O)—, where RA and RB are the R groups of the

**116**

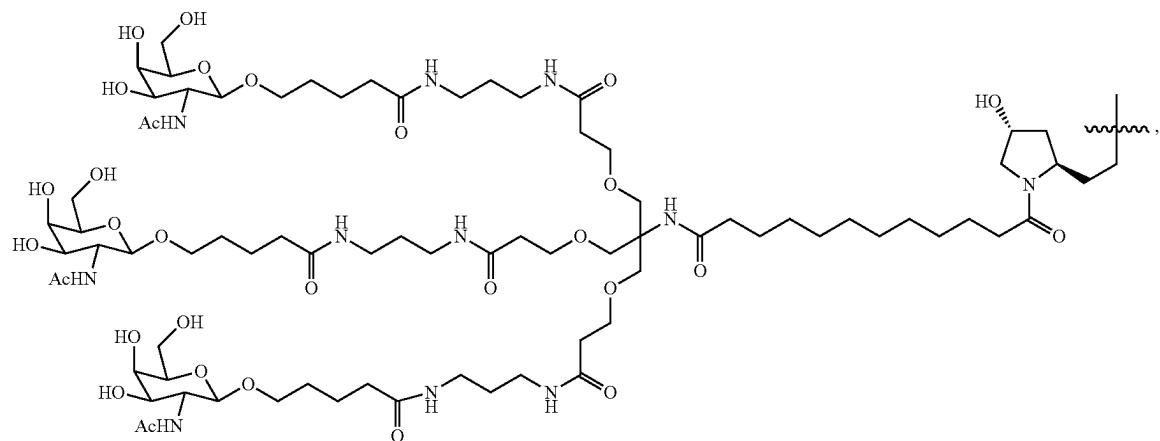
two adjacent amino acids. These candidates can be evaluated using methods analogous to those described above.

In some embodiments, an iRNA of the invention is conjugated to a carbohydrate through a linker. Non-limiting examples of iRNA carbohydrate conjugates with linkers of the compositions and methods of the invention include but are not limited to

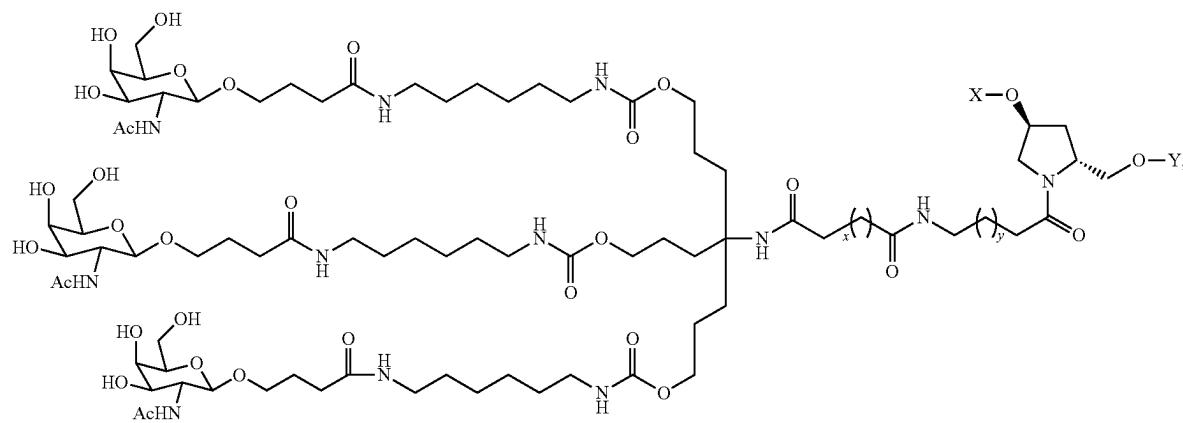
(Formula XXXVII)



(Formula XXXVIII)



(Formula XXXIX)


 $x = 1-30$   
 $y = 1-15$

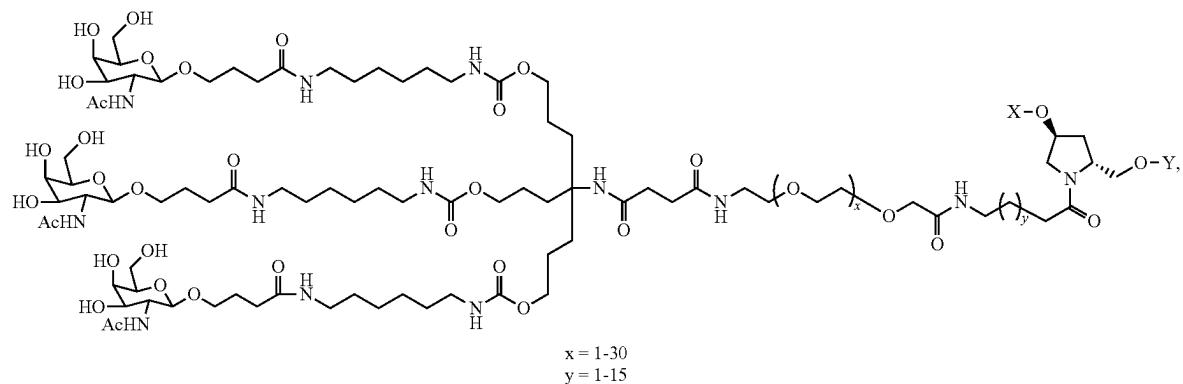
US 12,391,945 B2

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118

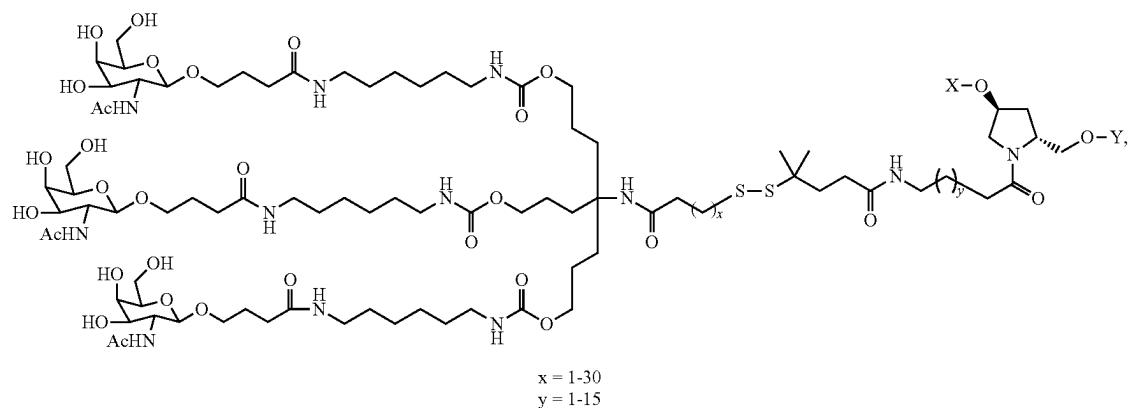
-continued

(Formula XL)



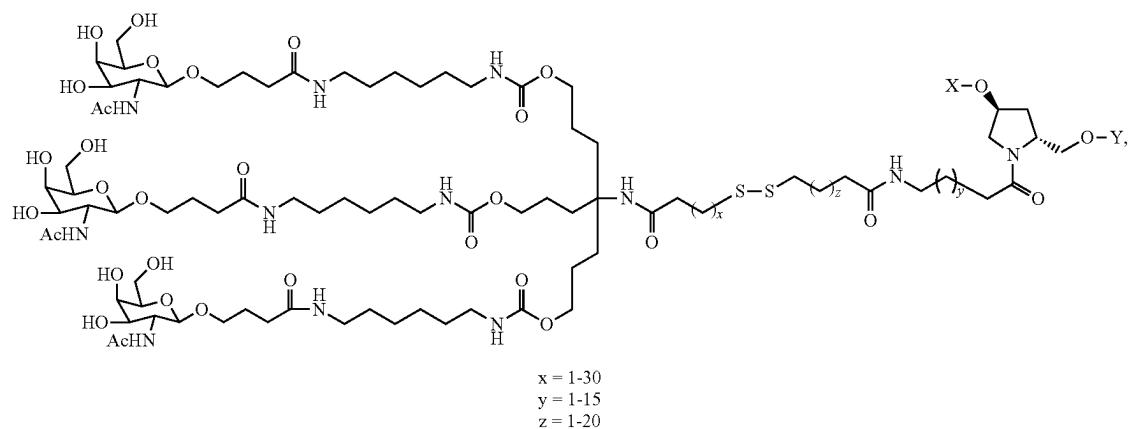
x = 1-30  
y = 1-15

(Formula XLI)



x = 1-30  
y = 1-15

(Formula XLII)



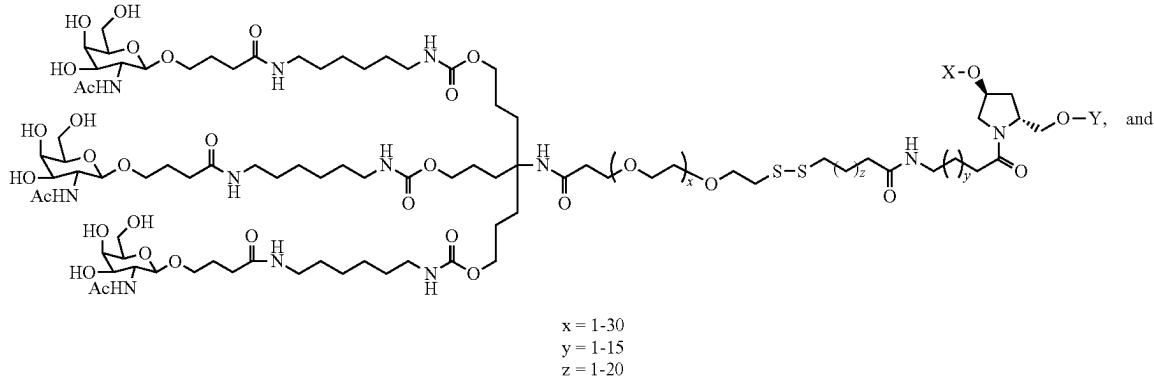
x = 1-30  
y = 1-15  
z = 1-20

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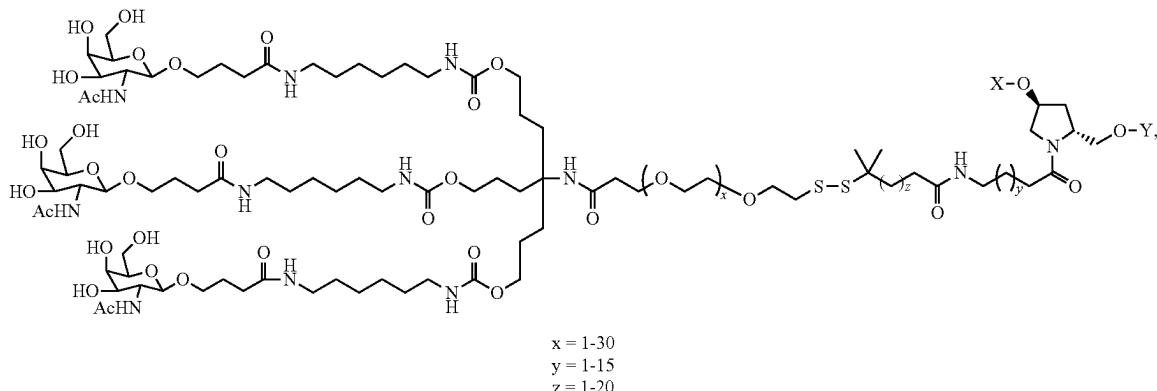
-continued

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(Formula XLIII)



(Formula XLIV)



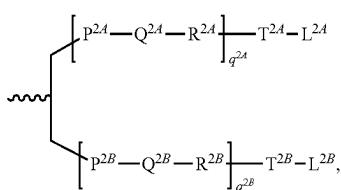
when one of X or Y is an oligonucleotide, the other is a hydrogen.

In certain embodiments of the compositions and methods of the invention, a ligand is one or more "GalNAc" 40 (N-acetylgalactosamine) derivatives attached through a bivalent or trivalent branched linker.

In certain embodiments, a dsRNA of the invention is conjugated to a bivalent or trivalent branched linker selected 45 from the group of structures shown in any of formula (XLV)-(XLVI):

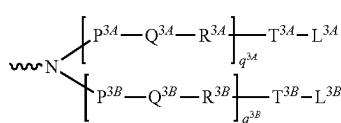
Formula XXXXV

50



Formula XLVI

55



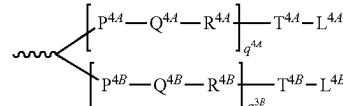
V)

60

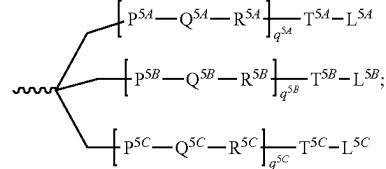
65

-continued

Formula XLVII



Formula XLVIII



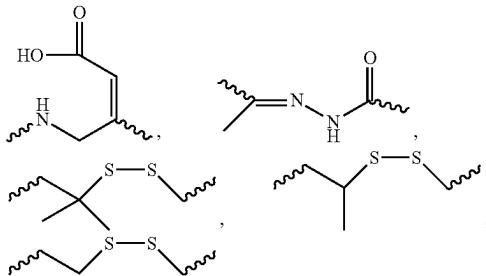
wherein:

q2A, q3B, q3A, q3B, q4A, q4B, q5A, q5B and q5C represent independently for each occurrence 0-20 and wherein the repeating unit can be the same or different; P<sup>2A</sup>, P<sup>2B</sup>, P<sup>3A</sup>, P<sup>3B</sup>, P<sup>4A</sup>, P<sup>4B</sup>, P<sup>5A</sup>, P<sup>5B</sup>, P<sup>5C</sup>, T<sup>2A</sup>, T<sup>2B</sup>, T<sup>3A</sup>, T<sup>3B</sup>, T<sup>4A</sup>, T<sup>4B</sup>, T<sup>4C</sup>, T<sup>5A</sup>, T<sup>5B</sup>, T<sup>5C</sup> are each independently for each occurrence absent, CO, NH, O, S, OC(O), NHC(O), CH<sub>2</sub>, CH<sub>2</sub>NH or CH<sub>2</sub>O;

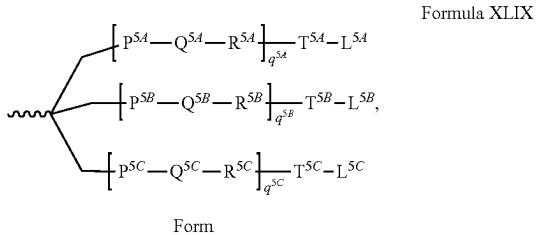
Q<sup>2A</sup>, Q<sup>2B</sup>, Q<sup>3A</sup>, Q<sup>3B</sup>, Q<sup>4A</sup>, Q<sup>4B</sup>, Q<sup>5A</sup>, Q<sup>5B</sup>, Q<sup>5C</sup> are independently for each occurrence absent, alkylene, substituted alkylene wherein one or more methylenes can be interrupted or terminated by one or more of O, S, S(O), SO<sub>2</sub>, N(R<sup>N</sup>), C(R<sup>1</sup>)=C(R<sup>11</sup>), C=C or C(O); R<sup>2A</sup>, R<sup>2B</sup>, R<sup>3A</sup>, R<sup>3B</sup>, R<sup>4A</sup>, R<sup>4B</sup>, R<sup>5A</sup>, R<sup>5B</sup>, R<sup>5C</sup> are each independently for each occurrence absent, NH, O, S,

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$\text{CH}_2$ ,  $\text{C}(\text{O})\text{O}$ ,  $\text{C}(\text{O})\text{NH}$ ,  $\text{NHCH}(\text{R}^a)\text{C}(\text{O})$ ,  $-\text{C}(\text{O})\text{CH}(\text{R}^a)-\text{NH}-$ ,  $\text{CO}$ ,  $\text{CH}=\text{N}-\text{O}$ ,



or heterocycl;  $\text{L}^{2A}$ ,  $\text{L}^{2B}$ ,  $\text{L}^{3A}$ ,  $\text{L}^{3B}$ ,  $\text{L}^{4A}$ ,  $\text{L}^{4B}$ ,  $\text{L}^{5A}$ ,  $\text{L}^{5B}$  and  $\text{L}^{5C}$  represent the ligand; i.e. each independently for each occurrence a monosaccharide (such as GalNAc), disaccharide, trisaccharide, tetrasaccharide, oligosaccharide, or polysaccharide; and  $\text{R}^a$  is H or amino acid side chain. Trivalent conjugating GalNAc derivatives are particularly useful for use with RNAi agents for inhibiting the expression of a target gene, such as those of formula (XLIX):



wherein  $\text{L}^{5A}$ ,  $\text{L}^{5B}$  and  $\text{L}^{5C}$  represent a monosaccharide, such as GalNAc derivative.

Examples of suitable bivalent and trivalent branched linker groups conjugating GalNAc derivatives include, but are not limited to, the structures recited above as formulas II, VII, XI, X, and XIII.

Representative U.S. Patents that teach the preparation of RNA conjugates include, but are not limited to, U.S. Pat. Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241; 5,391,723; 5,416,203; 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928; 5,688,941; 6,294,664; 6,320,017; 6,576,752; 6,783,931; 6,900,297; 7,037,646; and 8,106,022, the entire contents of each of which are hereby incorporated herein by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications can be incorporated in a single compound or even at a single nucleoside within an

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iRNA. The present invention also includes iRNA compounds that are chimeric compounds.

"Chimeric" iRNA compounds or "chimeras," in the context of this invention, are iRNA compounds, preferably dsRNA agents, that contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide in the case of a dsRNA compound. These iRNAs typically contain at least one region wherein the RNA is modified so as to confer upon the iRNA increased resistance to nuclease degradation, increased cellular uptake, or increased binding affinity for the target nucleic acid. An additional region of the iRNA can serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of iRNA inhibition of gene expression. Consequently, comparable results can often be obtained with shorter iRNAs when chimeric dsRNAs are used, compared to phosphorothioate deoxy dsRNAs hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

In certain instances, the RNA of an iRNA can be modified by a non-ligand group. A number of non-ligand molecules have been conjugated to iRNAs in order to enhance the activity, cellular distribution or cellular uptake of the iRNA, and procedures for performing such conjugations are available in the scientific literature. Such non-ligand moieties have included lipid moieties, such as cholesterol (Kubo, T. et al., *Biochem. Biophys. Res. Comm.*, 2007, 365(1):54-61; Letsinger et al., *Proc. Natl. Acad. Sci. USA*, 1989, 86:6553), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1994, 4:1053), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, 1992, 660:306; Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1993, 3:2765), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, 20:533), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., *EMBO J.*, 1991, 10:111; Kabanov et al., *FEBS Lett.*, 1990, 259:327; Svinarchuk et al., *Biochimie*, 1993, 75:49), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al., *Tetrahedron Lett.*, 1995, 36:3651; Shea et al., *Nucl. Acids Res.*, 1990, 18:3777), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14:969), or adamantane acetic acid (Manoharan et al., *Tetrahedron Lett.*, 1995, 36:3651), a palmitoyl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264:229), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277:923). Representative United States patents that teach the preparation of such RNA conjugates have been listed above. Typical conjugation protocols involve the synthesis of RNAs bearing an aminolinker at one or more positions of the sequence. The amino group is then reacted with the molecule being conjugated using appropriate coupling or activating reagents. The conjugation reaction can be performed either with the RNA still bound to the solid support or following cleavage of the RNA, in solution phase. Purification of the RNA conjugate by HPLC typically affords the pure conjugate.

#### V. Delivery of an RNAi Agent of the Disclosure

The delivery of a RNAi agent of the disclosure to a cell e.g., a cell within a subject, such as a human subject (e.g.,

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a subject in need thereof, such as a subject having a coronavirus-associated disorder, e.g., a subject having a coronavirus infection, e.g., a subject having Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or Middle East Respiratory Syndrome (MERS-CoV)), can be achieved in a number of different ways. For example, delivery may be performed by contacting a cell with an RNAi agent of the disclosure either *in vitro* or *in vivo*. In *in vivo* delivery may also be performed directly by administering a composition comprising an RNAi agent, e.g., a dsRNA, to a subject. Alternatively, *in vivo* delivery may be performed indirectly by administering one or more vectors that encode and direct the expression of the RNAi agent. These alternatives are discussed further below.

In general, any method of delivering a nucleic acid molecule (*in vitro* or *in vivo*) can be adapted for use with a RNAi agent of the disclosure (see e.g., Akhtar S. and Julian R L., (1992) *Trends Cell. Biol.* 2(5):139-144 and WO94/02595, which are incorporated herein by reference in their entireties). For *in vivo* delivery, factors to consider in order to deliver an RNAi agent include, for example, biological stability of the delivered agent, prevention of non-specific effects, and accumulation of the delivered agent in the target tissue. The non-specific effects of an RNAi agent can be minimized by local administration, for example, by direct injection or implantation into a tissue or topically administering the preparation. Local administration to a treatment site maximizes local concentration of the agent, limits the exposure of the agent to systemic tissues that can otherwise be harmed by the agent or that can degrade the agent, and permits a lower total dose of the RNAi agent to be administered. Several studies have shown successful knockdown of gene products when an RNAi agent is administered locally. For example, pulmonary system delivery, e.g., inhalation, of a dsRNA, e.g., SOD1, has been shown to effectively knockdown gene and protein expression in lung tissue and that there is excellent uptake of the dsRNA by the bronchioles and alveoli of the lung. Intraocular delivery of a VEGF dsRNA by intravitreal injection in cynomolgus monkeys (Tolentino, M J. et al., (2004) *Retina* 24:132-138) and subretinal injections in mice (Reich, S J. et al. (2003) *Mol. Vis.* 9:210-216) were also both shown to prevent neovascularization in an experimental model of age-related macular degeneration. In addition, direct intratumoral injection of a dsRNA in mice reduces tumor volume (Pille, J. et al. (2005) *Mol. Ther.* 11:267-274) and can prolong survival of tumor-bearing mice (Kim, W J. et al., (2006) *Mol. Ther.* 14:343-350; Li, S. et al., (2007) *Mol. Ther.* 15:515-523). RNA interference has also shown success with local delivery to the CNS by direct injection (Dorn, G. et al., (2004) *Nucleic Acids* 32:e49; Tan, P H. et al. (2005) *Gene Ther.* 12:59-66; Makimura, H. et al (2002) *BMC Neurosci.* 3:18; Shishkina, G T., et al. (2004) *Neuroscience* 129:521-528; Thakker, E R., et al. (2004) *Proc. Natl. Acad. Sci. U.S.A.* 101:17270-17275; Akaneya, Y., et al. (2005) *J. Neurophysiol.* 93:594-602) and to the lungs by intranasal administration (Howard, K A. et al., (2006) *Mol. Ther.* 14:476-484; Zhang, X. et al., (2004) *J. Biol. Chem.* 279:10677-10684; Bitko, V. et al., (2005) *Nat. Med.* 11:50-55). For administering a RNAi agent systemically for the treatment of a disease, the RNA can be modified or alternatively delivered using a drug delivery system; both methods act to prevent the rapid degradation of the dsRNA by endo- and exonucleases *in vivo*. Modification of the RNA or the pharmaceutical carrier can also permit targeting of the RNAi agent to the target tissue and avoid undesirable off-target effects

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(e.g., without wishing to be bound by theory, use of GNAs as described herein has been identified to destabilize the seed region of a dsRNA, resulting in enhanced preference of such dsRNAs for on-target effectiveness, relative to off-target effects, as such off-target effects are significantly weakened by such seed region destabilization). RNAi agents can be modified by chemical conjugation to lipophilic groups such as cholesterol to enhance cellular uptake and prevent degradation. For example, a RNAi agent directed against ApoB conjugated to a lipophilic cholesterol moiety was injected systemically into mice and resulted in knockdown of apoB mRNA in both the liver and jejunum (Soutschek, J. et al., (2004) *Nature* 432:173-178). Conjugation of an RNAi agent to an aptamer has been shown to inhibit tumor growth and mediate tumor regression in a mouse model of prostate cancer (McNamara, J O. et al., (2006) *Nat. Biotechnol.* 24:1005-1015). In an alternative embodiment, the RNAi agent can be delivered using drug delivery systems such as a nanoparticle, a dendrimer, a polymer, liposomes, or a cationic delivery system. Positively charged cationic delivery systems facilitate binding of molecule RNAi agent (negatively charged) and also enhance interactions at the negatively charged cell membrane to permit efficient uptake of an RNAi agent by the cell. Cationic lipids, dendrimers, or polymers can either be bound to an RNAi agent, or induced to form a vesicle or micelle (see e.g., Kim S H. et al., (2008) *Journal of Controlled Release* 129(2): 107-116) that encases an RNAi agent. The formation of vesicles or micelles further prevents degradation of the RNAi agent when administered systemically. Methods for making and administering cationic-RNAi agent complexes are well within the abilities of one skilled in the art (see e.g., Sorensen, D R., et al. (2003) *J. Mol. Biol.* 327:761-766; Verma, U N. et al., (2003) *Clin. Cancer Res.* 9:1291-1300; Arnold, A S et al. (2007) *J. Hypertens.* 25:197-205, which are incorporated herein by reference in their entirety). Some non-limiting examples of drug delivery systems useful for systemic delivery of RNAi agents include DOTAP (Sorensen, D R., et al (2003), supra; Verma, U N. et al., (2003), supra), Oligofectamine, "solid nucleic acid lipid particles" (Zimmermann, T S. et al., (2006) *Nature* 441:111-114), cardiolipin (Chien, P Y. et al., (2005) *Cancer Gene Ther.* 12:321-328; Pal, A. et al., (2005) *Int J. Oncol.* 26:1087-1091), polyethyleneimine (Bonnet M E. et al., (2008) *Pharm. Res.* August 16 Epub ahead of print; Aigner, A. (2006) *J. Biomed. Biotechnol.* 71659), Arg-Gly-Asp (RGD) peptides (Liu, S. (2006) *Mol. Pharm.* 3:472-487), and polyamidoamines (Tomalia, D A. et al., (2007) *Biochem. Soc. Trans.* 35:61-67; Yoo, H. et al., (1999) *Pharm. Res.* 16:1799-1804). In some embodiments, a RNAi agent forms a complex with cyclodextrin for systemic administration. Methods for administration and pharmaceutical compositions of RNAi agents and cyclodextrins can be found in U.S. Pat. No. 7,427,605, which is herein incorporated by reference in its entirety.

Certain aspects of the instant disclosure relate to a method of reducing the expression of a coronavirus target gene in a cell, comprising contacting said cell with the double-stranded RNAi agent of the disclosure. In one embodiment, the cell is a hepatic cell, optionally a hepatocyte. In one embodiment, the cell is an extrahepatic cell, optionally a pulmonary system cell.

Another aspect of the disclosure relates to a method of 65 reducing the expression of a coronavirus target gene in a subject, comprising administering to the subject the double-stranded RNAi agent of the disclosure.

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Another aspect of the disclosure relates to a method of treating a subject having a coronavirus-associated disorder, comprising administering to the subject a therapeutically effective amount of the double-stranded RNAi agent of the disclosure, thereby treating the subject. Non-limiting examples of coronavirus-associated diseases include, for example, Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or Middle East Respiratory Syndrome (MERS-CoV).

For ease of exposition the formulations, compositions and methods in this section are discussed largely with regard to modified siRNA compounds. It may be understood, however, that these formulations, compositions and methods can be practiced with other siRNA compounds, e.g., unmodified siRNA compounds, and such practice is within the disclosure. A composition that includes a RNAi agent can be delivered to a subject by a variety of routes. Exemplary routes include pulmonary system, intravenous, intraventricular, topical, rectal, anal, vaginal, nasal, and ocular.

In one embodiment, the double-stranded RNAi agent is administered by pulmonary system administration.

In one embodiment, the double-stranded RNAi agent is administered by inhalation.

In one embodiment, the double-stranded RNAi agent is administered by intranasal administration.

In one embodiment, the double-stranded RNAi agent is administered subcutaneously.

The RNAi agents of the disclosure can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically include one or more species of RNAi agent and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The pharmaceutical compositions of the present disclosure may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be pulmonary system, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, topical (including ophthalmic, vaginal, rectal, intranasal, transdermal), oral, or parenteral. Parenteral administration includes intravenous drip, subcutaneous, intraperitoneal, or intramuscular injection, or intrathecal or intraventricular administration.

The route and site of administration may be chosen to enhance targeting. For example, to target muscle cells, intramuscular injection into the muscles of interest would be a logical choice. Lung cells might be targeted by administering the RNAi agent in aerosol form. The vascular endothelial cells could be targeted by coating a balloon catheter with the RNAi agent and mechanically introducing the RNA.

Formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids, and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases,

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thickeners and the like may be necessary or desirable. Coated condoms, gloves, and the like may also be useful.

Compositions for oral administration include powders or granules, suspensions or solutions in water, syrups, elixirs or non-aqueous media, tablets, capsules, lozenges, or troches. In the case of tablets, carriers that can be used include lactose, sodium citrate and salts of phosphoric acid. Various disintegrants such as starch, and lubricating agents such as magnesium stearate, sodium lauryl sulfate and talc, are commonly used in tablets. For oral administration in capsule form, useful diluents are lactose and high molecular weight polyethylene glycols. When aqueous suspensions are required for oral use, the nucleic acid compositions can be combined with emulsifying and suspending agents. If desired, certain sweetening or flavoring agents can be added.

Compositions for intrathecal or intraventricular administration may include sterile aqueous solutions which may also contain buffers, diluents, and other suitable additives.

Formulations for parenteral administration may include sterile aqueous solutions which may also contain buffers, diluents, and other suitable additives. Intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir. For intravenous use, the total concentration of solutes may be controlled to render the preparation isotonic.

In one embodiment, the administration of the siRNA compound, e.g., a double-stranded siRNA compound, or ssRNA compound, composition is parenteral, e.g., intravenous (e.g., as a bolus or as a diffusible infusion), intradermal, intraperitoneal, intramuscular, intrathecal, intraventricular, intracranial, subcutaneous, transmucosal, buccal, sublingual, endoscopic, rectal, oral, vaginal, topical, pulmonary system, intranasal, urethral, or ocular. Administration can be provided by the subject or by another person, e.g., a health care provider. The medication can be provided in measured doses or in a dispenser which delivers a metered dose. Selected modes of delivery are discussed in more detail below.

## Pulmonary System Administration

In one embodiment, the double-stranded RNAi agent is administered by pulmonary system administration. The pulmonary system includes the upper pulmonary system and the lower pulmonary system. The upper pulmonary system includes the nose and the pharynx. The pharynx includes the nasopharynx, oropharynx, and laryngopharynx. The lower pulmonary system includes the larynx, trachea, carina, bronchi, bronchioles, and alveoli.

Pulmonary system administration may be intranasal administration or oral inhalative administration. Such administration permits both systemic and local delivery of the double stranded RNAi agents of the invention.

Intranasal administration may include instilling or insufflating a double stranded RNAi agent into the nasal cavity with syringes or droppers by applying a few drops at a time or via atomization. Suitable dosage forms for intranasal administration include drops, powders, nebulized mists, and sprays.

Oral inhalative administration may include use of device, e.g., a passive breath driven or active power driven single/-multiple dose dry powder inhaler (DPI), to deliver a double stranded RNAi agent to the pulmonary system. Suitable dosage forms for oral inhalative administration include powders and solutions. Suitable devices for oral inhalative administration include nebulizers, metered-dose inhalers, and dry powder inhalers. Dry powder inhalers are of the most popular devices used to deliver drugs, especially proteins to the lungs. Exemplary commercially available dry

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powder inhalers include Spinhaler (Fisons Pharmaceuticals, Rochester, NY) and Rotahaler (GSK, RTP, NC). Several types of nebulizers are available, namely jet nebulizers, ultrasonic nebulizers, vibrating mesh nebulizers. Jet nebulizers are driven by compressed air. Ultrasonic nebulizers use a piezoelectric transducer in order to create droplets from an open liquid reservoir. Vibrating mesh nebulizers use perforated membranes actuated by an annular piezoelement to vibrate in resonant bending mode. The holes in the membrane have a large cross-section size on the liquid supply side and a narrow cross-section size on the side from where the droplets emerge. Depending on the therapeutic application, the hole sizes and number of holes can be adjusted. Selection of a suitable device depends on parameters, such as nature of the drug and its formulation, the site of action, and pathophysiology of the lung. Aqueous suspensions and solutions are nebulized effectively. Aerosols based on mechanically generated vibration mesh technologies also have been used successfully to deliver proteins to lungs.

The amount of RNAi agent for pulmonary system administration may vary from one target gene to another target gene and the appropriate amount that has to be applied may have to be determined individually for each target gene. Typically, this amount ranges from 10 µg to 2 mg, preferably 50 µg to 1500 µg, more preferably 100 µg to 1000 µg.

#### Vector Encoded RNAi Agents of the Disclosure

RNAi agents targeting the coronavirus genome can be expressed from transcription units inserted into DNA or RNA vectors (see, e.g., Couture, A, et al., *TIG*, (1996), 12:5-10; WO 00/22113, WO 00/22114, and U.S. Pat. No. 6,054,299). Expression is preferably sustained (months or longer), depending upon the specific construct used and the target tissue or cell type. These transgenes can be introduced as a linear construct, a circular plasmid, or a viral vector, which can be an integrating or non-integrating vector. The transgene can also be constructed to permit it to be inherited as an extrachromosomal plasmid (Gassmann, et al., (1995) *Proc. Natl. Acad. Sci. USA* 92:1292).

The individual strand or strands of a RNAi agent can be transcribed from a promoter on an expression vector. Where two separate strands are to be expressed to generate, for example, a dsRNA, two separate expression vectors can be co-introduced (e.g., by transfection or infection) into a target cell. Alternatively, each individual strand of a dsRNA can be transcribed by promoters both of which are located on the same expression plasmid. In one embodiment, a dsRNA is expressed as inverted repeat polynucleotides joined by a linker polynucleotide sequence such that the dsRNA has a stem and loop structure.

RNAi agent expression vectors are generally DNA plasmids or viral vectors. Expression vectors compatible with eukaryotic cells, preferably those compatible with vertebrate cells, can be used to produce recombinant constructs for the expression of a RNAi agent as described herein. Delivery of RNAi agent expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that allows for introduction into a desired target cell.

Viral vector systems which can be utilized with the methods and compositions described herein include, but are not limited to, (a) adenovirus vectors; (b) retrovirus vectors, including but not limited to lentiviral vectors, moloney murine leukemia virus, etc.; (c) adeno-associated virus vectors; (d) herpes simplex virus vectors; (e) SV 40 vectors; (f) polyoma virus vectors; (g) papilloma virus vectors; (h)

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picornavirus vectors; (i) pox virus vectors such as an orthopox, e.g., vaccinia virus vectors or avipox, e.g. canary pox or fowl pox; and (j) a helper-dependent or gutless adenovirus. Replication-defective viruses can also be advantageous. Different vectors will or will not become incorporated into the cells' genome. The constructs can include viral sequences for transfection, if desired. Alternatively, the construct can be incorporated into vectors capable of episomal replication, e.g. EPV and EBV vectors. Constructs for the recombinant expression of a RNAi agent will generally require regulatory elements, e.g., promoters, enhancers, etc., to ensure the expression of the RNAi agent in target cells. Other aspects to consider for vectors and constructs are known in the art.

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#### VI. Compositions of the Invention

The present disclosure also provides compositions, including pharmaceutical compositions and formulations which include the RNAi agents of the disclosure.

For example, in one embodiment, the present invention provides compositions comprising two or more, e.g., 2, 3, or 4, dsRNA agents, e.g., dsRNA agents comprising a sense strand and an antisense strand forming a double stranded region, wherein each of the sense strands or each of the antisense strands is a sense strand or an antisense strand independently selected from the group consisting of any of the sense strands and antisense strands in any one of Table 2-5. In one embodiment, each of the sense strands or each of the antisense strands is a sense strand or an antisense strand independently selected from the sense strand or antisense strand of a duplex selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1184210, AD-1184270, AD-1184233, AD-1184271, AD-1184212, AD-1184228, AD-1184223, AD-1231490, AD-1231513, AD-1231485, AD-1231507, AD-1231471, AD-1231494, AD-1231496, and AD-1231497. In another embodiment, each of the sense strands or each of the antisense strands is a sense strand or an antisense strand of a duplex independently selected from the group consisting of AD-1184137, AD-1184147, AD-1184150, AD-1231490, AD-1231513, AD-1231485, AD-1231471, AD-1231496, and AD-1231497. In another embodiment, each of the sense strands and each of the antisense strands is a sense strand and an antisense strand of a duplex independently selected from the group consisting of AD-1184137 and AD-1184150. In one embodiment, the composition comprises a first dsRNA agent comprising the sense strand nucleotide sequence 5'-UAACAAUGUUGCUUUUCAAAC-3'(SEQ ID NO: 5) and an antisense strand comprising the nucleotide sequence 5'-GUUUGAAAAGCAACAUUGUUAGU-3' (SEQ ID NO: 6); and a second dsRNA agent comprising the sense strand nucleotide sequence 5'-ACUGUACAGUC-55 AAAAUGUCA-3' (SEQ ID NO: 7) and an antisense strand comprising the nucleotide sequence 5'-UGA-55 CAUUUUAGACUGUACAGUGG-3' (SEQ ID NO: 8). In one embodiment, the sense strand of the first dsRNA agent comprises the sense strand nucleotide sequence 5'-usasaca (Ahd)UfgUfUfGfcuuucaasasa-3' (SEQ ID NO: 9) and the 60 antisense strand of the first dsRNA agent comprises the nucleotide sequence 5'-VPUsUfsuugAfaaagcaaCfaU-fuguuagsu-3' (SEQ ID NO: 10); and the sense strand of the second dsRNA agent comprises the nucleotides sequence 5'-ascsgu(Ahd)CfaGfUfCfuaaauguscsa-3' (SEQ ID NO: 11) and the antisense strand of the second dsRNA agent comprises the nucleotide sequence 5'-VPUsGfsacaUfuuuu-gacUfgUfacagusgsg-3' (SEQ ID NO: 12), wherein a, g, c

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and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexadecyl-adenosine-3'-phosphate; and VP is Vinyl-phosphonate.

In another embodiment, provided herein are pharmaceutical compositions containing an RNAi agent, or a composition, as described herein, and a pharmaceutically acceptable carrier. The pharmaceutical compositions containing the RNAi agent or the composition are useful for treating a subject who would benefit from inhibiting or reducing the expression of a coronavirus genome, e.g., a subject having a coronavirus-associated disorder, e.g., a subject having a coronavirus infection, e.g., a subject having Severe Acute Respiratory Syndrome 2 (SARS-CoV-2; COVID-19), Severe Acute Respiratory Syndrome (SARS-CoV), or Middle East Respiratory Syndrome (MERS-CoV). Such pharmaceutical compositions are formulated based on the mode of delivery. One example is compositions that are formulated for direct delivery into the pulmonary system by intranasal administration or oral inhalative administration, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal or intranasal delivery. Another example is compositions that are formulated for systemic administration via parenteral delivery, e.g., by intravenous (IV), intramuscular (IM), or for subcutaneous (subQ) delivery.

In some embodiments, the pharmaceutical compositions of the invention are pyrogen free or non-pyrogenic.

The pharmaceutical compositions of the disclosure may be administered in dosages sufficient to inhibit expression of a coronavirus genome. In general, a suitable dose of an RNAi agent of the disclosure will be a flat dose in the range of about 0.001 to about 200.0 mg about once per month to about once per year, typically about once per quarter (i.e., about once every three months) to about once per year, generally a flat dose in the range of about 1 to 50 mg about once per month to about once per year, typically about once per quarter to about once per year.

After an initial treatment regimen (e.g., loading dose), the treatments can be administered on a less frequent basis.

The skilled artisan will appreciate that certain factors can influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a composition can include a single treatment or a series of treatments.

Advances in mouse genetics have generated a number of mouse models for the study of various coronavirus-associated diseases that would benefit from reduction in the expression of coronavirus. Such models can be used for in vivo testing of RNAi agents, as well as for determining a therapeutically effective dose. Suitable mouse models are known in the art and include, for example, the mouse models described elsewhere herein.

The pharmaceutical compositions of the present disclosure can be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration can be topical (e.g., by a transdermal patch), pulmonary system administration by intranasal administration or oral inhalative administration, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, epidermal and transdermal, oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intra-peritoneal or intramuscular injection or infusion; subdermal,

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e.g., via an implanted device; or intracranial, e.g., by intraparenchymal, intrathecal or intraventricular, administration.

The RNAi agents can be delivered in a manner to target a particular tissue, such as the liver, the lung (e.g., bronchioles, alveoli, or bronchus of the lung), or both the liver and lung.

Pharmaceutical compositions and formulations for topical administration can include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like can be necessary or desirable. Coated condoms, gloves and the like can also be useful. Suitable topical formulations include those in which the RNAi agents featured in the disclosure are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Suitable lipids and liposomes include neutral (e.g., dioleoylphosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearoylphosphatidyl choline) negative (e.g., dimyristoylphosphatidyl glycerol DMPG) and cationic (e.g., dioleyltrimethylammoniumpropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA). RNAi agents featured in the disclosure can be encapsulated within liposomes or can form complexes thereto, in particular to cationic liposomes. Alternatively, RNAi agents can be complexed to lipids, in particular to cationic lipids. Suitable fatty acids and esters include but are not limited to arachidonic acid, oleic acid, eicosanoic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a C<sub>1-20</sub> alkyl ester (e.g., isopropylmyristate IPM), monoglyceride, diglyceride or pharmaceutically acceptable salt thereof. Topical formulations are described in detail in U.S. Pat. No. 6,747,014, which is incorporated herein by reference.

#### A. RNAi Agent Formulations Comprising Membranous Molecular Assemblies

A RNAi agent for use in the compositions and methods of the disclosure can be formulated for delivery in a membranous molecular assembly, e.g., a liposome or a micelle. As used herein, the term "liposome" refers to a vesicle composed of amphiphilic lipids arranged in at least one bilayer, e.g., one bilayer or a plurality of bilayers. Liposomes include unilamellar and multilamellar vesicles that have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the RNAi agent composition. The lipophilic material isolates the aqueous interior from an aqueous exterior, which typically does not include the RNAi agent composition, although in some examples, it may. Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a tissue, the liposomal bilayer fuses with bilayer of the cellular membranes. As the merging of the liposome and cell progresses, the internal aqueous contents that include the RNAi agent are delivered into the cell where the RNAi agent can specifically bind to a target RNA and can mediate RNAi. In some cases the liposomes are also specifically targeted, e.g., to direct the RNAi agent to particular cell types.

A liposome containing an RNAi agent can be prepared by a variety of methods. In one example, the lipid component of a liposome is dissolved in a detergent so that micelles are formed with the lipid component. For example, the lipid component can be an amphipathic cationic lipid or lipid

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conjugate. The detergent can have a high critical micelle concentration and may be nonionic. Exemplary detergents include cholate, CHAPS, octylglucoside, deoxycholate, and lauroyl sarcosine. The RNAi agent preparation is then added to the micelles that include the lipid component. The cationic groups on the lipid interact with the RNAi agent and condense around the RNAi agent to form a liposome. After condensation, the detergent is removed, e.g., by dialysis, to yield a liposomal preparation of RNAi agent.

If necessary a carrier compound that assists in condensation can be added during the condensation reaction, e.g., by controlled addition. For example, the carrier compound can be a polymer other than a nucleic acid (e.g., spermine or spermidine). pH can also adjusted to favor condensation.

Methods for producing stable polynucleotide delivery vehicles, which incorporate a polynucleotide/cationic lipid complex as structural components of the delivery vehicle, are further described in, e.g., WO 96/37194, the entire contents of which are incorporated herein by reference. Liposome formation can also include one or more aspects of exemplary methods described in Felgner, P. L. et al., (1987) *Proc. Natl. Acad. Sci. USA* 8:7413-7417; U.S. Pat. Nos. 4,897,355; 5,171,678; Bangham et al., (1965) *M. Mol. Biol.* 23:238; Olson et al., (1979) *Biochim. Biophys. Acta* 557:9; Szoka et al., (1978) *Proc. Natl. Acad. Sci.* 75: 4194; Mayhew et al., (1984) *Biochim. Biophys. Acta* 775:169; Kim et al., (1983) *Biochim. Biophys. Acta* 728:339; and Fukunaga et al., (1984) *Endocrinol.* 115:757. Commonly used techniques for preparing lipid aggregates of appropriate size for use as delivery vehicles include sonication and freeze-thaw plus extrusion (see, e.g., Mayer et al., (1986) *Biochim. Biophys. Acta* 858:161. Microfluidization can be used when consistently small (50 to 200 nm) and relatively uniform aggregates are desired (Mayhew et al., (1984) *Biochim. Biophys. Acta* 775:169. These methods are readily adapted to packaging RNAi agent preparations into liposomes.

Liposomes fall into two broad classes. Cationic liposomes are positively charged liposomes which interact with the negatively charged nucleic acid molecules to form a stable complex. The positively charged nucleic acid/liposome complex binds to the negatively charged cell surface and is internalized in an endosome. Due to the acidic pH within the endosome, the liposomes are ruptured, releasing their contents into the cell cytoplasm (Wang et al. (1987) *Biochem. Biophys. Res. Commun.*, 147:980-985).

Liposomes, which are pH-sensitive or negatively charged, entrap nucleic acids rather than complex with them. Since both the nucleic acid and the lipid are similarly charged, repulsion rather than complex formation occurs. Nevertheless, some nucleic acid is entrapped within the aqueous interior of these liposomes. pH sensitive liposomes have been used to deliver nucleic acids encoding the thymidine kinase gene to cell monolayers in culture. Expression of the exogenous gene was detected in the target cells (Zhou et al. (1992) *Journal of Controlled Release*, 19:269-274).

One major type of liposomal composition includes phospholipids other than naturally-derived phosphatidylcholine. Neutral liposome compositions, for example, can be formed from dimyristoyl phosphatidylcholine (DMPC) or dipalmitoyl phosphatidylcholine (DPPC). Anionic liposome compositions generally are formed from dimyristoyl phosphatidylglycerol, while anionic fusogenic liposomes are formed primarily from dioleoyl phosphatidylethanolamine (DOPE). Another type of liposomal composition is formed from phosphatidylcholine (PC) such as, for example, soybean PC, and egg PC. Another type is formed from mixtures of phospholipid or phosphatidylcholine or cholesterol.

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Examples of other methods to introduce liposomes into cells in vitro and in vivo include U.S. Pat. Nos. 5,283,185; 5,171,678; WO 94/00569; WO 93/24640; WO 91/16024; Felgner, (1994) *J. Biol. Chem.* 269:2550; Nabel, (1993) *Proc. Natl. Acad. Sci.* 90:11307; Nabel, (1992) *Human Gene Ther.* 3:649; Gershon, (1993) *Biochem.* 32:7143; and Strauss, (1992) *EMBO J.* 11:417.

Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novasome™ I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novasome™ II (glyceryl distearate/cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver cyclosporin-A into the dermis of mouse skin. Results indicated that such non-ionic liposomal systems were effective in facilitating the deposition of cyclosporine A into different layers of the skin (Hu et al., (1994) *S.T.P. Pharma. Sci.*, 4(6):466).

Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome (A) comprises one or more glycolipids, such as monosialoganglioside G<sub>M1</sub>, or (B) is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. While not wishing to be bound by any particular theory, it is thought in the art that, at least for sterically stabilized liposomes containing gangliosides, sphingomyelin, or PEG-derivatized lipids, the enhanced circulation half-life of these sterically stabilized liposomes derives from a reduced uptake into cells of the reticuloendothelial system (RES) (Allen et al., (1987) *FEBS Letters*, 223:42; Wu et al., (1993) *Cancer Research*, 53:3765).

Various liposomes comprising one or more glycolipids are known in the art. Papahadjopoulos et al. (*Ann. N.Y. Acad. Sci.*, (1987), 507:64) reported the ability of monosialoganglioside G<sub>M1</sub>, galactocerebroside sulfate and phosphatidylinositol to improve blood half-lives of liposomes. These findings were expounded upon by Gabizon et al. (*Proc. Natl. Acad. Sci. U.S.A.*, (1988), 85:6949). U.S. Pat. No. 4,837,028 and WO 88/04924, both to Allen et al., disclose liposomes comprising (1) sphingomyelin and (2) the ganglioside G<sub>M1</sub> or a galactocerebroside sulfate ester. U.S. Pat. No. 5,543,152 (Webb et al.) discloses liposomes comprising sphingomyelin. Liposomes comprising 1,2-sn-dimyristoylphosphatidylcholine are disclosed in WO 97/13499 (Lim et al.).

In one embodiment, cationic liposomes are used. Cationic liposomes possess the advantage of being able to fuse to the cell membrane. Non-cationic liposomes, although not able to fuse as efficiently with the plasma membrane, are taken up by macrophages in vivo and can be used to deliver RNAi agents to macrophages.

Further advantages of liposomes include: liposomes obtained from natural phospholipids are biocompatible and biodegradable; liposomes can incorporate a wide range of water and lipid soluble drugs; liposomes can protect encapsulated RNAi agents in their internal compartments from metabolism and degradation (Rosoff, in "Pharmaceutical Dosage Forms," Lieberman, Rieger and Banker (Eds.), 1988, volume 1, p. 245). Important considerations in the

preparation of liposome formulations are the lipid surface charge, vesicle size and the aqueous volume of the liposomes.

A positively charged synthetic cationic lipid, N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride (DOTMA) can be used to form small liposomes that interact spontaneously with nucleic acid to form lipid-nucleic acid complexes which are capable of fusing with the negatively charged lipids of the cell membranes of tissue culture cells, resulting in delivery of RNAi agent (see, e.g., Felgner, P. L. et al., (1987) *Proc. Natl. Acad. Sci. USA* 8:7413-7417, and U.S. Pat. No. 4,897,355 for a description of DOTMA and its use with DNA).

A DOTMA analogue, 1,2-bis(oleoyloxy)-3-(trimethylammonia)propane (DOTAP) can be used in combination with a phospholipid to form DNA-complexing vesicles. Lipofectin™ Bethesda Research Laboratories, Gaithersburg, Md.) is an effective agent for the delivery of highly anionic nucleic acids into living tissue culture cells that comprise positively charged DOTMA liposomes which interact spontaneously with negatively charged polynucleotides to form complexes. When enough positively charged liposomes are used, the net charge on the resulting complexes is also positive. Positively charged complexes prepared in this way spontaneously attach to negatively charged cell surfaces, fuse with the plasma membrane, and efficiently deliver functional nucleic acids into, for example, tissue culture cells. Another commercially available cationic lipid, 1,2-bis(oleoyloxy)-3-(trimethylammonia)propane ("DOTAP") (Boehringer Mannheim, Indianapolis, Indiana) differs from DOTMA in that the oleoyl moieties are linked by ester, rather than ether linkages.

Other reported cationic lipid compounds include those that have been conjugated to a variety of moieties including, for example, carboxyspermine which has been conjugated to one of two types of lipids and includes compounds such as 5-carboxyspermylglycine diactaooleylamide ("DOGS") (Transfectam™, Promega, Madison, Wisconsin) and dipalmitoylphosphatidylethanolamine 5-carboxyspermyl-amide ("DPPE") (see, e.g., U.S. Pat. No. 5,171,678).

Another cationic lipid conjugate includes derivatization of the lipid with cholesterol ("DC-Chol") which has been formulated into liposomes in combination with DOPE (See, Gao, X. and Huang, L., (1991) *Biochim. Biophys. Res. Commun.* 179:280). Lipopolylysine, made by conjugating polylysine to DOPE, has been reported to be effective for transfection in the presence of serum (Zhou, X. et al., (1991) *Biochim. Biophys. Acta* 1065:8). For certain cell lines, these liposomes containing conjugated cationic lipids, are said to exhibit lower toxicity and provide more efficient transfection than the DOTMA-containing compositions. Other commercially available cationic lipid products include DMRIE and DMRIE-HP (Vical, La Jolla, California) and Lipofectamine (DOSPA) (Life Technology, Inc., Gaithersburg, Maryland). Other cationic lipids suitable for the delivery of oligonucleotides are described in WO 98/39359 and WO 96/37194.

Liposomal formulations are particularly suited for topical administration, liposomes present several advantages over other formulations. Such advantages include reduced side effects related to high systemic absorption of the administered drug, increased accumulation of the administered drug at the desired target, and the ability to administer RNAi agent into the skin. In some implementations, liposomes are used for delivering RNAi agent to epidermal cells and also to enhance the penetration of RNAi agent into dermal tissues, e.g., into skin. For example, the liposomes can be applied topically. Topical delivery of drugs formulated as

liposomes to the skin has been documented (see, e.g., Weiner et al., (1992) *Journal of Drug Targeting*, vol. 2,405-410 and du Plessis et al., (1992) *Antiviral Research*, 18:259-265; Mannino, R. J. and Fould-Fogerite, S., (1998) *Biotechniques* 6:682-690; Itani, T. et al., (1987) *Gene* 56:267-276; Nicolau, C. et al. (1987) *Meth. Enzymol.* 149:157-176; Straubinger, R. M. and Papahadjopoulos, D. (1983) *Meth. Enzymol.* 101:512-527; Wang, C. Y. and Huang, L., (1987) *Proc. Natl. Acad. Sci. USA* 84:7851-7855).

- 10 Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novosome I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novosome II (glyceryl distearate/cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver a drug into the dermis of mouse skin. Such formulations with RNAi agent are useful for treating a dermatological disorder.
- 15 20 Liposomes that include RNAi agents can be made highly deformable. Such deformability can enable the liposomes to penetrate through pores that are smaller than the average radius of the liposome. For example, transfersomes are a type of deformable liposomes. Transfersomes can be made by adding surface edge activators, usually surfactants, to a standard liposomal composition. Transfersomes that include RNAi agent can be delivered, for example, subcutaneously by injection in order to deliver RNAi agent to keratinocytes in the skin. In order to cross intact mammalian skin, lipid vesicles must pass through a series of fine pores, each with a diameter less than 50 nm, under the influence of a suitable transdermal gradient. In addition, due to the lipid properties, these transfersomes can be self-optimizing (adaptive to the shape of pores, e.g., in the skin), self-repairing, and can 25 frequently reach their targets without fragmenting, and often 30 self-loading.

Other formulations amenable to the present disclosure are described in PCT publication No. WO 2008/042973.

- 35 Transfersomes, yet another type of liposomes, are highly 40 deformable lipid aggregates which are attractive candidates for drug delivery vehicles. Transfersomes can be described as lipid droplets which are so highly deformable that they are easily able to penetrate through pores which are smaller than the droplet. Transfersomes are adaptable to the environment 45 in which they are used, e.g., they are self-optimizing (adaptive to the shape of pores in the skin), self-repairing, frequently reach their targets without fragmenting, and often self-loading. To make transfersomes it is possible to add surface edge-activators, usually surfactants, to a standard 50 liposomal composition. Transfersomes have been used to deliver serum albumin to the skin. The transfersome-mediated delivery of serum albumin has been shown to be as effective as subcutaneous injection of a solution containing serum albumin.

- 55 Surfactants find wide application in formulations such as those described herein, particularly in emulsions (including microemulsions) and liposomes. The most common way of classifying and ranking the properties of the many different types of surfactants, both natural and synthetic, is by the use 60 of the hydrophilic/lipophile balance (HLB). The nature of the hydrophilic group (also known as the "head") provides the most useful means for categorizing the different surfactants used in formulations (Rieger, in *Pharmaceutical Dosage Forms*, Marcel Dekker, Inc., New York, N.Y., 1988, p. 285).

- 65 If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are

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usable over a wide range of pH values. In general, their HLB values range from 2 to about 18 depending on their structure. Nonionic surfactants include nonionic esters such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

If the surfactant molecule carries a negative charge when it is dissolved or dispersed in water, the surfactant is classified as anionic. Anionic surfactants include carboxylates such as soaps, acyl lactylates, acyl amides of amino acids, esters of sulfuric acid such as alkyl sulfates and ethoxylated alkyl sulfates, sulfonates such as alkyl benzene sulfonates, acyl isethionates, acyl taurates and sulfosuccinates, and phosphates. The most important members of the anionic surfactant class are the alkyl sulfates and the soaps.

If the surfactant molecule carries a positive charge when it is dissolved or dispersed in water, the surfactant is classified as cationic. Cationic surfactants include quaternary ammonium salts and ethoxylated amines. The quaternary ammonium salts are the most used members of this class.

If the surfactant molecule has the ability to carry either a positive or negative charge, the surfactant is classified as amphoteric. Amphoteric surfactants include acrylic acid derivatives, substituted alkylamides, N-alkylbетaines and phosphatides.

The use of surfactants in drug products, formulations and in emulsions has been reviewed (Rieger, in *Pharmaceutical Dosage Forms*, Marcel Dekker, Inc., New York, N.Y., 1988, p. 285).

The RNAi agent for use in the methods of the disclosure can also be provided as micellar formulations. "Micelles" are defined herein as a particular type of molecular assembly in which amphipathic molecules are arranged in a spherical structure such that all the hydrophobic portions of the molecules are directed inward, leaving the hydrophilic portions in contact with the surrounding aqueous phase. The converse arrangement exists if the environment is hydrophobic.

A mixed micellar formulation suitable for delivery through transdermal membranes may be prepared by mixing an aqueous solution of the siRNA composition, an alkali metal C<sub>8</sub> to C<sub>22</sub> alkyl sulphate, and a micelle forming compounds. Exemplary micelle forming compounds include lecithin, hyaluronic acid, pharmaceutically acceptable salts of hyaluronic acid, glycolic acid, lactic acid, chamomile extract, cucumber extract, oleic acid, linoleic acid, linolenic acid, monoolein, monooleates, monolaurates, borage oil, evening of primrose oil, menthol, trihydroxy oxo cholanyl glycine and pharmaceutically acceptable salts thereof, glycerin, polyglycerin, lysine, polylysine, triolein, polyoxyethylene ethers and analogues thereof, polidocanol alkyl ethers and analogues thereof, chenodeoxycholate, deoxycholate, and mixtures thereof. The micelle forming compounds may be added at the same time or after addition of the alkali metal alkyl sulphate. Mixed micelles will form with substantially any kind of mixing of the ingredients but vigorous mixing in order to provide smaller size micelles.

In one method a first micellar composition is prepared which contains the siRNA composition and at least the alkali metal alkyl sulphate. The first micellar composition is then mixed with at least three micelle forming compounds to form a mixed micellar composition. In another method, the micellar composition is prepared by mixing the siRNA composition, the alkali metal alkyl sulphate and at least one

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of the micelle forming compounds, followed by addition of the remaining micelle forming compounds, with vigorous mixing.

Phenol or m-cresol may be added to the mixed micellar composition to stabilize the formulation and protect against bacterial growth. Alternatively, phenol or m-cresol may be added with the micelle forming ingredients. An isotonic agent such as glycerin may also be added after formation of the mixed micellar composition.

For delivery of the micellar formulation as a spray, the formulation can be put into an aerosol dispenser and the dispenser is charged with a propellant. The propellant, which is under pressure, is in liquid form in the dispenser. The ratios of the ingredients are adjusted so that the aqueous and propellant phases become one, i.e., there is one phase. If there are two phases, it is necessary to shake the dispenser prior to dispensing a portion of the contents, e.g., through a metered valve. The dispensed dose of pharmaceutical agent is propelled from the metered valve in a fine spray.

Propellants may include hydrogen-containing chlorofluorocarbons, hydrogen-containing fluorocarbons, dimethyl ether and diethyl ether. In certain embodiments, HFA 134a (1,1,1,2 tetrafluoroethane) may be used.

The specific concentrations of the essential ingredients can be determined by relatively straightforward experimentation. For absorption through the oral cavities, it is often desirable to increase, e.g., at least double or triple, the dosage for through injection or administration through the gastrointestinal tract.

#### Lipid Particles

RNAi agents, e.g., dsRNAs of in the disclosure may be fully encapsulated in a lipid formulation, e.g., a LNP, or other nucleic acid-lipid particle.

As used herein, the term "LNP" refers to a stable nucleic acid-lipid particle. LNPs typically contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (e.g., a PEG-lipid conjugate). LNPs are extremely useful for systemic applications, as they exhibit extended circulation lifetimes following intravenous (i.v.) injection and accumulate at distal sites (e.g., sites physically separated from the administration site). LNPs include "pSPLP," which include an encapsulated condensing agent-nucleic acid complex as set forth in WO 00/03683. The particles of the present disclosure typically have a mean diameter of about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 nm to about 90 nm, and are substantially nontoxic. In addition, the nucleic acids when present in the nucleic acid-lipid particles of the present disclosure are resistant in aqueous solution to degradation with a nuclease. Nucleic acid-lipid particles and their method of preparation are disclosed in, e.g., U.S. Pat. Nos. 5,976,567; 5,981,501; 6,534,484; 6,586,410; 6,815,432; United States Patent publication No. 2010/0324120 and WO 96/40964.

In one embodiment, the lipid to drug ratio (mass/mass ratio) (e.g., lipid to dsRNA ratio) will be in the range of from about 1:1 to about 50:1, from about 1:1 to about 25:1, from about 3:1 to about 15:1, from about 4:1 to about 10:1, from about 5:1 to about 9:1, or about 6:1 to about 9:1. Ranges intermediate to the above recited ranges are also contemplated to be part of the disclosure.

Certain specific LNP formulations for delivery of RNAi agents have been described in the art, including, e.g., "LNP01" formulations as described in, e.g., WO 2008/042973, which is hereby incorporated by reference.

Additional exemplary lipid-dsRNA formulations are identified in the table below.

		Ionizable/Cationic Lipid	cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
SNALP-1	1,2-Dilinoleyoxy-N,N-dimethylaminopropane (DLinDMA)		DLinDMA/DPPC/Cholesterol/PEG-cDMA (57.1/7.1/34.4/1.4) lipid:siRNA~7:1
2-XTC	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)		XTC/DPPC/Cholesterol/PEG-cDMA 57.1/7.1/34.4/1.4 lipid:siRNA~7:1
LNP05	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)		XTC/DSPC/Cholesterol/PEG-DMG 57.5/7.5/31.5/3.5 lipid:siRNA~6:1
LNP06	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)		XTC/DSPC/Cholesterol/PEG-DMG 57.5/7.5/31.5/3.5 lipid:siRNA~11:1
LNP07	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)		XTC/DSPC/Cholesterol/PEG-DMG 60/7.5/31/1.5, lipid:siRNA~6:1
LNP08	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)		XTC/DSPC/Cholesterol/PEG-DMG 60/7.5/31/1.5, lipid:siRNA~11:1
LNP09	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)		XTC/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP10	(3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-cyclopenta[d][1,3]dioxol-5-amine (ALN100)		ALN100/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP11	(6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3)		MC-3/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP12	1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (Tech G1)		Tech G1/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP13	XTC		XTC/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 33:1
LNP14	MC3		MC3/DSPC/Chol/PEG-DMG 40/15/40/5 Lipid:siRNA: 11:1
LNP15	MC3		MC3/DSPC/Chol/PEG-DSG/GalNAc-PEG-DSG 50/10/35/4.5/0.5 Lipid:siRNA: 11:1
LNP16	MC3		MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP17	MC3		MC3/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP18	MC3		MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 12:1
LNP19	MC3		MC3/DSPC/Chol/PEG-DMG 50/10/35/5 Lipid:siRNA: 8:1
LNP20	MC3		MC3/DSPC/Chol/PEG-DPG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP21	C12-200		C12-200/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 7:1

Ionizable/Cationic Lipid		cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
LNP22	XTC	XTC/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1

DSPC: distearoylphosphatidylcholine

DPPC: dipalmitoylphosphatidylcholine

PEG-DMG: PEG-didimyristoyl glycerol (C14-PEG, or PEG-C14) (PEG with avg mol wt of 2000)

PEG-DSG: PEG-distyryl glycerol (C18-PEG, or PEG-C18) (PEG with avg mol wt of 2000)

PEG-cDMA: PEG-carbamoyl-1,2-dimyristyloxypropylamine (PEG with avg mol wt of 2000)

SNALP (1,2-Dilinoleoyloxy-N,N-dimethylaminopropane (DLinDMA)) comprising formulations are described in WO 2009/127060, which is hereby incorporated by reference.

XTC comprising formulations are described in WO 2010/088537, the entire contents of which are hereby incorporated herein by reference.

MC3 comprising formulations are described, e.g., in United States Patent Publication No. 2010/0324120, the entire contents of which are hereby incorporated by reference.

ALNY-100 comprising formulations are described in WO 2010/054406, the entire contents of which are hereby incorporated herein by reference.

C12-200 comprising formulations are described in WO 2010/129709, the entire contents of which are hereby incorporated herein by reference.

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders can be desirable. In some embodiments, oral formulations are those in which dsRNAs featured in the disclosure are administered in conjunction with one or more penetration enhancer surfactants and chelators. Suitable surfactants include fatty acids or esters or salts thereof, bile acids or salts thereof. Suitable bile acids/salts include chenodeoxycholic acid (CDCA) and ursodeoxychenodeoxycholic acid (UDCA), cholic acid, dehydrocholic acid, deoxycholic acid, glucolic acid, glycholic acid, glycdeoxycholic acid, taurocholic acid, taurodeoxycholic acid, sodium tauro-24,25-dihydro-fusidate and sodium glycodihydrofusidate. Suitable fatty acids include arachidonic acid, undecanoic acid, oleic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a monoglyceride, a diglyceride or a pharmaceutically acceptable salt thereof (e.g., sodium). In some embodiments, combinations of penetration enhancers are used, for example, fatty acids/salts in combination with bile acids/salts. One exemplary combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. DsRNAs featured in the disclosure can be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. DsRNA complexing agents include poly-amino acids; polyimines; polyacrylates; poly-alkylacrylates, polyoxethanes, polyalkylcyanoacrylates; cationized gelatins, albumins, starches, acrylates, polyethylenglycols (PEG) and starches; polyalkylcyanoacrylates; DEAE-derivatized polyimines, pollulans, celluloses and starches. Suitable complexing agents include chitosan, N-trimethylchitosan, poly-L-lysine, polyhistidine, polyornithine, polyspermines, protamine, polyvinylpyridine, poly-thiodiethylaminomethylethylene P(TDAE), polyaminostyrene (e.g., p-amino), poly(methylcyanoacrylate), poly(ethylcyanoacrylate), poly(butylcyanoacrylate), poly(isobutylcyanoacrylate), poly(isohexylcyanoacrylate), DEAE-methacrylate, DEAE-hexylacrylate, DEAE-acrylamide, DEAE-albumin and DEAE-dextran, polymethylacrylate, polyhexylacrylate, poly(D,L-lactic acid), poly(DL-lac-

tic-co-glycolic acid (PLGA), alginate, and polyethyleneglycol (PEG). Oral formulations for dsRNAs and their preparation are described in detail in U.S. Pat. No. 6,887,906, U.S. 2003/0027780, and U.S. Pat. No. 6,747,014, each of which is incorporated herein by reference.

Compositions for pulmonary system delivery may include aqueous solutions, e.g., for intranasal or oral inhalative administration, suitable carriers composed of, e.g., lipids (liposomes, niosomes, microemulsions, lipidic micelles, solid lipid nanoparticles) or polymers (polymer micelles, dendrimers, polymeric nanoparticles, nonogels, nanocapsules), adjuvant, e.g., for oral inhalative administration. Aqueous compositions may be sterile and may optionally contain buffers, diluents, absorption enhancers and other suitable additives.

Compositions and formulations for parenteral, intraparenchymal (into the brain), intrathecal, intraventricular or intrahepatic administration can include sterile aqueous solutions which can also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Pharmaceutical compositions of the present disclosure include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions can be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids. Particularly preferred are formulations that target the brain when treating APP-associated diseases or disorders.

The pharmaceutical formulations of the present disclosure, which can conveniently be presented in unit dosage form, can be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

The compositions of the present disclosure can be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present disclosure can also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions can further contain substances which increase the

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viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol or dextran. The suspension can also contain stabilizers.

#### Additional Formulations

##### i. Emulsions

The compositions of the present disclosure can be prepared and formulated as emulsions. Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 m in diameter (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi et al., in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 301). Emulsions are often biphasic systems comprising two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions can be of either the water-in-oil (w/o) or the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase, the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase, the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions can contain additional components in addition to the dispersed phases, and the active drug which can be present as a solution in either aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants can also be present in emulsions as needed. Pharmaceutical emulsions can also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise, a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion can be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that can be incorporated into either phase of the emulsion. Emulsifiers can broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Synthetic surfactants, also known as surface active agents, have found wide applicability in the formulation of emul-

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sions and have been reviewed in the literature (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rieger, in Pharmaceutical Dosage Forms, Lieberman,

- 5 Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199).
- 10 Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The ratio of the hydrophilic to the hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants can be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic and amphoteric (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004,
- 15 Lippincott Williams & Wilkins (8th ed.), New York, NY Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

Naturally occurring emulsifiers used in emulsion formulations include lanolin, beeswax, phosphatides, lecithin and acacia. Absorption bases possess hydrophilic properties such that they can soak up water to form w/o emulsions yet retain their semisolid consistencies, such as anhydrous lanolin and hydrophilic petrolatum. Finely divided solids have also been used as good emulsifiers especially in combination with surfactants and in viscous preparations. These include polar inorganic solids, such as heavy metal hydroxides, nonswelling clays such as bentonite, attapulgite, hectorite, kaolin, montmorillonite, colloidal aluminum silicate and colloidal magnesium aluminum silicate, pigments and nonpolar solids such as carbon or glyceryl tristearate.

A large variety of non-emulsifying materials are also included in emulsion formulations and contribute to the properties of emulsions. These include fats, oils, waxes, fatty acids, fatty alcohols, fatty esters, humectants, hydrophilic colloids, preservatives and antioxidants (Block, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Hydrophilic colloids or hydrocolloids include naturally occurring gums and synthetic polymers such as polysaccharides (for example, acacia, agar, alginic acid, carrageenan, guar gum, karaya gum, and tragacanth), cellulose derivatives (for example, carboxymethylcellulose and carboxypolycellulose), and synthetic polymers (for example, carbomers, cellulose ethers, and carboxyvinyl polymers). These disperse or swell in water to form colloidal solutions that stabilize emulsions by forming strong interfacial films around the dispersed-phase droplets and by increasing the viscosity of the external phase.

Since emulsions often contain a number of ingredients such as carbohydrates, proteins, sterols and phosphatides that can readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation. Antioxidants used can be free radical scav-

engers such as tocopherols, alkyl gallates, butylated hydroxyanisole, butylated hydroxytoluene, or reducing agents such as ascorbic acid and sodium metabisulfite, and antioxidant synergists such as citric acid, tartaric acid, and lecithin.

The application of emulsion formulations via dermatological, oral and parenteral routes and methods for their manufacture have been reviewed in the literature (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Emulsion formulations for oral delivery have been very widely used because of ease of formulation, as well as efficacy from an absorption and bioavailability standpoint (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Mineral-oil base laxatives, oil-soluble vitamins and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

## ii. Microemulsions

In one embodiment of the present disclosure, the compositions of RNAi agents and nucleic acids are formulated as microemulsions. A microemulsion can be defined as a system of water, oil and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically, microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: Controlled Release of Drugs: Polymers and Aggregate Systems, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 185-215). Microemulsions commonly are prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used, and on the structure and geometric packing of the polar heads and hydrocarbon tails of the surfactant molecules (Schott, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 271).

The phenomenological approach utilizing phase diagrams has been extensively studied and has yielded a comprehensive knowledge, to one skilled in the art, of how to formulate microemulsions (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich N G., and Ansel H C., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel

Dekker, Inc., New York, N.Y., volume 1, p. 245; Block, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Bunker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335). Compared to conventional emulsions, microemulsions offer the advantage of solubilizing water-insoluble drugs in a formulation of thermodynamically stable droplets that are formed spontaneously.

Surfactants used in the preparation of microemulsions include, but are not limited to, ionic surfactants, non-ionic surfactants, Brij 96, polyoxyethylene oleyl ethers, polyglycerol fatty acid esters, tetraglycerol monolaurate (ML310), tetraglycerol monooleate (M0310), hexaglycerol monooleate (P0310), hexaglycerol pentaoleate (P0500), decaglycerol monocaprate (MCA750), decaglycerol monooleate (M0750), decaglycerol sequioleate (S0750), decaglycerol decaoleate (DA0750), alone or in combination with cosurfactants. The cosurfactant, usually a short-chain alcohol such as ethanol, 1-propanol, and 1-butanol, serves to increase the interfacial fluidity by penetrating into the surfactant film and consequently creating a disordered film because of the void space generated among surfactant molecules. Microemulsions can, however, be prepared without the use of cosurfactants and alcohol-free self-emulsifying microemulsion systems are known in the art. The aqueous phase can typically be, but is not limited to, water, an aqueous solution of the drug, glycerol, PEG300, PEG400, polyglycerols, propylene glycols, and derivatives of ethylene glycol. The oil phase can include, but is not limited to, materials such as Captex 300, Captex 355, Capmul MCM, fatty acid esters, medium chain (C8-C12) mono, di, and tri-glycerides, polyoxyethylated glyceryl fatty acid esters, fatty alcohols, polyglycolized glycerides, saturated polyglycolized C8-C10 glycerides, vegetable oils and silicone oil.

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (see e.g., U.S. Pat. Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides et al., Pharmaceutical Research, 1994, 11, 1385-1390; Ritschel, Meth. Find. Exp. Clin. Pharmacol., 1993, 13, 205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of drug absorption due to surfactant-induced alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (see e.g., U.S. Pat. Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides et al., Pharmaceutical Research, 1994, 11, 1385; Ho et al., J. Pharm. Sci., 1996, 85, 138-143). Often microemulsions can form spontaneously when their components are brought together at ambient temperature. This can be particularly advantageous when formulating thermolabile drugs, peptides or RNAi agents. Microemulsions have also been effective in the transdermal delivery of active components in both cosmetic and pharmaceutical applications. It is expected that the microemulsion compositions and formulations of the present disclosure will facilitate the increased systemic absorption of RNAi agents and nucleic acids from the gastrointestinal tract, as well as improve the local cellular uptake of RNAi agents and nucleic acids.

Microemulsions of the present disclosure can also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the RNAi agents and nucleic acids of the

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present disclosure. Penetration enhancers used in the micro-emulsions of the present disclosure can be classified as belonging to one of five broad categories—surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92). Each of these classes has been discussed above.

iii. Microparticles

An RNAi agent of the disclosure may be incorporated into a particle, e.g., a microparticle. Microparticles can be produced by spray-drying, but may also be produced by other methods including lyophilization, evaporation, fluid bed drying, vacuum drying, or a combination of these techniques.

iv. Penetration Enhancers

In one embodiment, the present disclosure employs various penetration enhancers to effect the efficient delivery of nucleic acids, particularly RNAi agents, to the skin of animals. Most drugs are present in solution in both ionized and nonionized forms. However, usually only lipid soluble or lipophilic drugs readily cross cell membranes. It has been discovered that even non-lipophilic drugs can cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

Penetration enhancers can be classified as belonging to one of five broad categories, i.e., surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, NY, 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92). Each of the above mentioned classes of penetration enhancers are described below in greater detail.

Surfactants (or “surface-active agents”) are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous solution and another liquid, with the result that absorption of RNAi agents through the mucosa is enhanced. In addition to bile salts and fatty acids, these penetration enhancers include, for example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether) (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, NY, 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92); and perfluorochemical emulsions, such as FC-43. Takahashi et al., J. Pharm. Pharmacol., 1988, 40, 252).

Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C<sub>1-20</sub> alkyl esters thereof (e.g., methyl, isopropyl and t-butyl), and mono- and di-glycerides thereof (i.e., oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, etc.) (see e.g., Touitou, E., et al. Enhancement in Drug Delivery, CRC Press, Danvers, MA, 2006; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; El Hariri et al., J. Pharm. Pharmacol., 1992, 44, 651-654).

The physiological role of bile includes the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (see e.g., Malmsten, M. Surfactants and polymers in drug

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delivery, Informa Health Care, New York, NY, 2002; Brunton, Chapter 38 in: Goodman & Gilman's The Pharmacological Basis of Therapeutics, 9th Ed., Hardman et al. Eds., McGraw-Hill, New York, 1996, pp. 934-935). Various natural bile salts, and their synthetic derivatives, act as penetration enhancers. Thus the term “bile salts” includes any of the naturally occurring components of bile as well as any of their synthetic derivatives. Suitable bile salts include, for example, cholic acid (or its pharmaceutically acceptable sodium salt, sodium cholate), dehydrocholic acid (sodium dehydrocholate), deoxycholic acid (sodium deoxycholate), gluchocholic acid (sodium glucocholate), glycholic acid (sodium glycocholate), glycocodeoxycholic acid (sodium glycocodeoxycholate), taurocholic acid (sodium taurocholate), taurodeoxycholic acid (sodium taurodeoxycholate), chenodeoxycholic acid (sodium chenodeoxycholate), ursodeoxycholic acid (UDCA), sodium tauro-24,25-dihydro-fusidate (STDHF), sodium glycodihydrofusidate and polyoxyethylene-9-lauryl ether (POE) (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, NY, 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92; Swinyard, Chapter 39 In: Remington's Pharmaceutical Sciences, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, Pa., 1990, pages 782-783; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Yamamoto et al., J. Pharm. Exp. Ther., 1992, 263, 25; Yamashita et al., J. Pharm. Sci., 1990, 79, 579-583).

Chelating agents, as used in connection with the present disclosure, can be defined as compounds that remove metallic ions from solution by forming complexes therewith, with the result that absorption of RNAi agents through the mucosa is enhanced. With regards to their use as penetration enhancers in the present disclosure, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for catalysis and are thus inhibited by chelating agents (Jarrett, J. Chromatogr., 1993, 618, 315-339). Suitable chelating agents include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium salicylate, 5-methoxysalicylate and homovanillic), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones (enamines)(see e.g., Katdare, A. et al., Excipient development for pharmaceutical, biotechnology, and drug delivery, CRC Press, Danvers, MA, 2006; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Buur et al., J. Control Rel., 1990, 14, 43-51).

As used herein, non-chelating non-surfactant penetration enhancing compounds can be defined as compounds that demonstrate insignificant activity as chelating agents or as surfactants but that nonetheless enhance absorption of RNAi agents through the alimentary mucosa (see e.g., Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33). This class of penetration enhancers includes, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92); and non-steroidal anti-inflammatory agents such as diclofenac sodium, indomethacin and phenylbutazone (Yamashita et al., J. Pharm. Pharmacol., 1987, 39, 621-626).

Agents that enhance uptake of RNAi agents at the cellular level can also be added to the pharmaceutical and other compositions of the present disclosure. For example, cationic lipids, such as lipofectin (Junichi et al, U.S. Pat. No. 5,705,188), cationic glycerol derivatives, and polycationic

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molecules, such as polylysine (WO 97/30731), are also known to enhance the cellular uptake of dsRNAs.

Other agents can be utilized to enhance the penetration of the administered nucleic acids, including glycols such as ethylene glycol and propylene glycol, pyrrols such as 2-pyrrol, azones, and terpenes such as limonene and menthone.

**vi. Excipients**

In contrast to a carrier compound, a "pharmaceutical carrier" or "excipient" is a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The excipient can be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, etc., when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutical carriers include, but are not limited to, binding agents (e.g., pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, etc.); fillers (e.g., lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, etc.); lubricants (e.g., magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, etc.); disintegrants (e.g., starch, sodium starch glycolate, etc.); and wetting agents (e.g., sodium lauryl sulphate, etc.).

Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can also be used to formulate the compositions of the present disclosure. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

Formulations for topical administration of nucleic acids can include sterile and non-sterile aqueous solutions, non-aqueous solutions in common solvents such as alcohols, or solutions of the nucleic acids in liquid or solid oil bases. The solutions can also contain buffers, diluents and other suitable additives. Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can be used.

Suitable pharmaceutically acceptable excipients include, but are not limited to, water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

**vii. Other Components**

The compositions of the present disclosure can additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions can contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or can contain additional materials useful in physically formulating various dosage forms of the compositions of the present disclosure, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present disclosure. The formulations can be sterilized and, if desired, mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavor-

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ings or aromatic substances and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

Aqueous suspensions can contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol or dextran. The suspension can also contain stabilizers.

In some embodiments, pharmaceutical compositions featured in the disclosure include (a) one or more RNAi agents and (b) one or more agents which function by a non-RNAi mechanism and which are useful in treating a coronavirus-associated disorder. Examples of such agents include, but are not limited to SSRIs, venlafaxine, bupropion, and atypical antipsychotics.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population).

The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>. Compounds that exhibit high therapeutic indices are preferred.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of compositions featured herein in the disclosure lies generally within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods featured in the disclosure, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range of the compound or, when appropriate, of the polypeptide product of a target sequence (e.g., achieving a decreased concentration of the polypeptide) that includes the IC<sub>50</sub> (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

In addition to their administration, as discussed above, the RNAi agents featured in the disclosure can be administered in combination with other known agents effective in treatment of pathological processes mediated by nucleotide repeat expression. In any event, the administering physician can adjust the amount and timing of RNAi agent administration on the basis of results observed using standard measures of efficacy known in the art or described herein.

## VII. Kits

In certain aspects, the instant disclosure provides kits that include a suitable container containing a pharmaceutical formulation of a siRNA compound, e.g., a double-stranded siRNA compound, or siRNA compound, (e.g., a precursor, e.g., a larger siRNA compound which can be processed into a siRNA compound, or a DNA which encodes an siRNA compound, e.g., a double-stranded siRNA compound, or siRNA compound, or precursor thereof). In certain embodiments the individual components of the pharmaceutical formulation may be provided in one container. Alternatively, it may be desirable to provide the components of the pharmaceutical formulation separately in two or more containers, e.g., one container for a siRNA compound prepara-

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tion, and at least another for a carrier compound. The kit may be packaged in a number of different configurations such as one or more containers in a single box. The different components can be combined, e.g., according to instructions provided with the kit. The components can be combined according to a method described herein, e.g., to prepare and administer a pharmaceutical composition. The kit can also include a delivery device. For example, the kit can include a delivery device suitable for pulmonary system administration, e.g., a device suitable for oral inhalative administration including nebulizers, metered-dose inhalers, and dry powder inhalers.

### VIII. Methods for Inhibiting Coronavirus Expression

The present disclosure also provides methods of inhibiting expression of a coronavirus genome in a cell. The methods include contacting a cell with an RNAi agent, e.g., double stranded RNAi agent, a composition comprising a double stranded RNAi agent of the invention, or a pharmaceutical compositions comprising a double stranded RNAi agent of the invention in an amount effective to inhibit expression of a coronavirus genome in the cell, thereby inhibiting expression of coronavirus in the cell. In some embodiments, the methods include contacting a cell with two or more double stranded RNAi agents, as described herein, e.g., any two or more, e.g., 2, 3, or 4, of the dsRNA agents selected from the group of dsRNA agents in Tables 2-5. In certain embodiments of the methods including two or more double stranded RNAi agents, the two or more double stranded RNAi agents may be present in the same composition, in separate compositions, or any combination thereof. In some embodiments, the methods of the invention include contacting a cell with a composition comprising two or more, e.g., 2, 3, or 4, double stranded RNAi agents of the invention, e.g., any two or more of the dsRNA agents selected from the group of dsRNA agents in Tables 2-5. In certain embodiments of the disclosure, expression of a coronavirus genome is inhibited preferentially in the pulmonary system (e.g., lung, bronchial, alveoli) cells. In other embodiments of the disclosure, expression of a coronavirus genome is inhibited preferentially in the liver (e.g., hepatocytes). In certain embodiments of the disclosure, expression of a coronavirus genome is inhibited in the pulmonary system (e.g., lung, bronchial, alveoli) cells and in liver (e.g., hepatocytes) cells.

Contacting of a cell with a RNAi agent, e.g., a double stranded RNAi agent, may be done in vitro or in vivo. Contacting a cell in vivo with the RNAi agent includes contacting a cell or group of cells within a subject, e.g., a human subject, with the RNAi agent. Combinations of in vitro and in vivo methods of contacting a cell are also possible.

In some embodiments of the methods of the invention which include contacting a cell with two or more double stranded RNAi agents, as described herein, e.g., any two or more, e.g., 2, 3, or 4, of the dsRNA agents selected from the group of dsRNA agents in Tables 2-5, the cell may be contacted with a first agent (or a composition comprising a first agent) at a first time, a second agent (or a composition comprising a second agent) at a second time, a third agent (or a composition comprising a third agent) at a third time, and a fourth agent (or a composition comprising a fourth agent) at a fourth time; or the cell may be contacted with all of the agents (or a composition comprising all of the agents) at the same time. Alternatively, the cell may be contacted

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with a first agent (or a composition comprising a first agent) at a first time and a second, third, and/or fourth agent (or a composition comprising a second, third, and/or fourth agent) at a second time. Other combinations of contacting the cell with two or more agents (or compositions comprising two or more dsRNA agents) of the invention are also contemplated.

Contacting a cell may be direct or indirect, as discussed above. Furthermore, contacting a cell may be accomplished via a targeting ligand, including any ligand described herein or known in the art. In some embodiments, the targeting ligand is a carbohydrate moiety, e.g., a GaINAc ligand, or any other ligand that directs the RNAi agent to a site of interest.

The term "inhibiting," as used herein, is used interchangeably with "reducing," "silencing," "downregulating," "suppressing" and other similar terms, and includes any level of inhibition. In certain embodiments, a level of inhibition, e.g., for an RNAi agent of the instant disclosure, can be assessed in cell culture conditions, e.g., wherein cells in cell culture are transfected via Lipofectamine<sup>TM</sup>-mediated transfection at a concentration in the vicinity of a cell of 10 nM or less, 1 nM or less, etc. Knockdown of a given RNAi agent can be determined via comparison of pre-treated levels in cell culture versus post-treated levels in cell culture, optionally also comparing against cells treated in parallel with a scrambled or other form of control RNAi agent. Knockdown in cell culture of, e.g., preferably 50% or more, can thereby be identified as indicative of "inhibiting" or "reducing," "downregulating" or "suppressing", etc. having occurred. It is expressly contemplated that assessment of targeted mRNA or encoded protein levels (and therefore an extent of "inhibiting", etc. caused by a RNAi agent of the disclosure) can also be assessed in in vivo systems for the RNAi agents of the instant disclosure, under properly controlled conditions as described in the art.

The phrase "inhibiting expression of a coronavirus genome" or "inhibiting expression of coronavirus," as used herein, includes inhibition of expression of any coronavirus genome as well as variants or mutants of a coronavirus genome that encode a coronavirus protein. Thus, the coronavirus genome may be a wild-type coronavirus genome, a mutant coronavirus genome, or a transgenic coronavirus genome in the context of a genetically manipulated cell, group of cells, or organism.

"Inhibiting expression of a coronavirus genome" includes any level of inhibition of a coronavirus genome, e.g., at least partial suppression of the expression of a coronavirus genome, such as an inhibition by at least 20%. In certain embodiments, inhibition is by at least 30%, at least 40%, preferably at least 50%, at least about 60%, at least 70%, at least about 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%; or to below the level of detection of the assay method. In a preferred method, inhibition is measured at a 10 nM concentration of the siRNA using the luciferase assay provided in Example 1.

The expression of a coronavirus genome may be assessed based on the level of any variable associated with coronavirus genome expression, e.g., coronavirus RNA level or coronavirus protein level or coronavirus replication.

Inhibition may be assessed by a decrease in an absolute or relative level of one or more of these variables compared with a control level. The control level may be any type of control level that is utilized in the art, e.g., a pre-dose baseline level, or a level determined from a similar subject, cell, or sample that is untreated or treated with a control (such as, e.g., buffer only control or inactive agent control).

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In some embodiments of the methods of the disclosure, expression of a coronavirus genome is inhibited by at least 20%, 30%, 40%, preferably at least 50%, 60%, 70%, 80%, 85%, 90%, or 95%, or to below the level of detection of the assay. In certain embodiments, the methods include a clinically relevant inhibition of expression of coronavirus, e.g. as demonstrated by a clinically relevant outcome after treatment of a subject with an agent to reduce the expression of a coronavirus genome.

Inhibition of the expression of a coronavirus genome may be manifested by a reduction of the amount of genome expressed by a first cell or group of cells (such cells may be present, for example, in a sample derived from a subject) in which a coronavirus genome is transcribed and which has or have been treated (e.g., by contacting the cell or cells with a RNAi agent of the disclosure, or by administering a RNAi agent of the disclosure to a subject in which the cells are or were present) such that the expression of a coronavirus genome is inhibited, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has not or have not been so treated (control cell(s) not treated with a RNAi agent or not treated with a RNAi agent targeted to the genome of interest). The degree of inhibition may be expressed in terms of:

$$\frac{(\text{genome in control cells}) - (\text{genome in treated cells})}{\text{(genome in control cells)}} \times 100\%$$

In other embodiments, inhibition of the expression of a coronavirus genome may be assessed in terms of a reduction of a parameter that is functionally linked to a coronavirus genome expression, e.g., coronavirus protein expression. Coronavirus genome silencing may be determined in any cell expressing a coronavirus genome, either endogenous or heterologous from an expression construct, and by any assay known in the art.

Inhibition of the expression of a coronavirus protein may be manifested by a reduction in the level of the coronavirus protein that is expressed by a cell or group of cells (e.g., the level of protein expressed in a sample derived from a subject). As explained above, for the assessment of genome suppression, the inhibition of protein expression levels in a treated cell or group of cells may similarly be expressed as a percentage of the level of protein in a control cell or group of cells.

A control cell or group of cells that may be used to assess the inhibition of the expression of a coronavirus genome includes a cell or group of cells that has not yet been contacted with an RNAi agent of the disclosure. For example, the control cell or group of cells may be derived from an individual subject (e.g., a human or animal subject) prior to treatment of the subject with an RNAi agent.

The level of coronavirus genome that is expressed by a cell or group of cells may be determined using any method known in the art for assessing RNA expression. In one embodiment, the level of expression of coronavirus in a sample is determined by detecting a transcribed polynucleotide, or portion thereof, e.g., RNA of the coronavirus genome. RNA may be extracted from cells using RNA extraction techniques including, for example, using acid phenol/guanidine isothiocyanate extraction (RNAzol B; Biogenesis), RNeasy™ RNA preparation kits (Qiagen®) or PAXgene (PreAnalytix, Switzerland). Typical assay formats utilizing ribonucleic acid hybridization include nuclear run-on assays, RT-PCR, RNase protection assays, northern blot-

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ting, in situ hybridization, and microarray analysis. Circulating coronavirus genome may be detected using methods described in WO2012/177906, the entire contents of which are hereby incorporated herein by reference.

In some embodiments, the level of expression of coronavirus is determined using a nucleic acid probe. The term "probe", as used herein, refers to any molecule that is capable of selectively binding to a specific coronavirus nucleic acid or protein, or fragment thereof. Probes can be synthesized by one of skill in the art, or derived from appropriate biological preparations. Probes may be specifically designed to be labeled. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

Isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or northern analyses, polymerase chain reaction (PCR) analyses and probe arrays. One method for the determination of RNA levels involves contacting the isolated RNA with a nucleic acid molecule (probe) that can hybridize to coronavirus RNA. In one embodiment, the RNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated RNA on an agarose gel and transferring the RNA from the gel to a membrane, such as nitrocellulose. In an alternative embodiment, the probe(s) are immobilized on a solid surface and the RNA is contacted with the probe(s), for example, in an Affymetrix® gene chip array. A skilled artisan can readily adapt known RNA detection methods for use in determining the level of coronavirus RNA.

An alternative method for determining the level of expression of coronavirus in a sample involves the process of nucleic acid amplification or reverse transcriptase (to prepare cDNA) of for example mRNA in the sample, e.g., by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Pat. No. 4,683,202), ligase chain reaction (Barany (1991) *Proc. Natl. Acad. Sci. USA* 88:189-193), self sustained sequence replication (Guatelli et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi et al. (1988) *Bio/Technology* 6:1197), rolling circle replication (Lizardi et al., U.S. Pat. No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. In particular aspects of the disclosure, the level of expression of coronavirus is determined by quantitative fluorogenic RT-PCR (i.e., the TaqMan™ System), by a Dual-Glo® Luciferase assay, or by other art-recognized method for measurement of coronavirus genome expression or protein level.

The expression level of coronavirus RNA may be monitored using a membrane blot (such as used in hybridization analysis such as northern, Southern, dot, and the like), or microwells, sample tubes, gels, beads or fibers (or any solid support comprising bound nucleic acids). See U.S. Pat. Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, which are incorporated herein by reference. The determination of coronavirus expression level may also comprise using nucleic acid probes in solution.

In some embodiments, the level of RNA expression is assessed using branched DNA (bDNA) assays or real time PCR (qPCR). The use of this PCR method is described and

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exemplified in the Examples presented herein. Such methods can also be used for the detection of coronavirus nucleic acids.

The level of coronavirus protein expression may be determined using any method known in the art for the measurement of protein levels. Such methods include, for example, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, fluid or gel precipitin reactions, absorption spectroscopy, a colorimetric assays, spectrophotometric assays, flow cytometry, immunodiffusion (single or double), immunoelectrophoresis, western blotting, radioimmunoassay (RIA), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, electrochemiluminescence assays, and the like. Such assays can also be used for the detection of proteins indicative of the presence or replication of coronavirus proteins.

In some embodiments, the efficacy of the methods of the disclosure in the treatment of a coronavirus-related disease is assessed by a decrease in coronavirus genome level (e.g., by assessment of a coronavirus level, e.g., in the lung, by biopsy, or otherwise).

In some embodiments, the efficacy of the methods of the disclosure in the treatment of a coronavirus-related disease is assessed by a decrease in coronavirus genome level (e.g., by assessment of a liver sample for coronavirus level, by biopsy, or otherwise).

In some embodiments of the methods of the disclosure, the RNAi agent is administered to a subject such that the RNAi agent is delivered to a specific site within the subject. The inhibition of expression of a coronavirus genome may be assessed using measurements of the level or change in the level of coronavirus genome or coronavirus protein in a sample derived from a specific site within the subject, e.g., lung and/or liver cells. In certain embodiments, the methods include a clinically relevant inhibition of expression of coronavirus, e.g. as demonstrated by a clinically relevant outcome after treatment of a subject with an agent to reduce the expression of coronavirus.

As used herein, the terms detecting or determining a level of an analyte are understood to mean performing the steps to determine if a material, e.g., protein, RNA, is present. As used herein, methods of detecting or determining include detection or determination of an analyte level that is below the level of detection for the method used.

#### IX. Methods of Treating or Preventing Coronavirus-Associated Diseases

The present disclosure also provides methods of using an RNAi agent of the disclosure, two or more, e.g., 2, 3, or 4, double stranded RNAi agents of the disclosure (e.g., each agent independently targeting a portion of a coronavirus genome), a composition (such as a pharmaceutical composition) containing a RNAi agent of the disclosure, two or more, e.g., 2, 3, or 4, compositions (such as pharmaceutical compositions), each independently comprising a double stranded RNAi agent of the invention, or a composition comprising two or more, e.g., 2, 3, or 4, double stranded RNAi agents of the disclosure to reduce or inhibit coronavirus expression in a cell. The methods include contacting the cell with a dsRNA of the disclosure, a composition of the disclosure, or a pharmaceutical composition of the disclosure and maintaining the cell for a time sufficient to obtain degradation of the RNA transcripts of a coronavirus genome, thereby inhibiting expression of the coronavirus

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genome in the cell. Reduction in gene expression can be assessed by any methods known in the art. For example, a reduction in the expression of coronavirus may be determined by determining the RNA expression level of a coronavirus genome using methods routine to one of ordinary skill in the art, e.g., northern blotting, qRT-PCR; by determining the protein level of a coronavirus protein using methods routine to one of ordinary skill in the art, such as western blotting, immunological techniques.

10 In the methods of the disclosure the cell may be contacted in vitro or in vivo, i.e., the cell may be within a subject.

A cell suitable for treatment using the methods of the disclosure may be any cell that expresses a coronavirus genome. A cell suitable for use in the methods of the disclosure may be a mammalian cell, e.g., a primate cell (such as a human cell or a non-human primate cell, e.g., a monkey cell or a chimpanzee cell), a non-primate cell (such as a rat cell, or a mouse cell. In one embodiment, the cell is a human cell, e.g., a human lung cell. In one embodiment, the cell is a human cell, e.g., a human liver cell. In one embodiment, the cell is a human cell, e.g., a human lung cell and a human liver cell.

Coronavirus genome expression is inhibited in the cell by at least about 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 25 96, 97, 98, 99, or about 100%, i.e., to below the level of detection. In preferred embodiments, coronavirus expression is inhibited by at least 50%.

The *in vivo* methods of the disclosure may include administering to a subject a composition containing a RNAi agent, where the RNAi agent includes a nucleotide sequence that is complementary to at least a part of target coronavirus sequence, e.g., an RNA transcript of the coronavirus genome, of the coronavirus to be treated. In some embodiments, the subject is administered two or more, e.g., 2, 3, or 30 4, compositions, each independently comprising an RNAi agent of the invention. The compositions may be the same or different. In other embodiments, the subject is administered a composition comprising two or more, e.g., 2, 3, or 4, dsRNA agents, each independently targeting a portion of the 35 coronavirus genome.

When the organism to be treated is a mammal such as a human, the composition can be administered by any means known in the art including, but not limited to oral, intraperitoneal, or parenteral routes, including intracranial (e.g., 45 intraventricular, intraparenchymal, and intrathecal), intravenous, intramuscular, subcutaneous, transdermal, airway (aerosol), nasal, rectal, and topical (including buccal and sublingual) administration. In certain embodiments, the compositions are administered by intravenous infusion or 50 injection. In certain embodiments, the compositions are administered by subcutaneous injection. In certain embodiments, the compositions are administered by pulmonary system delivery, e.g., inhalation or intranasal delivery.

In some embodiments, the administration is via a depot 55 injection. A depot injection may release the RNAi agent in a consistent way over a prolonged time period. Thus, a depot injection may reduce the frequency of dosing needed to obtain a desired effect, e.g., a desired inhibition of coronavirus, or a therapeutic or prophylactic effect. A depot injection may also provide more consistent serum concentrations. Depot injections may include subcutaneous injections or intramuscular injections. In preferred embodiments, the depot injection is a subcutaneous injection.

In one embodiment, the double-stranded RNAi agent is 60 administered by pulmonary system administration, e.g., intranasal administration or oral inhalative administration. Pulmonary system administration may be via a syringe, a

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dropper, atomization, or use of device, e.g., a passive breath driven or active power driven single/-multiple dose dry powder inhaler (DPI) device.

The mode of administration may be chosen based upon whether local or systemic treatment is desired and based upon the area to be treated. The route and site of administration may be chosen to enhance targeting.

In one aspect, the present disclosure also provides methods for inhibiting the expression of a coronavirus genome in a mammal. The methods include administering to the mammal a dsRNA that targets a coronavirus genome in a cell of the mammal and maintaining the mammal for a time sufficient to obtain degradation of the RNA transcript of the coronavirus genome, thereby inhibiting expression of the coronavirus genome in the cell. In some embodiments, the dsRNA is present in a composition, such as a pharmaceutical composition. In some embodiments, the mammal is administered two or more, e.g., 2, 3, or 4, dsRNA agents of the invention. In some embodiments, each dsRNA agent administered to the subject is independently present in a composition. In other embodiments, the mammal is administered a composition comprising two or more, e.g., 2, 3, or 4, dsRNAs of the invention.

Reduction in genome expression can be assessed by any methods known it the art and by methods, e.g. qRT-PCR, described herein. Reduction in protein production can be assessed by any methods known it the art and by methods, e.g. ELISA, described herein. In one embodiment, a lung biopsy sample serves as the tissue material for monitoring the reduction in coronavirus genome or protein expression (or of a proxy therefore).

The present disclosure further provides methods of treatment of a subject in need thereof. The treatment methods of the disclosure include administering an RNAi agent of the disclosure to a subject, e.g., a subject that would benefit from inhibition of coronavirus expression, in a therapeutically effective amount of a RNAi agent targeting a coronavirus genome or a pharmaceutical composition comprising a RNAi agent targeting a coronavirus genome. In some embodiments, the subject is administered a therapeutically effective amount of two or more, e.g., 2, 3, or 4, dsRNA agents of the invention. In some embodiments, each dsRNA agent administered to the subject is independently present in a composition. In other embodiments, the subject is administered a composition comprising two or more, e.g., 2, 3, or 4, dsRNAs of the invention.

In addition, the present disclosure provides methods of preventing, treating or inhibiting the progression of a coronavirus-associated disease or disorder, such as severe acute respiratory syndrome (SARS), the Middle East respiratory syndrome (MERS), and severe acute respiratory syndrome-2 (SARS-2). The methods include administering to the subject a therapeutically effective amount of any of the RNAi agent, e.g., dsRNA agents, or the pharmaceutical composition provided herein, thereby preventing, treating, or inhibiting the progression of the coronavirus-associated disease or disorder in the subject. In some embodiments, the mammal is administered a therapeutically effective amount of two or more, e.g., 2, 3, or 4, dsRNA agents of the invention. In some embodiments, each dsRNA agent administered to the subject is independently present in a composition. In other embodiments, the mammal is administered a composition comprising two or more, e.g., 2, 3, or 4, dsRNAs of the invention.

In some embodiments of the methods of the invention which include administering two or more double stranded RNAi agents, as described herein, e.g., any two or more, e.g., 2, 3, or 4, of the dsRNA agents selected from the group

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of dsRNA agents in Tables 2-5, the subject may be administered a first agent (or a composition comprising a first agent) at a first time, a second agent (or a composition comprising a second agent) at a second time, a third agent (or a compositions comprising a third agent) at a third time, and a fourth agent (or a composition comprising a fourth agent) at a fourth time; or the subject may be administered all of the agents (or a composition comprising all of the agents at the same time, Alternatively, the subject may be administered a first agent (or a composition comprising a first agent) at a first time and a second, third, and/or fourth agent (or a compostion comprising a second, third and/or fourth agent) at a second time. Other combinations of contacting the cell with two or more agents of the invention are also contemplated.

An RNAi agent of the disclosure may be administered as a "free RNAi agent." A free RNAi agent is administered in the absence of a pharmaceutical composition. The naked RNAi agent may be in a suitable buffer solution. The buffer solution may comprise acetate, citrate, prolamine, carbonate, or phosphate, or any combination thereof. In one embodiment, the buffer solution is phosphate buffered saline (PBS). The pH and osmolarity of the buffer solution containing the RNAi agent can be adjusted such that it is suitable for administering to a subject.

Alternatively, an RNAi agent of the disclosure may be administered as a pharmaceutical composition, such as a dsRNA liposomal formulation.

Subjects that would benefit from a reduction or inhibition 30 of coronavirus genome expression are those having a coronavirus-associated disease, e.g., subjects of an age greater than 60 years and/or subjects who are immunocompromised.

The disclosure further provides methods for the use of a RNAi agent or a pharmaceutical composition thereof, e.g., 35 for treating a subject that would benefit from reduction or inhibition of coronavirus expression, e.g., a subject having a coronavirus-associated disorder, in combination with other pharmaceuticals or other therapeutic methods, e.g., with known pharmaceuticals or known therapeutic methods, such 40 as, for example, those which are currently employed for treating these disorders. For example, in certain embodiments, an RNAi agent targeting coronavirus is administered in combination with, e.g., an agent useful in treating a coronavirus-associated disorder as described elsewhere herein or as otherwise known in the art. For example, additional agents and treatments suitable for treating a subject that would benefit from reduction in coronavirus expression, e.g., a subject having a coronavirus-associated disorder, may include agents currently used to treat symptoms of coronavirus. The RNAi agent and additional therapeutic agents may be administered at the same time or in the same combination, e.g., via pulmonary system administration, or the additional therapeutic agent can be administered as part of a separate composition or at separate times or by another method known in the art or described herein.

Exemplary additional therapeutics and treatments include, for example, an antiviral agent, an immune stimulator, a therapeutic vaccine, a viral entry inhibitor, and a combination of any of the foregoing.

In one embodiment, the method includes administering a composition featured herein such that expression of the target coronavirus genome is decreased, for at least one month. In preferred embodiments, expression is decreased for at least 2 months, or 6 months.

Preferably, the RNAi agents useful for the methods and compositions featured herein specifically target RNAs (primary or processed) of the target coronavirus genome. Com-

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positions and methods for inhibiting the expression of these genes using RNAi agents can be prepared and performed as described herein.

Administration of the dsRNA according to the methods of the disclosure may result in a reduction of the severity, signs, symptoms, or markers of such diseases or disorders in a patient with a coronavirus-associated disorder. By "reduction" in this context is meant a statistically significant or clinically significant decrease in such level. The reduction can be, for example, at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or about 100%.

Efficacy of treatment or prevention of disease can be assessed, for example by measuring disease progression, disease remission, symptom severity, reduction in pain, quality of life, dose of a medication required to sustain a treatment effect, level of a disease marker or any other measurable parameter appropriate for a given disease being treated or targeted for prevention. It is well within the ability of one skilled in the art to monitor efficacy of treatment or prevention by measuring any one of such parameters, or any combination of parameters. It is well within the ability of one skilled in the art to monitor efficacy of treatment or prevention by measuring any one of such parameters, or any combination of parameters. In connection with the administration of a RNAi agent targeting coronavirus or pharmaceutical composition thereof, "effective against" a coronavirus-associated disorder indicates that administration in a clinically appropriate manner results in a beneficial effect for at least a statistically significant fraction of patients, such as an improvement of symptoms, a cure, a reduction in disease, extension of life, improvement in quality of life, or other effect generally recognized as positive by medical doctors familiar with treating coronavirus-associated disorders and the related causes.

A treatment or preventive effect is evident when there is a statistically significant improvement in one or more parameters of disease status, or by a failure to worsen or to develop symptoms where they would otherwise be anticipated. As an example, a favorable change of at least 10% in a measurable parameter of disease, and preferably at least 20%, 30%, 40%, 50%, or more can be indicative of effective treatment. Efficacy for a given RNAi agent drug or formulation of that drug can also be judged using an experimental animal model for the given disease as known in the art. When using an experimental animal model, efficacy of treatment is evidenced when a statistically significant reduction in a marker or symptom is observed.

Alternatively, the efficacy can be measured by a reduction in the severity of disease as determined by one skilled in the art of diagnosis based on a clinically accepted disease severity grading scale. Any positive change resulting in e.g., lessening of severity of disease measured using the appropriate scale, represents adequate treatment using a RNAi agent or RNAi agent formulation as described herein.

Subjects can be administered a therapeutic amount of dsRNA, such as about 0.01 mg/kg to about 200 mg/kg.

The RNAi agent can be administered via the pulmonary system over a period of time, on a regular basis. In certain embodiments, after an initial treatment regimen, the treatments can be administered on a less frequent basis. Administration of the RNAi agent can reduce coronavirus genome levels, e.g., in a cell, tissue, blood, lung sample or other compartment of the patient by at least 20%, 30%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or at least about 99% or more. In a preferred embodiment, administration of the RNAi agent can reduce

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coronavirus genome levels, e.g., in a cell, tissue, blood, pulmonary system sample or other compartment of the patient by at least 50%.

Before administration of a full dose of the RNAi agent, patients can be administered a smaller dose, such as a 5% infusion reaction, and monitored for adverse effects, such as an allergic reaction. In another example, the patient can be monitored for unwanted immunostimulatory effects, such as increased cytokine (e.g., TNF-alpha or INF-alpha) levels.

Alternatively, the RNAi agent can be administered by pulmonary system administration or subcutaneously, i.e., by subcutaneous injection. One or more injections may be used to deliver the desired, e.g., monthly dose of RNAi agent to a subject. The injections may be repeated over a period of time. The administration may be repeated on a regular basis. In certain embodiments, after an initial treatment regimen, the treatments can be administered on a less frequent basis. A repeat-dose regime may include administration of a therapeutic amount of RNAi agent on a regular basis, such as monthly or extending to once a quarter, twice per year, once per year. In certain embodiments, the RNAi agent is administered about once per month to about once per quarter (i.e., about once every three months).

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the RNAi agents and methods featured in the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

An informal Sequence Listing is filed herewith and forms part of the specification as filed.

This invention is further illustrated by the following examples which should not be construed as limiting. The entire contents of all references, patents and published patent applications cited throughout this application, as well as the Figures and the Sequence Listing, are hereby incorporated herein by reference.

## EXAMPLES

### Example 1. siRNA Synthesis

#### Source of Reagents

Where the source of a reagent is not specifically given herein, such reagent can be obtained from any supplier of reagents for molecular biology at a quality/purity standard for application in molecular biology.

#### siRNA Design

The selection of siRNA designs targeting coronavirus was driven by two primary factors: a) potency and b), the desire to employ siRNA with near-perfect matches with greater than 90% fractional coverage of the known coronaviruses sequences, e.g., SARS-CoV, MERS-CoV and SARS-CoV-2.

A detailed list of a set of the unmodified siRNA sense and antisense strand sequences targeting SARS-CoV-2 is shown in Table 2 and 4.

A detailed list of a set of the modified siRNA sense and antisense strand sequences targeting SARS-CoV-2 is shown in Tables 3 and 5.

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**siRNA Synthesis**

siRNAs were synthesized and annealed using routine methods known in the art. Briefly, siRNA sequences were synthesized on a 1  $\mu$ mol scale using a Mermade 192 synthesizer (BioAutomation) with phosphoramidite chemistry on solid supports. The solid support was controlled pore glass (500-1000 Å) loaded with a custom GaINAc ligand (3'-GalNAc conjugates), universal solid support (AM Chemicals), or the first nucleotide of interest. Ancillary synthesis reagents and standard 2-cyanoethyl phosphoramidite monomers (2'-deoxy-2'-fluoro, 2'-O-methyl, RNA, DNA) were obtained from Thermo-Fisher (Milwaukee, WI), Hongene (China), or Chemgenes (Wilmington, MA, USA). Additional phosphoramidite monomers were procured from commercial suppliers, prepared in-house, or procured using custom synthesis from various CMOs. Phosphoramidites were prepared at a concentration of 100 mM in either acetonitrile or 9:1 acetonitrile:DMF and were coupled using 5-Ethylthio-1H-tetrazole (ETT, 0.25 M in acetonitrile) with a reaction time of 400 s. Phosphorothioate linkages were generated using a 100 mM solution of 3-((Dimethylamino-methylidene) amino)-3H-1,2,4-dithiazole-3-thione (DDTT, obtained from Chemgenes (Wilmington, MA, USA)) in anhydrous acetonitrile/pyridine (9:1 v/v). Oxidation time was 5 minutes. All sequences were synthesized with final removal of the DMT group ("DMT-Off").

Upon completion of the solid phase synthesis, solid-supported oligoribonucleotides were treated with 300  $\mu$ L of Methylamine (40% aqueous) at room temperature in 96 well plates for approximately 2 hours to afford cleavage from the solid support and subsequent removal of all additional base-labile protecting groups. For sequences containing any natural ribonucleotide linkages (2'-OH) protected with a tert-butyl dimethyl silyl (TBDMS) group, a second deprotection step was performed using TEA.3HF (triethylamine trihydrofluoride). To each oligonucleotide solution in aqueous methylamine was added 200  $\mu$ L of dimethyl sulfoxide (DMSO) and 300  $\mu$ L TEA.3HF and the solution was incubated for approximately 30 mins at 60° C. After incubation, the plate was allowed to come to room temperature and crude oligonucleotides were precipitated by the addition of 1 mL of 9:1 acetonitrile:ethanol or 1:1 ethanol:isopropanol. The plates were then centrifuged at 4° C. for 45 mins and the supernatant carefully decanted with the aid of a multichannel pipette. The oligonucleotide pellet was resuspended in 20 mM NaOAc and subsequently desalting using a HiTrap size exclusion column (5 mL, GE Healthcare) on an Agilent LC system equipped with an autosampler, UV detector, conductivity meter, and fraction collector. Desalted samples were collected in 96 well plates and then analyzed by LC-MS and UV spectrometry to confirm identity and quantify the amount of material, respectively.

Duplexing of single strands was performed on a Tecan liquid handling robot. Sense and antisense single strands were combined in an equimolar ratio to a final concentration of 10  $\mu$ M in 1 $\times$  PBS in 96 well plates, the plate sealed, incubated at 100° C. for 10 minutes, and subsequently allowed to return slowly to room temperature over a period of 2-3 hours. The concentration and identity of each duplex was confirmed and then subsequently utilized for in vitro screening assays.

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**Example 2. In Vitro Screening of siRNA Duplexes****SARS-CoV-02 Expression Plasmid Construction**

5 Dual-Glo® Luciferase constructs generated in the psi-CHECK-2 vector which was obtained from Promega (Catalog No. C8021 (Madison, WI)). The SARS-CoV-2 vector sequences were synthesized and incorporated into the psi-CHECK2 vector by Blue Heron Biotech (Bothell, WA). The final constructs are referred to CV-concat-02 and CV-concat-21 (see, FIG. 2). The nucleotide sequence of SARS-CoV-2 incorporated into the psiCHECK-2 vector to generate CV-concat-02 is provided in SEQ ID NO:3 and the nucleotide sequence of SARS-CoV-2 incorporated into the psi-CHECK-2 vector to generate CV-concat-21 is provided in SEQ ID NO:4,

**Cell Culture and Transfections**

20 Cos7 cells (ATCC, Manassas, VA) were grown to near confluence at 37° C. in an atmosphere of 5% CO<sub>2</sub> in DMEM (ATCC) supplemented with 10% FBS, before being released from the plate by trypsinization. Cos7 cells were co-transfected with psiCHECK2-CV-concat-02 or psiCHECK2-CV-concat-21 plasmids and siRNA in 384-well plates at a density of 5 $\times$ 10<sup>4</sup> cells per well using Lipofectamine™ 2000 transfection reagent (Catalog No. 11668019, Invitrogen (Carlsbad, CA)). For each well of a 384 well plate, 0.1  $\mu$ L of Lipofectamine was added to 50 ng of plasmid vector in 5  $\mu$ L of Opti-MEM and allowed to complex at room temperature for 15 minutes. The mixture was then added to the cells which were resuspended in 40  $\mu$ L of fresh complete media. Cells were incubated for 48 hours before luciferase is measured.

Single dose experiments are performed at 1 nM or 10 nM final duplex concentration.

**Dual-Glo® Luciferase Assay (Promega, Cat No. E2980)**

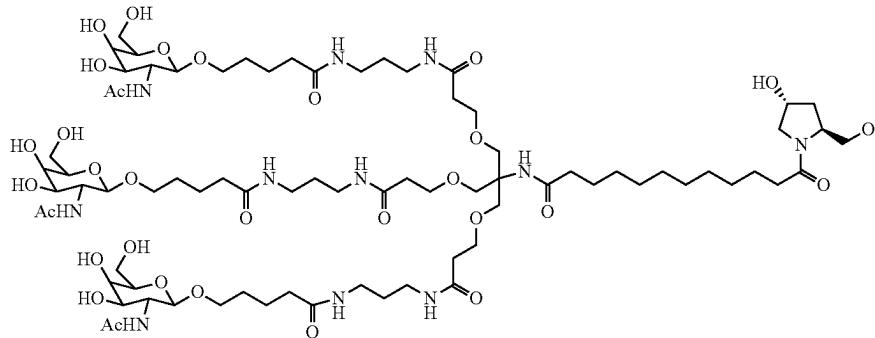
40 Forty-eight hours after the siRNAs were transfected, Firefly (transfection control) and *Renilla* (fused to SARS-CoV-2 target sequence) luciferase were measured. First, media was removed from cells. Then Firefly luciferase activity was measured by adding 20  $\mu$ L of Dual-Glo® Luciferase Reagent equal to the culture medium volume to each well and mix. The mixture was incubated at room temperature for 30 minutes before luminescence (500 nm) was measured on a Spectramax (Molecular Devices) to detect the Firefly luciferase signal. *Renilla* luciferase activity was measured by adding 20  $\mu$ L of room temperature of Dual-Glo® Stop & Glo® Reagent to each well and the plates are incubated for 10-15 minutes before luminescence was again measured to determine the *Renilla* luciferase signal. The Dual-Glo® Stop & Glo® Reagent, quench the firefly luciferase signal and sustain luminescence for the *Renilla* luciferase reaction. siRNA activity was determined by normalizing the *Renilla* (SARS-CoV-2) signal to the Firefly (control) signal within each well. The magnitude of siRNA activity was then assessed relative to cells that were transfected with the same vector but are not treated with siRNA or are treated with a non-targeting siRNA. All transfections are done at n=4 or greater.

The results of the single dose screens of the duplexes in 65 Tables 2 and 3 are provided in Table 6 and the results of the single dose screens of the duplexes in Tables 4 and 5 are provided in Table 7.

TABLE 1

Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds.

Abbreviation	Nucleotide(s)
A	Adenosine-3'-phosphate
Ab	beta-L-adenosine-3'-phosphate
Abs	beta-L-adenosine-3'-phosphorothioate
Af	2'-fluoroadenosine-3'-phosphate
Afs	2'-fluoroadenosine-3'-phosphorothioate
As	adenosine-3'-phosphorothioate
C	cytidine-3'-phosphate
Cb	beta-L-cytidine-3'-phosphate
Cbs	beta-L-cytidine-3'-phosphorothioate
Cf	2'-fluorocytidine-3'-phosphate
Cfs	2'-fluorocytidine-3'-phosphorothioate
Cs	cytidine-3'-phosphorothioate
G	guanosine-3'-phosphate
Gb	beta-L-guanosine-3'-phosphate
Gbs	beta-L-guanosine-3'-phosphorothioate
Gf	2'-fluoroguanosine-3'-phosphate
Gfs	2'-fluoroguanosine-3'-phosphorothioate
Gs	guanosine-3'-phosphorothioate
T	5'-methyluridine-3'-phosphate
Tf	2'-fluoro-5-methyluridine-3'-phosphate
Tfs	2'-fluoro-5-methyluridine-3'-phosphorothioate
Ts	5-methyluridine-3'-phosphorothioate
U	Uridine-3'-phosphate
Uf	2'-fluorouridine-3'-phosphate
Ufs	2'-fluorouridine-3'-phosphorothioate
Us	uridine-3'-phosphorothioate
N	any nucleotide, modified or unmodified
a	2'-O-methyladenosine-3'-phosphate
as	2'-O-methyladenosine-3'-phosphorothioate
c	2'-O-methylcytidine-3'-phosphate
cs	2'-O-methylcytidine-3'-phosphorothioate
g	2'-O-methylguanosine-3'-phosphate
gs	2'-O-methylguanosine-3'-phosphorothioate
t	2'-O-methyl-5-methyluridine-3'-phosphate
ts	2'-O-methyl-5-methyluridine-3'-phosphorothioate
u	2'-O-methyluridine-3'-phosphorothioate
us	2'-O-methyluridine-3'-phosphorothioate linkage
s	phosphorothioate linkage
L96	N-[tris(GalNAc-alkyl)-amidodecanoyl]-4-hydroxyprolinol(Hyp-(GalNAc-alkyl)3)



Y34	2-hydroxymethyl-tetrahydrofuran-4-methoxy-3-phosphate (abasic 2'-OMe furanose)
Y44	inverted abasic DNA (2-hydroxymethyl-tetrahydrofuran-5-phosphate)
L10	N-(cholesterylcarboxamidocaproyl)-4-hydroxyprolinol (Hyp-C6-Chol)
(Agn)	Adenosine-glycol nucleic acid (GNA)
(Cgn)	Cytidine-glycol nucleic acid (GNA)
(Ggn)	Guanosine-glycol nucleic acid (GNA)
(Tgn)	Thymidine-glycol nucleic acid (GNA) S-Isomer
P	Phosphate
VP	Vinyl-phosphonate
dA	2'-deoxyadenosine-3'-phosphate
dAs	2'-deoxyadenosine-3'-phosphorothioate
dC	2'-deoxycytidine-3'-phosphate
dCs	2'-deoxycytidine-3'-phosphorothioate
dG	2'-deoxyguanosine-3'-phosphate
dGs	2'-deoxyguanosine-3'-phosphorothioate
dT	2'-deoxythymidine-3'-phosphate
dTs	2'-deoxythymidine-3'-phosphorothioate
dU	2'-deoxyuridine

TABLE 1-continued

Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds.

Abbreviation	Nucleotide(s)
dUs	2'-deoxyuridine-3'-phosphorothioate
(C2p)	cytidine- 2'-phosphate
(G2p)	guanosine- 2'-phosphate
(U2p)	uridine- 2'-phosphate
(A2p)	adenosine- 2'-phosphate
(Ahd)	2'-O-hexadecyl-adenosine-3'-phosphate
(Ahds)	2'-O-hexadecyl-adenosine-3'-phosphorothioate
(Chd)	2'-O-hexadecyl-cytidine-3'-phosphate
(Chds)	2'-O-hexadecyl-cytidine-3'-phosphorothioate
(Ghd)	2'-O-hexadecyl-guanosine-3'-phosphate
(Ghds)	2'-O-hexadecyl-guanosine-3'-phosphorothioate
(Uhd)	2'-O-hexadecyl-uridine-3'-phosphate
(Uhds)	2'-O-hexadecyl-uridine-3'-phosphorothioate

TABLE 2  
Unmodified Sense and Antisense Strand Coronavirus\_dRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO:	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Strand of the Viral RNA Targeted by the Agent
AD-1183935	AUCUGUUUCUCAAACGAAACU	17	AAGGUUCGUUAGAGAACAGAUC	372	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	55	77	TRUE	TRUE	FALSE	+
AD-1183936	UCUGUUUCUCAAACGAAACU	18	AAAGGUUCGUUAGAGAACAGAU	373	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	56	78	TRUE	TRUE	FALSE	+
AD-1183937	GUUCUCUAAAACGAAUUAA	19	UUUAAAAGUUCGUUAGAGAACAGA	374	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	59	81	TRUE	TRUE	FALSE	+
AD-1183938	CUGCUUAAGGUUUCGUCCGU	20	CACGGACGAAACCGUAAACGAGC	375	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	188	210	TRUE	TRUE	FALSE	+
AD-1183939	GGUGUGACCGAAAGGUAGA	21	AUCUUACCUUUCGUACACCC	376	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	245	267	TRUE	TRUE	FALSE	+
AD-1183940	CCGAAAGGUAGAUGGAGAG	22	GCUCUCCAUCUACCUUCUCCGU	377	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	252	274	TRUE	TRUE	FALSE	+
AD-1183941	AAACACACGUCCAAUCAGU	23	AAUCAGGUUGGAGCUGUGUUUU	378	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	295	317	TRUE	TRUE	FALSE	+
AD-1183942	ACAGACGUCCAACUCAGUU	24	CAAACUGGUUGGGACGUUGUU	379	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	297	319	TRUE	TRUE	FALSE	+
AD-1183943	GUCCAAUCAGUUTGCCGU	25	AACAGGC2AACUGAGUUGGAGC	380	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	303	325	TRUE	TRUE	FALSE	+
AD-1183944	CUUCUUCGUAGAACGGUAA	26	AUTAACCGGUUCUACGAAGAAGA	381	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	627	649	TRUE	TRUE	FALSE	+
AD-1183945	UUCUUCGUAGAACGGUAAU	27	UAUUAACCCGUUCUACGAGAAG	382	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	628	650	TRUE	TRUE	FALSE	+
AD-1183946	UCUCGUAGAACGGUAAUA	28	UUAUUACCGGUUCUACGAGAAGA	383	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	629	651	TRUE	TRUE	FALSE	+
AD-1183947	UUCUUAAAACUUCUUCUCAA	29	CUUGAAAGAGAUUAGGUAGGAA	384	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	2156	2178	TRUE	FALSE	FALSE	-
AD-1183948	UCACCUAAAUCUAGGGUUU	30	UAAAAGCCUUGAAUUAUGGUAGA	385	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	2365	2387	TRUE	FALSE	FALSE	-

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS? SARS2?	Targets MERS?	Targeted by the Agent	
AD-1183949	CUCUGGAAUUAACACAUU	31	GAAGUGUGUUAAAUCGAGA	386	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	2418	2440	TRUE	FALSE	FALSE	
AD-1183950	CUUCUCAUAAAGUACUUU	32	GAAAAGGACUUAAGAACAG	387	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	2813	2835	TRUE	FALSE	FALSE	
AD-1183951	ACUCUUCUUCUACAAUC	33	GUGAUUUGAGAAAGAGGU	388	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3066	3088	TRUE	FALSE	FALSE	
AD-1183952	UUAUUUAAAACUACUGACA	34	UUGUCAGTAAGUUUAAAUAAC	389	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3353	3375	TRUE	TRUE	+	
AD-1183953	UAUCUACACAAACUUAAA	35	CUUUAGAGGUUGUGUAGAUAC	390	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3747	3769	TRUE	FALSE	FALSE	
AD-1183954	AUCUUGUUUUUCUGUCAA	36	GTUGAACAGAGAAAACAGAUG	391	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3929	3951	TRUE	FALSE	FALSE	
AD-1183955	CACUUUUAUCCCCUUTUA	37	UUBAGAGGGUGUAUAAAUG	392	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	4848	4870	TRUE	FALSE	FALSE	
AD-1183956	UCUCUGAAAGUAGUGGAA	38	UUUCCACUACUUCUAGAGAC	393	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6403	6425	TRUE	TRUE	+	
AD-1183957	UCUGAAAGAGUAGUGGAAA	39	AUUUCCACUACUUCUAGAG	394	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6405	6427	TRUE	TRUE	+	
AD-1183958	CUGAGAAAGUAGGGAAA	40	GAUUUCCACUACUUCUAGAG	395	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6406	6428	TRUE	TRUE	+	
AD-1183959	AGUGGAAAUCCUACAUAC	41	UGUAUGGGAGGUUUUCCACUA	396	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6416	6438	TRUE	TRUE	+	
AD-1183960	GUGGAAAUCUACAUACA	42	CUGUAUGGGAGGUUUUCCACU	397	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6417	6439	TRUE	TRUE	+	
AD-1183961	GCUCUUCUAAACCUAUAA	43	UUUUAUGGGGUUAGAGGC	398	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	9454	9476	TRUE	FALSE	FALSE	
AD-1183962	AUGGUUCACCAUCUGGUU	44	AAACACCCGAUGGUGAACCAU	399	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	10408	10430	TRUE	TRUE	+	

TABLE 2-continued

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO: Sequence 5' to 3'	Antisense Strand SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Strand of the Viral RNA	Targeted by the Agent
AD-1183963 A	CAUGGGAGAGGGGUUUU	45 UAAAACCACACUACCAAGA	A	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	10483	10505	TRUE	TRUE	FALSE	+	
AD-1183964 A	CAGCUAAUUCUAUGUUAA	46 UUUUACAUAGAUUAUGACGU	G	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	10501	10523	TRUE	FALSE	FALSE	-	
AD-1183965 G	UUUUGAUUGTGUTGACAAU	47 CAUTGUCUACACAUCAAAAG	G	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	10931	10953	TRUE	TRUE	FALSE	+	
AD-1183966 G	AUGGUAAUGCUUUAGAUCAA	48 CUUGAUCUAAAGCAUACCAA	A	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	11431	11453	TRUE	TRUE	FALSE	+	
AD-1183967 U	GCUGAGAUCCUAAAGGUGA	49 AUGACUCUUAGGGAUCAUAGCC	C	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	12843	12865	TRUE	TRUE	FALSE	+	
AD-1183968 G	ACACACUUAACACAUUA	50 CUAUUGUUAAGAUUGU	GU	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13140	13162	TRUE	FALSE	FALSE	-	
AD-1183969 C	UAAGAUGUGUGUACACACA	51 GUGUGUGACACAAUCUUAA	C	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13148	13170	TRUE	TRUE	FALSE	+	
AD-1183970 G	AGAUGUUGUACACACAU	52 CAGUGUGUACACAAUCUU	A	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13150	13172	TRUE	TRUE	FALSE	+	
AD-1183971 C	GGUGUGUACACACUGGU	53 GUACCAAGGUGUACACAAACA	U	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13154	13176	TRUE	TRUE	FALSE	+	
AD-1183972 G	CAGGCACTAGUACUGAUC	54 CGCAUCAGUACUAGGCCUGU	G	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13509	13531	TRUE	TRUE	FALSE	+	
AD-1183973 G	CCGCUAUUCUAAACUUAA	55 CUUUAAGUUAGAUAGCGGU	G	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13743	13765	TRUE	FALSE	FALSE	-	
AD-1183974 C	UUUAAAUAUUGGGAUCAGA	56 GUCUGAUCCCCAAUAUUAAA	A	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14296	14318	TRUE	FALSE	TRUE	+	
AD-1183975 A	UUUAAAUAUUGGGAUCAGC	57 UGUCUGAUCCCCAAUAUUAAA	U	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14297	14319	TRUE	FALSE	TRUE	+	
AD-1183976 C	CACCUACAGUUUUGGACCA	58 GUGGUCC2AAACUUGUAGGUGG	G	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14403	14425	TRUE	TRUE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1183977	AAUCAGGAUGUAAAACUACA U	59	AUGUAAGUUUACAUCCGAAUA	414	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14504	14526	TRUE	TRUE	FALSE	+
AD-1183978	AGGAUGAAAACUTACAUAGC U	60	AGCUAUGGAAAGUUUACAUCCUG	415	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14508	14530	TRUE	TRUE	FALSE	+
AD-1183979	ACAAUGUGCUUUUCAACAU G	61	CAGUUUGAAAAGCACAUUGUU A	416	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14646	14668	TRUE	TRUE	FALSE	+
AD-1183980	UGUGUGCUUUUCAACUGUCA A	62	UUGACAGGUUGAAAAGCACAU U	417	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14650	14672	TRUE	TRUE	FALSE	+
AD-1183981	UUGCUUUUCAACUGUCAA C	63	GUUUGACAGGUUGAAAAGAAC A	418	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14652	14674	TRUE	TRUE	FALSE	+
AD-1183982	GCTUUUCAACUGUCAACC C	64	GGGUUUGACAGGUUGAAAAGCA A	419	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14654	14676	TRUE	TRUE	FALSE	+
AD-1183983	UAUGACAUUUGUGUGUCAAA G	65	CUUGAGACAGCAAAGCUAUAG A	420	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14696	14718	TRUE	TRUE	FALSE	+
AD-1183984	GUUUCUUUAGGAAGGAAGU U	66	AAUCUUCUUCUUAAGAACCC C	421	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14718	14740	TRUE	TRUE	FALSE	+
AD-1183985	UUUCUUUAGGAAGGAAGUU C	67	GAACUUCUUCUUAAGAACCC C	422	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14719	14741	TRUE	TRUE	FALSE	+
AD-1183986	AGGAAGGGAAAGUUUGUGAA U	68	AUUCAAAGGAACUCCUCCUU A	423	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14727	14749	TRUE	TRUE	FALSE	+
AD-1183987	AAACAUUUCUUCUUGCUAG G	69	CCUGAGGAAAGAGAACGUUU U	424	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14751	14773	TRUE	TRUE	FALSE	+
AD-1183988	ACUUCUUUUGUGUCAGGAU G	70	CAUCCUGGCAAAAGAGAGUG U	425	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14754	14776	TRUE	TRUE	FALSE	+
AD-1183989	AAUGUGUGAUAAUCAGAAC C	71	AGUGUGUCUAGAUACACAUUG U	426	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14824	14846	TRUE	TRUE	FALSE	+
AD-1183990	CCAUUUAAAUCGGGUA A	72	CUTACCCCAUUUAAAUGGA A	427	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14951	14973	TRUE	TRUE	FALSE	+

TABLE 2-continued

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Strand of the Viral RNA Targeted by the Agent
AD-1183991 G	CAAUGAGUUAUGAGGAUAA	73 A	CUTGAUCCUCAUAAUCUAGUA	428	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14991	15013	TRUE	TRUE	FALSE	+
AD-1183992 C	UGCAAAAGAAUAGAGCUCCA	74 U	GUGCGAGCUCUAUUCUUUGCAC	429	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15085	15107	TRUE	TRUE	TRUE	+
AD-1183993 C	GCAAGAAUAGAGGGUCGAC	75 C	GGUGCGAGCUCUAUUCUUUGCA	430	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15086	15108	TRUE	TRUE	TRUE	+
AD-1183994 G	CAAGAAUAGAGGUCGACC	76 A	CGGUGCGAGCUCUAUUCUUUGC	431	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15087	15109	TRUE	TRUE	TRUE	+
AD-1183995 U	AAAGAAUAGAGCUCGACCG	77 C	ACGGUGCGAGCUCUAUUCUUUG	432	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15088	15110	TRUE	TRUE	TRUE	+
AD-1183996 U	UGUCUCUACUUCGUAGUAUA	78 C	AUGAUACUACAGAUCAGACAC	433	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15115	15137	TRUE	TRUE	FALSE	+
AD-1183997 C	CUCUACUACUAGUACUAGUA	79 C	GUGAUAGUACUACAGAUAGAGA	434	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15118	15140	TRUE	TRUE	FALSE	+
AD-1183998 A	UCACCUUAVGGGTUGGGAUU	80 G	UAAUCCUCAACCCAUAAAGUGAG	435	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15274	15296	TRUE	TRUE	TRUE	+
AD-1183999 U	CACCUUAVGGGTUGGGAUUA	81 G	AURAUCCCAAACCCAUAAAGGUA	436	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15275	15297	TRUE	TRUE	TRUE	+
AD-1184000 C	ACCUUAVGGGTUGGGAUAU	82 A	GRUAUCCCAACCCAUAAAGGUG	437	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15276	15298	TRUE	TRUE	TRUE	+
AD-1184001 C	CCUUAUGGGUUGGGAUUAUC	83 G	GGAAUAUCCCAACCCAUABAGGU	438	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15277	15299	TRUE	TRUE	TRUE	+
AD-2 1184002 A	ACUUGUUUUCUGCUUGCAAC	84 A	UGUUUGCCAGGAGAACAGUG	439	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15343	15365	TRUE	TRUE	FALSE	+
AD-1184003 U	CUUGUUUUCUGCUUGCAACA	85 G	AUGUUUGGGAGGAAGAACAGAU	440	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15344	15366	TRUE	TRUE	FALSE	+
AD-1184004 G	CACACACUGCUUAUGCUAAUA	86 C	CUAAUAGCAUAAAGCAGUUGGG	441	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15493	15515	TRUE	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184005	UGAGGUGUCUCUUAUAGAAAAUA G	87	CAUUUCUUAAGAGACACUCAU A	442	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15622	15644	TRUE	TRUE	FALSE	+
AD-1184006	UGGACUGAGACUGACCUCAC U	88	AGUAAGGGCAGUGUCAGGCCAA C	443	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15836	15858	TRUE	TRUE	FALSE	+
AD-1184007	UUACCCAGAUCCAUCAAGAA U	89	AUUCUUGAUGGAUCUGGGUAAG G	444	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15928	15950	TRUE	TRUE	FALSE	+
AD-1184008	GAUGGUACACUUUAUGAUAGA A	90	UUAAUCAUUAAGGUACCAUCU G	445	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15989	16011	TRUE	TRUE	FALSE	+
AD-1184009	AAACAUCCUAUACAGGAUA U	91	AUACUCCUGAUUAGGAUGUUUA G	446	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	16049	16071	TRUE	TRUE	FALSE	+
AD-1184010	AACAUCCUAUACAGGAU G	92	CAUACUCCUGAUUAGGAUGUU A	447	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	16050	16072	TRUE	TRUE	FALSE	+
AD-1184011	AGGAGUAUGCUGAUGUCUU C	93	GAAGAGCACUCAGCAUACUCUG A	448	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	16062	16084	TRUE	TRUE	FALSE	+
AD-1184012	CCUGAGUTUUAUGGGCUAU G	94	CAUAGCCUCAUAAAACUCAGGU U	449	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	16190	16212	TRUE	TRUE	FALSE	+
AD-1184013	GCAGCAGAAACGCCUAAAGC U	95	AGCUUUGAGCCGUUCUGUGCA A	450	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	16634	16656	TRUE	TRUE	FALSE	+
AD-1184014	CCUGGUATCGGUAAAGGICA U	96	AUGACUCUUACCAGUACAGGU G	451	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17084	17106	TRUE	TRUE	FALSE	+
AD-1184015	UAUAGAUAAAUGUAGAAA U	97	AUUCUACUACAUUUAUCUAG G	452	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17212	17234	TRUE	TRUE	FALSE	+
AD-1184016	CUGCUGAAAUUUGUGACACU G	98	CAGUGUCACAAUUCACCGAG A	453	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17568	17590	TRUE	TRUE	FALSE	+
AD-1184017	GCUGAAAATGUTUGACACTGU G	99	CACAGUGUCAACAUUUCAGCA G	454	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17570	17592	TRUE	TRUE	FALSE	+
AD-1184018	UGAAAATGGUGACACUGA G	100	CUCACAGUGUCAACAAUUCAG C	455	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17572	17594	TRUE	TRUE	FALSE	+

TABLE 2-continued

## Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Strand of the Viral RNA Targeted by the Agent
AD-1184019	AAAUTUGUGACACUGUGAGU	101	CAUCACAGUGUAAACAUUUC	456	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17574	17596	TRUE	TRUE	FALSE	+
AD-1184020	UGUGACACUGUGAGGUU	102	AAAGCACUCACAGUGAACAA	457	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17578	17600	TRUE	TRUE	FALSE	+
AD-1184021	GCAUGAUGUUCAUCUGGAA	103	AUTGGAGUGAAAACAUGUGCG	458	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17677	17699	TRUE	TRUE	FALSE	+
AD-1184022	UUCACCUCUAAAUUCACAGA	104	UUCUGUGAAUUAAGGUGAA	459	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17770	17792	TRUE	TRUE	TRUE	+
AD-1184022	UUCACCUCUAAAUUCACAGA	104	UUCUGUGAAUUAAGGUGAA	459	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17770	17792	TRUE	TRUE	TRUE	+
AD-1184023	UCACCUUAAAUUCACAGA	105	AUUCUGUGAAUUAAGGUGA	460	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17771	17793	TRUE	TRUE	TRUE	+
AD-1184024	ACCUUAAAUCACAGAUG	106	GCAGAUUCUGUGAAUUAAGGUG	461	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17773	17795	TRUE	TRUE	TRUE	+
AD-1184025	CCUUAUAAUUCACAGAUGC	107	AGCAUUCUGUGAAUUAAGGU	462	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17774	17796	TRUE	FALSE	TRUE	+
AD-1184025	CCUUAUAAUUCACAGAUGC	107	AGCAUUCUGUGAAUUAAGGU	462	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17774	17796	TRUE	FALSE	TRUE	+
AD-1184026	UAUAAUUCACAGAUGC	108	UACAGCAUUCUGUGAAUUAAG	463	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17777	17799	TRUE	FALSE	TRUE	+
AD-1184027	AACUGUUAAUCACAGG	109	CCCUGUGAGAAUCAACGUUU	464	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17827	17849	TRUE	TRUE	FALSE	+
AD-1184028	GAAUAUGACUAUGCUAUU	110	GAUAUAGCAUAGCUAUUUC	465	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17832	17852	TRUE	TRUE	FALSE	+
AD-1184029	CUGUCUAAAGGUCCUUA	111	GAUAGAGCCUUUAUGGAAAGU	466	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17963	17990	TRUE	FALSE	FALSE	-
AD-1184030	CUCACUCUAAUGGCUUU	112	AAAACCC2AUCAUAGAGAAGU	467	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	18197	18219	TRUE	TRUE	FALSE	+

TABLE 2-continued

## Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO: Sequence 5' to 3'	Antisense Strand SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS? SARS2?	Targets MERS? MERS?	Strand of the Viral RNA Targeted by the Agent
AD- 1184031 A	AGGUCCUAUUUUACAAAAU	113 A	UAUUUGGAAAUAUGGCCUG	468 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	18628	18650	TRUE	FALSE	FALSE -
AD- 1184032 U	UUUACAAAUAUTUGAUACU	114 C	AAGUAUCAAAUUGUUUAAAC	469 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	19566	19588	TRUE	TRUE	FALSE +
AD- 1184033 A	AUAUACUCAACUGUGCUAU	115 U	UAUUGACACAGUGAGUUAUU	470 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	20794	20816	TRUE	TRUE	FALSE +
AD- 1184034 C	UAGGUACUTUCUUTUGAACU	116 U	GAAGGUCAAAAGAAGUACUAC	471 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	23092	23114	TRUE	TRUE	FALSE +
AD- 1184035 U	UGGUAAACACUAAUAGUAAA	117 A	AUUUACUAAUUAUGGUACAC	472 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	23712	23734	TRUE	FALSE	FALSE -
AD- 1184036 G	CAAUACCACUAAACCACAA	118 GA	CUTAUAGGUUUAUGGUAAUG	473 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24270	24292	TRUE	FALSE	FALSE -
AD- 1184037 A	AAUGGUUCUTCAUAGGAACCA	119 U	UGGGUUCUCAUAGGAAACAUUC	474 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24300	24322	TRUE	TRUE	FALSE +
AD- 1184038 C	UUCUGCUAAUCUTUGCGCUA	120 C	GUAGCAGGAAGAUAGCGGAAG	475 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24620	24642	TRUE	TRUE	FALSE +
AD- 1184039 A	CUGCUAAUCUUGUGCUACU	121 A	UAGUAGCAGCAAGAUAGCAGA	476 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24622	24644	TRUE	TRUE	FALSE +
AD- 1184040 G	AUCAUACAUCCAGAUUU	122 C	CAACAUCUGGUGAUGUAU	477 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	25033	25055	TRUE	TRUE	FALSE +
AD- 1184041 A	GUCAAUUACAUUACACUA	123 UC	UUAUGGUAAUUGUAUUGAC	478 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	25362	25384	TRUE	TRUE	FALSE +
AD- 1184042 U	ACGACGATACUACGGGCC	124 G	AGGCACGGCUAGUAGUCCGUC	479 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26192	26214	TRUE	TRUE	FALSE +
AD- 1184043 U	CGACGACUACUAGGUGCCU	125 C	AAGGCACCUAGUAGUCCGUC	480 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26193	26215	TRUE	TRUE	FALSE +
AD- 1184044 G	ACGACUACUAGGUGCCUU	126 G	CAAAGGCGACGUAGUAGCUC	481 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26195	26217	TRUE	TRUE	FALSE +

TABLE 2-continued

## Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Strand of the Viral RNA Targeted by the Agent
AD-1184045	CGACUACUAGCGGCCUTUG U	127	ACAAAGGGACCGUAGUAGCGU	482	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26196	26218	TRUE	TRUE	FALSE	+
AD-1184046	GAGUACGAAACUUAUGUACUC A	128	UGAGUACAUAAAGUUCGUACUCA	483	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26231	26253	TRUE	TRUE	FALSE	+
AD-1184047	UACGAACTUUAUGGUACUAU C	129	GAAGUGAGUACAUAAAGUUCGUAC	484	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26234	26256	TRUE	TRUE	FALSE	+
AD-1184048	UACUCAUUCGUUUCGGAGA G	130	CUCUUCCAAAAGCAAGUAGUAC	485	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26246	26268	TRUE	TRUE	FALSE	+
AD-1184049	UAGGUAAAUGCGUACUUCUU U	131	AAGAAAGUACGCUAUUACUAU	486	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26280	26302	TRUE	TRUE	FALSE	+
AD-1184050	UUCUUGGUUUCGUGUUUC U	132	ACGUUACUCCAAAGCAGAAA A	487	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26301	26323	TRUE	TRUE	FALSE	+
AD-1184051	UUCGGGGAUUUCUUGCUAGU U	133	AACUAGGAAAGAAUACCACGAAA G	488	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26309	26331	TRUE	TRUE	FALSE	+
AD-1184052	UAGCCAUCUUCUACUGCGUU C	134	GAAGGCCTGUAAAGGAUGGUAG U	489	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26334	26356	TRUE	TRUE	FALSE	+
AD-1184053	AGCCAUCUUCUACUGCGCTUC G	135	CGTAGGCCAGUAGGAUGGCCA G	490	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26335	26357	TRUE	TRUE	FALSE	+
AD-1184054	GCCAUUCUACUGGCCUTUG A	136	UCGAAGGCCAGUAGGAUGGCCU A	491	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26336	26358	TRUE	TRUE	FALSE	+
AD-1184055	CCAUCUUCUACUGGCCUUCA U	137	AUGGAAGGCCAGUAGGUGGCC U	492	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26337	26359	TRUE	TRUE	FALSE	+
AD-1184056	ACUGCGCTUUCGAUUGUGUGC G	138	CGCACAC2AUCAAGGCCAGUA A	493	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26345	26367	TRUE	TRUE	FALSE	+
AD-1184057	UGCGCUUCGAAUUGUGGCCU A	139	UAGGCACACAAUCGAAGGCCAG U	494	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26347	26369	TRUE	TRUE	FALSE	+
AD-1184058	CGCUUCGAAUUGUGGCCUAC U	140	AGUACGC2ACACAUCAUCGAGCGC A	495	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26349	26371	TRUE	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184059	GCUUCGATUGUGUGGUACU	141	CAGUACGGCACAAUCGAAGCG	496	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26350	26372	TRUE	TRUE	FALSE	+
AD-1184060	GUUCCUGAUCCUUCGGGCUA	142	UUAGACCAGAACGUAGCGAACU	497	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26450	26472	TRUE	TRUE	FALSE	+
AD-1184061	UUCCUGAUCCUUCGGGCUAA	143	UUUAGACCAGAACGUAGCGAAC	498	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26451	26473	TRUE	TRUE	FALSE	+
AD-1184062	CCUGAUCUTCUGGUCAAC	144	CGUUUAGGCCAGAGAUAGGA	499	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26453	26475	TRUE	TRUE	FALSE	+
AD-1184063	UCUUCUGGUCAAAACGAAUC	145	UAGUUUGUUUAGCCAGAGAU	500	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26458	26480	TRUE	TRUE	FALSE	+
AD-1184064	CUUCUGGUCAAAACGAAUC	146	UJAGUUUCGUUAGACCAAGAA	501	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26459	26481	TRUE	TRUE	FALSE	+
AD-1184065	GGAAACCUCUAAUACGUUUC	147	GGAAACCUCUAAUACGUUUC	502	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26579	26601	TRUE	TRUE	FALSE	+
AD-1184066	UGCUACACGAAAGCCTUU	148	GAAGGGCUUCGUGAUGUAGCAA	503	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27030	27052	TRUE	TRUE	FALSE	+
AD-1184067	GCUBCAUCACGAAAGCUUUC	149	AAGAAAGCCGUUCGUGAUGUAGCA	504	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27031	27053	TRUE	TRUE	FALSE	+
AD-1184068	CUACAUCCGAAAGCUUUCU	150	AAGAAAGCCGUUCGUGAUGUAGC	505	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27032	27054	TRUE	TRUE	FALSE	+
AD-1184069	ACGUUUUUCUUAUACAUU	151	CAAUUUGUAUAGAAGCGGUU	506	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27043	27065	TRUE	TRUE	FALSE	+
AD-1184070	UGUACAGGAAAGGACAAACAG	152	UCUGUUUGUACUTUACUGACAA	507	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27180	27202	TRUE	TRUE	FALSE	+
AD-1184071	AAGUGACACAGAUGUUTCA	153	AUGAAAACPUUCUGUUGUACUUA	508	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27188	27210	TRUE	TRUE	FALSE	+
AD-1184072	CUACUCUAAAUAUACAUUA	154	CUAAAUGGUAAAUAUAGACUAG	509	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28021	28043	TRUE	FALSE	FALSE	-

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA	Targeted by the Agent
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	MERS?		
AD-1184073	CCCCAAGGGUUUACCCAAUAA	155	AUUAUUGGGUAAAACCUCGGGC	510	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28395	28417	TRUE	TRUE	FALSE	+	
AD-1184074	UACCCAAUAAAUCUGCGCU	156	AGGACGCAAGAUUAUUGGUAAA	511	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28405	28427	TRUE	TRUE	FALSE	+	
AD-1184075	GAUGACCAAAUUGGUACUAUA	157	GUAGUAGGCCAAUUTGGGUACUC	512	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28512	28534	TRUE	TRUE	FALSE	+	
AD-1184076	GCUACUACCGAAAGAGCUACC	158	UGGUAGGCUUCUUGGUAGUAGGCC	513	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28525	28547	TRUE	TRUE	FALSE	+	
AD-1184077	UCGGGCUAGAACUCCUCUAA	159	CUTUGAGGGAGGTGGUAGGCAGAU	514	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28741	28763	TRUE	TRUE	FALSE	+	
AD-1184078	CGUGGCUACAAUCUCCUCAG	160	CCUUGGAGGAAAGUUGUAGCAGGA	515	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28742	28764	TRUE	TRUE	FALSE	+	
AD-1184079	UGCUCACAAUCUCCUAAAGGA	161	UUCGUUAGGGAAAGUUGUAGCAG	516	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28744	28766	TRUE	TRUE	FALSE	+	
AD-1184080	UACAAACUUCUCAAGGAAACA	162	UGGUUCUUGAGGAAGUUGUAG	517	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28747	28769	TRUE	TRUE	FALSE	+	
AD-1184081	ACAAACUUCUCAAGGAAACA	163	GUUGGUCCUUGAGGAAGUUGUAG	518	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28748	28770	TRUE	TRUE	FALSE	+	
AD-1184082	ACUUCUCUCAAGGAAACA	164	AAUGUUGUCCUUGAGGAAGUUGUAG	519	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28751	28773	TRUE	TRUE	FALSE	+	
AD-1184083	UCCUCAAGGAACAAUUGC	165	GGCAAUGGUUGUCCUUGGGAA	520	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28754	28776	TRUE	TRUE	FALSE	+	
AD-1184084	CAAGGAACAAUUGCCAAA	166	UUUUGGCAUAGUGUUCUUGUAG	521	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28758	28780	TRUE	TRUE	FALSE	+	
AD-1184085	AAGGAACAAUUGCCAAA	167	CUUUUGGCAUAGUGUUCUUGUAG	522	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28759	28781	TRUE	TRUE	FALSE	+	
AD-1184086	ACAUUGCCAAAAGGCCUUCUA	168	GUAGAAGGCCUUTUGCAAUUGUU	523	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28767	28789	TRUE	TRUE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184087	GACAGAUAGAACCGCUGA	169	CUCAAAGCUGGUCUCAUCGUCA	524	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28944	28966	TRUE	TRUE	FALSE	+
AD-1184088	CAACUGUGACUAGAACU	170	AGAUUUCCUAGUGACAGUUGG	525	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29001	29023	TRUE	TRUE	FALSE	+
AD-1184089	GUCCAGAACAAACCCAGGA	171	UUCUUGGGUUUUGUGGACC	526	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29104	29126	TRUE	TRUE	FALSE	+
AD-1184090	GGCCGCAAAUUGCAAAUU	172	CAAAUUGGCAAUTUGGCCA	527	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29173	29195	TRUE	TRUE	FALSE	+
AD-1184091	GCAUGGAAGUCACCUUCG	173	CCGAAAGGGUGUGACUUCAGGC	528	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29233	29255	TRUE	TRUE	FALSE	+
AD-1184092	UAUAGUCUACUCUTUGGAG	174	UCUGCACAAAGGUAGACUAAU	529	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29595	29617	TRUE	TRUE	FALSE	+
AD-1184093	UAGUCUACUCUUGUGCAGAA	175	AUUCUGCACAGAGUAGCUAU	530	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29597	29619	TRUE	TRUE	FALSE	+
AD-1184094	AGUCUACUCUUGGCGAGAU	176	CAUUCUGGACAAGAGUAGACUA	531	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29598	29620	TRUE	TRUE	FALSE	+
AD-1184095	UCUACUCUUGGCGAGAUGA	177	UUCAUUCUGGACAAGAGUAGAC	532	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29600	29622	TRUE	TRUE	FALSE	+
AD-1184096	CUCUUGGGAGAUGAAUUC	178	AGRAUUCAUUCUGGACAAAGAGU	533	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29604	29626	TRUE	TRUE	FALSE	+
AD-1184097	UAGGUAAAUCUAAUCACAA	179	AUGUGAGAUAGUACAUAC	534	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29650	29672	TRUE	TRUE	FALSE	+
AD-1184098	UAACUUAAAUCUACAUAGC	180	UGCUAUGGAGAUAAAACUUA	535	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29654	29676	TRUE	TRUE	FALSE	+
AD-1184099	UUUAAUCUACAUAGCAUC	181	AUAUUGCUAUGUGAGAUAAA	536	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29658	29680	TRUE	TRUE	FALSE	+
AD-1184100	UUAAUCUACAUAGCAACU	182	AAGAUUGCUAUGUGAGAUAAA	537	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29659	29681	TRUE	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184101	GGGGAGACUUGAAAAGGCCA C	183 A	GGGGCUCUUUCAAGUCCUCCU	538 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29699 29721	TRUE	TRUE	FALSE	FALSE	+	
AD-1184102	GUAGAACUUCUUCUAAACCG A	184 A	UGUUUAGAGAACAGAUCAUA	539 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	51	73	TRUE	TRUE	FALSE	+	
AD-1184103	AGAUCUGUCUCUAAACGGA C	185 C	GUUCGUUAGAGACAGGUCAUA	540 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	53	75	TRUE	TRUE	FALSE	+	
AD-1184104	UUCUCUAAACGAAACUUAAA A	186 A	UUUUAAAGGUUCGUUAGAAC	541 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	60	82	TRUE	TRUE	FALSE	+	
AD-1184105	UCUCUAAACGAAACUUAAA U	187 AC	AUUUAAAAGGUUCGUUAGAGA	542 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	61	83	TRUE	TRUE	FALSE	+	
AD-1184106	CUAACGAAACUUAAAACU G	188 G	CAGAUUUAAAGGUUCGUUAGA	543 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	64	86	TRUE	TRUE	FALSE	+	
AD-1184107	UAAACGAAACUUAAAACUG U	189 A	ACAGAUUUAAAGGUUCGUUAG	544 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	65	87	TRUE	TRUE	FALSE	+	
AD-1184108	AAACGAAACUUAAAACUGU G	190 G	CACAGAUUUAAAGGUUCGUUA	545 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	66	88	TRUE	TRUE	FALSE	+	
AD-1184109	ACGAAACUUAAAACUGGU G	191 U	CACACAGAUUUAAAGGUUCGUU	546 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	68	90	TRUE	TRUE	FALSE	+	
AD-1184110	GCUGCUUACGGUUCGUCCG U	192 U	ACGGACGAAACCGUAGCAGCC	547 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	187	209	TRUE	TRUE	FALSE	+	
AD-1184111	UGCUUACGGUUCGUCCGUG U	193 C	ACACGGACGAAACCGUAGCAG	548 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	189	211	TRUE	TRUE	FALSE	+	
AD-1184112	GCUUACGGUUCGUCCGUGU U	194 G	AACACGGACGAAACCGUAGCCA	549 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	190	212	TRUE	TRUE	FALSE	+	
AD-1184113	CUUACGGUUCGUCCGUGU G	195 A	CAACACGGACGAAACCGUAGGC	550 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	191	213	TRUE	TRUE	FALSE	+	
AD-1184114	UUACGGUUCGUCCGUGUG C	196 C	GCACACGGACGAAACCGUAGG	551 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	192	214	TRUE	TRUE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS? SARS2?	Targets MERS?	Targeted by the Agent	
AD-1184115	UGUGACCCAAAGGUAGAUGG	197	CCAUCUACCUUUCGGUACAC	552	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	247	269	TRUE	TRUE	FALSE	
AD-1184116	GACCGAAAGGUAAAGGAGG	198	UCUCCAUACUACUUUCGGUCA	553	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	250	272	TRUE	TRUE	FALSE	
AD-1184117	AAAACACACGUCCAACUCAAG	199	ACUGAGUUGGACGUUUUC	554	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	294	316	TRUE	TRUE	FALSE	
AD-1184118	CACACGUCCAAACUAGUUTG	200	GCAACACUGAGUUGGACGUUGU	555	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	298	320	TRUE	TRUE	FALSE	
AD-1184119	ACACGUCCAAACUCAGUUGC	201	GGCAAACUGAGUUGGACGUUG	556	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	299	321	TRUE	TRUE	FALSE	
AD-1184120	CACGUCCAAACUCAGUUGCC	202	AGGCAAAACUGAGUUGGACGUUG	557	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	300	322	TRUE	TRUE	FALSE	
AD-1184121	ACGUCCAAACUCAGUUGCCU	203	CAGGCAAACUGAGUUGGACGU	558	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	301	323	TRUE	TRUE	FALSE	
AD-1184122	CGUCCAAACUCAGUUGCCUG	204	ACAGGCAAACUGAGUUGGACGU	559	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	302	324	TRUE	TRUE	FALSE	
AD-1184123	GUUCUUCUUCGUAGAACCG	205	ACCGGUUCUACGAAAGAACCC	560	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	624	646	TRUE	TRUE	FALSE	
AD-1184124	UUCCUUCUUCGUAGAACGU	206	UACCGGUUCUACGAAAGAAC	561	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	625	647	TRUE	TRUE	FALSE	
AD-1184125	UCUUCUUCUAGAACGGA	207	UACCCGUUCUACGAAAGAAC	562	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	626	648	TRUE	TRUE	FALSE	
AD-1184126	AUCUUCUUCUUCGUUCUU	208	GAAGAAGGCCAAGAACGAAU	563	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3179	3201	TRUE	FALSE	FALSE	
AD-1184127	GGUUAUUAAAACUACUGA	209	GUCAGUAGUUUUAAAACCA	564	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3351	3373	TRUE	TRUE	FALSE	
AD-1184128	UCUACACAAACUCAAAAGA	210	UUCUUUAAGAGUUGGUAGA	565	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	3745	3767	TRUE	FALSE	FALSE	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences												Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent	
AD-1184129	AAGAGAGUGGGAAAUCCU	211	UAGGAUUTUCCACUACUCUUC	566	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6409	6431	TRUE	TRUE	FALSE	+	
AD-1184130	ACAAUUGGUACUUUACUA	212	CUAGAAAAGUACACA AUUGUA	567	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6794	6816	TRUE	TRUE	FALSE	+	
AD-1184131	ACACUCUAAACAGUAUUCUU	213	AAGAAAUACUGUUAAGAGUGUC	568	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	6862	6884	TRUE	FALSE	FALSE	-	
AD-1184132	AUGUACAAACUAUUGUUAUG	214	CCAUAAACAAUAGUUGUCAAU	569	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	7529	7551	TRUE	TRUE	FALSE	+	
AD-1184133	UGUACAAACUAUUGUUAUGG	215	ACCAUAAACAAUAGUUGUACAU	570	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	7530	7552	TRUE	TRUE	FALSE	+	
AD-1184134	CCAGCAGUUUUCUGUGCU	216	UACACCACAGAAAACUCCUGGU	571	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	9306	9328	TRUE	TRUE	FALSE	+	
AD-1184135	UCAUGUGGUAGUGUUGGUU	217	AAAACCAACACUACCAUGAA	572	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	10482	10504	TRUE	TRUE	FALSE	+	
AD-1184136	CACUGUACAGUCUAAAUGU	218	GACAUUUUAGACGUACGUGG	573	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	11831	11853	TRUE	TRUE	FALSE	+	
AD-1184137	ACUGUACAGUCUAAAUGUC	219	UGACAUUUUAGACGUACAGUG	574	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	12212	12234	TRUE	TRUE	FALSE	+	
AD-1184138	UUUGAAUGUGGCUAAAUCUG	220	CCAUACCUUCAUUAGGUUGUU	575	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	12967	12989	TRUE	TRUE	FALSE	+	
AD-1184139	ACACCUAAAAGGGU AUG	221	UACCAUACCUUCAUUAGGUUG	576	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	12969	12991	TRUE	TRUE	FALSE	+	
AD-1184140	AACCUAAAAGGGU AUGU	222	AAUCCUUUAGGAUUGGGUGAU	577	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13263	13290	TRUE	TRUE	FALSE	+	
AD-1184141	UCAUCCAAAUCUAAAGGAU	223	CCGAGAGCGUACAGACUGUG	578	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13364	13386	TRUE	TRUE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences												Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent	
AD-1184143	ACGGUUUUGGGGUAAAGUGC	224 U	GCACUUACACGCCAACCGGUU	579	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13465	13487	TRUE	TRUE	FALSE	+	
AD-1184144	AGGCACAUAGUACGAUGGUG	225 U	ACGCACAUAGUAUAGUGCCUG	580	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13510	13532	TRUE	TRUE	FALSE	+	
AD-1184145	UUCUACUUUGGUAAAAGA	226 C	CUCUAAACUACAAGUAGAAU	581	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13639	13661	TRUE	TRUE	FALSE	+	
AD-1184146	CUCUAAACUACCAACAUAGAG	227 A	UCUCUACUUGGGAGUAGAGA	582	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13669	13691	TRUE	TRUE	FALSE	+	
AD-1184147	UUGUGAUGAUAAUUAUCA	228 A	UUGAAAUUAUCAUCAUCAAAC	583	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13891	13913	TRUE	TRUE	FALSE	+	
AD-1184148	UGUGAUGAUAAUUAUCAA	229 C	AUTGAAAUAAUCAUCAUCAA	584	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	13892	13914	TRUE	TRUE	FALSE	+	
AD-1184149	AUCAGGAUAAACUUAUCAU	230 A	UAUGUAAGUUUACAUCCUGAUU	585	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14505	14527	TRUE	TRUE	FALSE	+	
AD-1184150	UAAAGAAUGUUGCUUUCAAA	5 U	GTTTGGAAAAGCAACATUGUAG	6	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14644	14666	TRUE	TRUE	FALSE	+	
AD-1184151	UUUUCAAACUGUCAAACCG	231 C	CCGGGUUUGACAGUUUAGAAAG	586	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14656	14678	TRUE	TRUE	FALSE	+	
AD-1184152	ACUGUCAAAACCGGUAAUU	232 U	AAAAUACCGGGTUUGAGAGUU	587	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14663	14685	TRUE	TRUE	FALSE	+	
AD-1184153	CUUUAAGGAGGAUUCUUG	233 A	AAGAGACUUCUCCUCCUAGA	588	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14722	14744	TRUE	TRUE	FALSE	+	
AD-1184154	UUUAAGGAGGAUUCUUG	234 A	AACAGAACUUCUCCUCCUAAAG	589	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14723	14745	TRUE	TRUE	FALSE	+	
AD-1184155	UUAAGGAGGAAGUUCUUG	235 G	CAACAGAACUUCUCCUAAAG	590	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14724	14746	TRUE	TRUE	FALSE	+	
AD-1184156	UAAGGAGGAAGUUCUUG	236 A	UCAACAGAACUUCUCCUAAAG	591	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14725	14747	TRUE	TRUE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences												Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent	
AD- 1184157	AAAACACUTUCUCCUUGGUC	2337	UGGCCAAAGAAGAGGUUU AA	592	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14749	14771	TRUE	TRUE	FALSE	+	
AD- 1184158	GGUAAGGGCUAGACUUUAUA	2338	AUAUAAAAGUCUAGCCUACCC C	593	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14966	14988	TRUE	TRUE	FALSE	+	
AD- 1184159	GUAGGCUGAGACUUAUUAU	2339	CAUAAUAGUCUAGCCUACCC C	594	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	14967	14989	TRUE	TRUE	FALSE	+	
AD- 1184160	GAUCAAGAUGCACUUUCGC	240	UGCGAAAAAGUGCAUCUGAUCC U	595	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15005	15027	TRUE	TRUE	FALSE	+	
AD- 1184161	UAGCUGGGUGCUACUACGU	241	UACAGAUAGAGAACCAACUAC G	596	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15108	15130	TRUE	TRUE	FALSE	+	
AD- 1184162	GGUGUCUCUAUCUGUAC	242	ACUACUACAGAUAGACACCA G	597	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15113	15135	TRUE	TRUE	FALSE	+	
AD- 1184163	UCUCUAAUCGUAGUACU AUG	243	UCAUAGGUACUACAGAUAGAGAC A	598	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15117	15139	TRUE	TRUE	FALSE	+	
AD- 1184164	UUGUUCUGGCUCGAAACAU	244	UAUGGUUCGGAGCAAGAACAG U	599	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15345	15367	TRUE	TRUE	FALSE	+	
AD- 1184165	UUCACUAAUAGUAAACCAG	245	CCUGGUTUACAAUAGGAAAC C	600	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15451	15473	TRUE	TRUE	FALSE	+	
AD- 1184166	ACACACUGCUUAUGCUAAUAG	246	ACUAAUAGCAUAGCAGUGUG G	601	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15494	15516	TRUE	TRUE	FALSE	+	
AD- 1184167	CAAUCGUUAUGCUAAUAGU	247	CACUAAUAGCAUAGCAGUG G	602	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15495	15517	TRUE	TRUE	FALSE	+	
AD- 1184168	AACUGCUUAUGCUAAUAGUG	248	ACACUAAUAGCAUAGCAGUG U	603	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15496	15518	TRUE	TRUE	FALSE	+	
AD- 1184169	ACUGCUUAUGCUAAUAGUG	249	AACACUAAUAGCAUAGCAGUG G	604	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15497	15519	TRUE	TRUE	FALSE	+	
AD- 1184170	CACUCAUAAAGUCUGUGUG	250	ACACACAGACUUAUGGUG C	605	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15609	15631	TRUE	FALSE	FALSE	-	

TABLE 2-continued

## Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS? SARS2?	Targets MERS?	Strand of the Viral RNA	Targeted by the Agent
AD-1184171	GAGUGUCUCUAGAAUAG A	251	UCUAUUUCUAAGAGACACUCA	606	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15623	15645	TRUE	TRUE	FALSE	+
AD-1184172	ACUGAGACUGACCUACUAA	252	UUAGUAGGUCAGUCUAGUC	607	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15839	15861	TRUE	TRUE	FALSE	+
AD-1184173	CAUACAAGCUAGUAAAACA G	253	CUGUUAAUCUAGCAUUGUAUGU	608	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15884	15906	TRUE	TRUE	FALSE	+
AD-1184174	ACAGAUGGUACACUUAAGAU U	254	AAUCAUAGUGUACCAUCUGUU	609	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15986	16008	TRUE	TRUE	FALSE	+
AD-1184175	CAGAUGGUACACUUAUGAUU G	255	CAAUCAUAGGUACCAUCUGU	610	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	15987	16009	TRUE	TRUE	FALSE	+
AD-1184176	AGGAGAGUACCCUUUGAAA A	256	UUUUCAAGGGGUACUCUCCUA	611	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	16819	16841	TRUE	TRUE	FALSE	+
AD-1184177	UAUCUCAGAUGAGUUUUCUA G	257	CUGAAAAACUCAUCUGAGAUU	612	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17005	17027	TRUE	TRUE	FALSE	+
AD-1184178	AUCUCAGAUGAGUUUUCUAG C	258	GCUGAGAAAACUCAUCUGGAAUA	613	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17006	17028	TRUE	TRUE	FALSE	+
AD-1184179	AUGUGCAAAUUAUCAAAAG G	259	CCUUUUGAUAAUUGCACAUU	614	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17028	17050	TRUE	TRUE	FALSE	+
AD-1184180	GUUGCAAUUUAUCAAAAGGU U	260	AACCUUUTGAAUAAUUGGAACA	615	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17030	17052	TRUE	TRUE	FALSE	+
AD-1184181	GUACUGGUAGAGUCAUUUU G	261	CAAAAUGCUCUACCAQUACC A	616	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17088	17110	TRUE	TRUE	FALSE	+
AD-1184182	UACUGGUAAAGAGUCAUUUTG C	262	GCaaaaUGACUCUACAGGUAC	617	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17089	17111	TRUE	TRUE	FALSE	+
AD-1184183	GUAGAGGUGUUTGUAUAAAUU C	263	GAAUUUACUAAAACACUACUA	618	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17252	17274	TRUE	TRUE	FALSE	+
AD-1184184	AGAGGUUUTGUAUAAAUTC A	264	UUGAAAUUACUAAAACACUCA	619	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17254	17276	TRUE	TRUE	FALSE	+

TABLE 2-continued

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO: Sequence 5' to 3'	Antisense Strand SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Strand of the Viral RNA Targeted by the Agent
AD- 1184185 U	GUGGUGUUAGUAAAUCAAAG	2655 ACUUUGAUUUUAUCAAAACACU C	620 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17257 17279	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184186 A	GUUUUGAUAAAUCAAAGUG	2656 UCACUUUGAAUUUAUCAAAACA C	621 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17259 17281	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184187 U	CACACUAGAACCCAGAAUAUU	2657 AAAAUUUCCGGGTUCUAUGUGGC C	622 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17479 17501	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184188 C	ACACUAGAACCCAGAAUAUU	2658 GAAAUAUCUGGUUCUAGUGUG C	623 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17480 17502	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184189 U	GAAAUGGUGGACAGUGAG	2659 ACUCACAGUGUCACAAUUAUCA G	624 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17573 17595	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184190 U	CCCCUGCUUGGAGAAGCUG	2700 ACAGCUUWUCUCCANGGCCU U	625 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17743 17765	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184191 G	CUUAUAAUUCACAGAAUGCU	2711 CAGCAUTUCUGUGAAUUAAGG U	626 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17775 17797	TRUE	FALSE	TRUE	TRUE	+	
AD- 1184191 G	CUUAUAAUUCACAGAAUGCU	2711 CAGCAUTUCUGUGAAUUAAGG U	626 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17775 17797	TRUE	FALSE	TRUE	TRUE	+	
AD- 1184192 U	UUAAAUAUUCACAGAAUGCUG	2722 ACAGCAUTUCUGUGAAUUAAGG G	627 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17776 17798	TRUE	FALSE	TRUE	TRUE	+	
AD- 1184193 A	AAU AUGACUAUGCUAUUC	2733 UGAAUAUGACAUAGCUAUUC U	628 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17853 17875	TRUE	TRUE	FALSE	TRUE	+	
AD- 1184194 C	AUAUGACUAUGCUAUUCA	2744 GUGAAUAUGACAUAGCUAUU C	629 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17854 17876	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184195 U	UAUGACUAUGCUAUUCA	2755 AGUGAAUAUGACAUAGCUAUU U	630 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	17855 17877	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184196 G	AAGACUCAUUCUAGAUGUG	2766 CCCAUCAUAGAGAUGAGCUUC U	631 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	18193 18215	TRUE	TRUE	FALSE	FALSE	+	
AD- 1184197 U	AGACUCAUUCUAGAUGGG	2777 ACCCAUC2AUAGAGAUGAGCUUU C	632 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	18194 18216	TRUE	TRUE	FALSE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS? SARS2?	Targets MERS?	Targeted by the Agent	
AD-1184198 C	UCAGAGUUUAGAAAUGGG	278 G	GCCACAUUUUCUAAACUCUGAA	633 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	19615	19637	TRUE	TRUE	FALSE	+	
AD-1184199 A	ACCAUCAACTUUUCAUAU	279 GU	UAUUAUAGAAAAGUUGAGGU	634 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	20152	20174	TRUE	FALSE	FALSE	-	
AD-1184200 A	CUCCAUAAACGAAUAGUCG	280 U	UGAACACAUUAUCGUUUUAGGAGA	635 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	20315	20337	TRUE	FALSE	FALSE	-	
AD-1184201 A	CAUAGGAUAAAACUUCUA	281 A	UJAGAAAGUUUUAUUCCUAUGG	636 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	20413	20435	TRUE	FALSE	FALSE	-	
AD-1184202 C	CCUAAUUAUACAAACUUG	282 A	GCACAAGUUUGUAAUUAUAGGA	637 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	22548	22570	TRUE	TRUE	FALSE	+	
AD-1184203 C	GCTUGUAAAACAAUCUAGCU	283 U	GAGCUAACGUUUUACAGCG	638 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24443	24465	TRUE	TRUE	FALSE	+	
AD-1184204 C	CUUGUUAAAACAACUAGCUC	284 G	GGAGCUAACGUUUUACAGC	639 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24444	24466	TRUE	TRUE	FALSE	+	
AD-1184205 A	CUUGCGGUACUAAAAGUC	285 U	UGACAUUUAGUAGCAGGAAAGA	640 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	24630	24652	TRUE	TRUE	FALSE	+	
AD-1184206 G	ACUUAUGGAUUGUUUAGCA	286 C	CUCAUAAAACAAUCCAUAGUU	641 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	25387	25409	TRUE	TRUE	FALSE	+	
AD-1184207 C	CGACGACGACUACUAGCCUG	287 U	GCACGCUAGUAGUCGUCCUGG	642 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26190	26212	TRUE	TRUE	FALSE	+	
AD-1184208 C	GACGACGACUACUAGCCUG	288 G	GGACCGGUAGUAGUCGUCCUG	643 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26191	26213	TRUE	TRUE	FALSE	+	
AD-1184209 U	AUGAGUACGAACUUAUGUAC	289 A	AGUACAUAGUAGUACUCAUC	644 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26229	26251	TRUE	TRUE	FALSE	+	
AD-1184210 U	CGAACUUUAUGUACUAUTCG	290 A	ACGAUAGZAGUACAUAGUCGU	645 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26236	26258	TRUE	TRUE	FALSE	+	
AD-1184211 U	GAACUUUAUGUACUACUCCU	291 U	AACGAAUAGAGUACAUAAACUCCG	646 BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26237	26259	TRUE	TRUE	FALSE	+	

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184212	AACUUAUGGUACAUUCCGUU	292	AAACGAAUAGGUACAUUAGGUUC	647	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26238	26260	TRUE	TRUE	FALSE	+
AD-1184213	ACUUAUGGUACAUUCCGUU	293	GAACGAAUAGGUACAUUAGGUU	648	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26239	26261	TRUE	TRUE	FALSE	+
AD-1184214	CUUAUGGUACAUUCCGUU	294	CGAACGGAAUAGGUACAUUAGGU	649	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26240	26262	TRUE	TRUE	FALSE	+
AD-1184215	UUAGGUACAUUCCGUU	295	CCGAAACGGAAUAGGUACAUUAGG	650	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26241	26263	TRUE	TRUE	FALSE	+
AD-1184216	UAUGGUACAUUCCGUU	296	UCCGAAACGGAAUAGGUACAUUAAA	651	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26242	26264	TRUE	TRUE	FALSE	+
AD-1184217	AUGGUACAUUCCGUU	297	UUCCGAAACGGAAUAGGUACAUAAA	652	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26243	26265	TRUE	TRUE	FALSE	+
AD-1184218	UGUACUCAUUCGUUUCGAA	298	CUUCCGAAACGGAAUAGGUACAU	653	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26244	26266	TRUE	TRUE	FALSE	+
AD-1184219	GUACUCAUUCGUUUCGAA	299	UCUUCGCCAACGGAAUAGGUACAA	654	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26245	26267	TRUE	TRUE	FALSE	+
AD-1184220	CAGGUACGUUAAUAGGUAAU	300	UAUUAUCAUUAUACGUACCUGU	655	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26268	26290	TRUE	TRUE	FALSE	+
AD-1184221	AGGUACGUUAAUAGGUAAU	301	CUAUUAUCAUUAUACGUACCUG	656	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26269	26291	TRUE	TRUE	FALSE	+
AD-1184222	UAAUAGGUAAUAGGUACUU	302	GAAGUACGUUAAUACGUUUAAA	657	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26277	26299	TRUE	TRUE	FALSE	+
AD-1184223	UCUUGGUUUCGGGUUACUU	303	AAGAAUACCGAACGGAAAGAA	658	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26302	26324	TRUE	TRUE	FALSE	+
AD-1184224	CUGGUUUCGGGUUACUU	304	CAAGAAUACCGAACGGAAAGAA	659	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26303	26325	TRUE	TRUE	FALSE	+
AD-1184225	UUGGUUUCGGGUUACUU	305	GCAAGAAUACCGAACGGAAAG	660	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26304	26326	TRUE	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184226	UGCUUUCGUGGUAAUCUGC	306	AGCAAGAAUACCACGAAAGCAA	661	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26305	26327	TRUE	TRUE	FALSE	+
AD-1184227	GCUUUCGUGGUAAUCUGC	307	UAGCAAGAAUACCACGAAAGCA	662	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26306	26328	TRUE	TRUE	FALSE	+
AD-1184228	UUUCGGGUAAUCUGUGAG	308	ACUAGCAAGAAUACCACGAAAG	663	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26308	26330	TRUE	TRUE	FALSE	+
AD-1184229	CUGGCUGUGAUUGUGUGCG	309	ACGCACACAAUUCGAAGGCCAGU	664	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26346	26368	TRUE	TRUE	FALSE	+
AD-1184230	GUACUGCUGCAAUAUUGUA	310	UUAACAAUUAUUGCAGCAGUACG	665	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26365	26387	TRUE	TRUE	FALSE	+
AD-1184231	CUGCUGCAAUAUUGUAACG	311	ACGUUACAAUAUUGCAGCAGU	666	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26368	26390	TRUE	TRUE	FALSE	+
AD-1184232	UGCUGCAAUAUUGUAACGU	312	CACGUUACAAUAUUGCAGCAG	667	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26369	26391	TRUE	TRUE	FALSE	+
AD-1184233	GCUGCAAUAUUGUAACGUG	313	UCACGUUACAAUAUUGGAGCA	668	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26370	26392	TRUE	TRUE	FALSE	+
AD-1184234	CUGCAAUAUUGUAACGUGA	314	CUCACGUUACAAUAUUGCAGC	669	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26371	26393	TRUE	TRUE	FALSE	+
AD-1184235	AGAGUUCUGAUUCUGGU	315	GACCAAGAAUCAUCAGGAACCUA	670	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26447	26469	TRUE	TRUE	FALSE	+
AD-1184236	CUGAUCUUCUGGUAAACGG	316	UCCGUUAGACCGAGACAGG	671	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26454	26476	TRUE	TRUE	FALSE	+
AD-1184237	GAUCUUCUGGUAAACGAA	317	GUUCGUUAGACCAAGACAUCA	672	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26456	26478	TRUE	TRUE	FALSE	+
AD-1184238	ACAAUGGAAACCUGUAAUAG	318	CCUAAUACUAGGUUCCAUUGUU	673	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26574	26596	TRUE	TRUE	FALSE	+
AD-1184239	CAAUGGAAACCUGUAAUAGG	319	ACCUUAAUACUAGGUUCCAUUGU	674	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26575	26597	TRUE	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	Targets MERS?	Targeted by the Agent
AD-1184240	AAUGGAAACCAGGUAAUAGGU	320	AACCUAUATACUAGGUCCAUUG	675	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26576	26598	TRUE	TRUE	FALSE	+
AD-1184241	AUGGAACCUAGGUAAUAGGUU	321	AAACCUAUACUAGGUCCAUU	676	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26577	26599	TRUE	TRUE	FALSE	+
AD-1184242	AACCUAGGUAAUAGGUUUCCU	322	UAGGAAACCUAUACUAGGUUC	677	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26581	26603	TRUE	TRUE	FALSE	+
AD-1184243	ACCUAGGUAAUAGGUUUCCUA	323	AUAGGAAACCUAUACUAGGUU	678	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	26582	26604	TRUE	TRUE	FALSE	+
AD-1184244	UACAUCAACGAAUCUUUUUU	324	UAGGAAACCGUUUCGGAGUAG	679	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27033	27055	TRUE	TRUE	FALSE	+
AD-1184245	ACAUCAACGAAACGUUUUUA	325	AUAGGAAACGCCUUCGGAGUUA	680	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27034	27056	TRUE	TRUE	FALSE	+
AD-1184246	CAUGACGAAACGCUUUCUUAU	326	AAUAGGAAAGCGUUCGGAGU	681	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27035	27057	TRUE	TRUE	FALSE	+
AD-1184247	AUCACGAAACGGCUUUCUUAU	327	UAAAAGGAAAGCGUUCGGAGU	682	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27036	27058	TRUE	TRUE	FALSE	+
AD-1184248	UCACGAAACGGCUUUCUUAUA	328	GUAUAAAGAAAGCGUUCGGAGU	683	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27037	27059	TRUE	TRUE	FALSE	+
AD-1184249	CACGAAACGCUUUCUUAUAC	329	UGUAUAAAGAAAGCGUUCGGAGA	684	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27038	27060	TRUE	TRUE	FALSE	+
AD-1184250	ACGAAACGGCUUUCUUAUACA	330	UGUAAAUAAGAAAGCGUUCGGUG	685	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27039	27061	TRUE	TRUE	FALSE	+
AD-1184251	CGAACGCUUUCUUAUACAA	331	UUUGUAAAAGAAAGCGUUCGGU	686	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27040	27062	TRUE	TRUE	FALSE	+
AD-1184252	GUAGUGAGAACAGAUGGUU	332	GAACACAUUGUGUCAUUCACU	687	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27186	27208	TRUE	TRUE	FALSE	+
AD-1184253	UUAGCCUTUCUGCUAUUCU	333	AAGGAAUAGCAGAAAGGCCAAA	688	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27793	27815	TRUE	TRUE	FALSE	+

TABLE 2-continued

## Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS? SARS2?	Targets MERS? MERS?	Strand of the Viral RNA Targeted by the Agent
AD-1184254	UAGCCUUUCUGCUAUUCUU G	334	CAAGGAUJAGCAGAAAGGUAA A	689	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27794	27816	TRUE	FALSE	+
AD-1184255	AGCCUUUCUGCUAUUCUUG U	335	ACAGGAAUAGCGAAAAGCUA A	690	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27795	27817	TRUE	FALSE	+
AD-1184256	CCUUUCUGCUAUUCUUGUU U	336	AAACAAGGAAUAGCAGAAAGGC U	691	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27797	27819	TRUE	FALSE	+
AD-1184257	CUTUCUGCUAUUCUUGUU U	337	AAACACAAGGAAUAGCAGAAAGG C	692	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27798	27820	TRUE	FALSE	+
AD-1184258	UUUCUGCUAUUCUUGUU A	338	UUAAAACAGGAAUAGCAGAAAG G	693	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27799	27821	TRUE	FALSE	+
AD-1184259	UUCUGCUAUUCUUGUU A	339	UJAAAACCAAGGAAUAGCAGAAA G	694	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27800	27822	TRUE	FALSE	+
AD-1184260	UCUGCUAUUCUUGUU U	340	AUAAAACCAAGGAAUAGCAGAAA A	695	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27801	27823	TRUE	FALSE	+
AD-1184261	CUGCUAUUCUUGUU U	341	AAUAAAACCAAGGAAUAGCAGAA A	696	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	27802	27824	TRUE	FALSE	+
AD-1184262	CCAGGUUACCCAAUAAA C	342	GUAUUAUGGGUAAACCUUGGG G	697	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28397	28419	TRUE	FALSE	+
AD-1184263	AAGGUUACCCAAUAAU G	343	CAGUAAUUGGGUAAACCUUG G	698	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28399	28421	TRUE	FALSE	+
AD-1184264	AGGUUACCCAAUAAA C	344	GAGGUAAUUGGGUAAACCU G	699	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28400	28422	TRUE	FALSE	+
AD-1184265	ACCGAAUAAUACUGCG G	345	CAAGACGGAGUAAUUGGGUA A	700	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28406	28428	TRUE	FALSE	+
AD-1184266	AGUCAGAUGACCAA C	346	GCCAAUUTGGCAUCGGACUG C	701	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28506	28528	TRUE	FALSE	+
AD-1184267	GUCCAGAUGACCA U	347	AGCCAAUUTGGCAUCGGACU G	702	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28507	28529	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	MERS?	Targeted by the Agent
AD-1184268	AUUGCCAAAAGGCCUCUACG C	348	GCGUAGAGGCCUTUGGAAUG U	703	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28769	28791	TRUE	TRUE	FALSE	+
AD-1184269	UUGCCAAAAGGCCUCUACGC A	349	UGCUGAGAGGCCUUUGCAAU G	704	BetaCoV/Wuhan-Hu-1/2019 EPLISL_402125	28770	28792	TRUE	TRUE	FALSE	+
AD-1184270	GGCAGUCAGGCCUCUUCUGG U	350	ACGAGAACGGCTUGACGCCG C	705	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	28806	28828	TRUE	TRUE	FALSE	+
AD-1184271	AACUGUCACUAAGAAUCUG C	351	GCAGAUUUCUUAUGACAGUUU G	706	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29003	29025	TRUE	TRUE	FALSE	+
AD-1184272	UGUGACUAAAAGAAUCUGGUG C	352	GCAGCAGAUUUCUUAUGACAG U	707	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29006	29028	TRUE	TRUE	FALSE	+
AD-1184273	AACUGUGACUCUUCUUCUG C	353	GGAGGAAGAACAGACAGUUU G	708	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29441	29463	TRUE	TRUE	FALSE	+
AD-1184274	UCUUGGGAGAAUGAAUUCU C	354	GAGAAUUCAUUCUGCACAGAG U	709	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29605	29627	TRUE	TRUE	FALSE	+
AD-1184275	CUUGUGGAGAAUGAAUUCUC G	355	CGAGAAUUCAUUCUGCACAGA G	710	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29606	29628	TRUE	TRUE	FALSE	+
AD-1184276	UUGUGGAGAAUGAAUUCUCG U	356	ACGAGAAUUCAUUCUGCACAA G	711	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29607	29629	TRUE	TRUE	FALSE	+
AD-1184277	UGUGGAGAAUUCUCGUUAC G	357	UACGAGAAUUCAUUCUGCACAA G	712	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29608	29630	TRUE	TRUE	FALSE	+
AD-1184278	GUGGAGAAUUCUCGUUAC A	358	UUACGAGAAUUCAUUCUGCAC A	713	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29609	29631	TRUE	TRUE	FALSE	+
AD-1184279	UGCGAGAAUUCUCGUUAC C	359	GUUACGAGAAUUCAUUCUGCAC A	714	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29610	29632	TRUE	TRUE	FALSE	+
AD-1184280	GCAGAAUUCGUUAC C	360	AGUUACGAGAAUUCAUUCUGCA C	715	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29611	29633	TRUE	TRUE	FALSE	+
AD-1184281	CAGRAUGAAUUCUCGUUACU A	361	UAGUUACGAGAAUUCAUUCUGC A	716	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29612	29634	TRUE	TRUE	FALSE	+

TABLE 2-continued

Unmodified Sense and Antisense Strand Coronavirus dsRNA Sequences											Strand of the Viral RNA	Targeted by the Agent
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO	Target RNA Accession Version	mRNA start	mRNA end	Targets SARS2?	Targets SARS?	MERS?		
AD-1184282	UAAUCUCACAUAGCAAUUU	362	AAAGAUUCCUAUGUGAGAUUA	717	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29660	29682	TRUE	TRUE	FALSE	+	+
AD-1184283	UCUGACAUAGCAAUCUAAA	363	AUTAAAAGAUUGCUAUGUGAGA	718	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29663	29685	TRUE	TRUE	FALSE	+	+
AD-1184284	CUCACAUAGCAAUCUUAAA	364	GAUAAAAGAUUGCUAUGUGAG	719	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29664	29686	TRUE	TRUE	FALSE	+	
AD-1184285	UCACAUAGGAAUCUUAAAUC	365	UGAUAAAAGAUUGCUAUGUGA	720	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29665	29687	TRUE	TRUE	FALSE	+	+
AD-1184286	CACAUAGGAAUCUUAAAUC	366	CUGAUAAAAGAUUGCUAUGUGA	721	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29666	29688	TRUE	TRUE	FALSE	+	+
AD-1184287	GAGCCCUAAUGGUAAAAAU	367	UAUUUUUACACAUAGGCCUCU	722	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29796	29818	TRUE	TRUE	FALSE	+	
AD-1184288	GCCCCUAAUGGUAAAAAUAA	368	AUAAAUUUACACAUAGGGCU	723	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29798	29820	TRUE	TRUE	FALSE	+	
AD-1184289	CCCUAAUGGUAAAAAUAAU	369	AAUAAAUUUACACAUAGGGC	724	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29799	29821	TRUE	TRUE	FALSE	+	+
AD-1184290	CCUUAUGGUAAAAAUAAU	370	AAAUAUUUUACACAUAGGG	725	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29800	29822	TRUE	TRUE	FALSE	+	+
AD-1184291	CCCAUGGUAAUUUAAUAGCU	371	AAGCUAUAAAUCACAUAGGG	726	BetaCoV/Wuhan-Hu-1/2019 EPL_ISL_402125	29834	29856	TRUE	TRUE	FALSE	+	

TABLE 3  
Modified Sense and Antisense Strand Coronavirus dsRNA Sequences

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	Strand of the Viral RNA Targeted by the Agent
AD-1183935	asucug (Uhd) Ufcuffufuaaccaa ususa	727 VPusAfscudTc (G2p) unuagaAfcaAfccg auscstu	1082 AGATCTGTCTCTAAACGAA CTT	+
AD-1183936	uscsugu (Uhd) CfucfufAfaacgaa ususa	728 VPusAfscadTt (C2p) guuuuAgAfafaca gususc	1083 GATCTGTTCTCTAAACGAAAC TTT	+
AD-1183937	gsusucu (Chd) UfAFAFcFgaaacuu asasa	729 VPusAfscudAa (G2p) uucguuAfAgfaga acsasg	1084 CTGTTCTCTAAACGAACTTT AAA	+
AD-1183938	cusugcu (Uhd) AfFcGfGFUfuucgccc gsusa	730 VPusAfscgdGa (C2p) gaaaaccGfufAfagca gscsc	1085 GGCTGCTTACGGTTTCGTCCT GTG	+
AD-1183939	gsgsugu (Ghd) AfCcFGFafaagguaa gsasa	731 VPusAfscudTa (C2p) cauucggfufCfcafac cscsg	1086 CGGGTGTGACCCGAAAGGTA AGAT	+
AD-1183940	cscgaa (Ahd) GfFgufAfAfaguggaa asgsa	732 VPusAfscudTc (C2p) aeuuuAfcuFuucg gsuse	1087 GACCGRAAGGTAAAGATGGAA GAGC	+
AD-1183941	asasaca (Chd) AfFcGfUFFcacaacuccag susu	733 VPusAfscudGa (G2p) uuggaccGfufGfugu uussuc	1088 GAAAACACACTCCAACTCA GTT	+
AD-1183942	asacaca (Chd) GfUcFcFIAfacucagu susu	734 VPusAfscadAa (G2p) aguuggAfGfugu gususu	1089 AAMACACACTCCAACTCAGT TTG	+
AD-1183943	gsusccca (Ahd) CfucFAfGfuuuggccu gsusa	735 VPusAfscadcg (C2p) aaacugAfGfuggg acsgsu	1090 AGTCCAAACTCAGTTGCCT GTT	+
AD-1183944	csusucu (Uhd) CfGUfAfGfacaacggu asasa	736 VPusAfscudCc (G2p) uucuuuAfGfaga agsasa	1091 TTCTCTTCGTAAGAACGCTT AAT	+
AD-1183945	ususccuu (Chd) GfUAAAfGfacaacggu asusa	737 VPusAfscudAc (C2p) guuuuuAfGfaga asgsa	1092 TCTTCCTCGTAAGAACGGTA ATA	+
AD-1183946	uscsuuc (Ghd) UfAfGfAfacgguaa ususa	738 VPusAfscudTa (C2p) cgnucuUfAfGfaga asasg	1093 CCTCTTCGTAAGAACGGTAA TAA	+
AD-1183947	ususccu (Uhd) AfAfAfCfufucucuuc asasa	739 VPusAfscudAa (G2p) agaaaguUfAfagg aasbsg	1094 CCTTCCTTAACACTCTCTCTCA AG	-
AD-1183948	uscsacc (Uhd) AfAfUfUfcaaggccu ususa	740 VPusAfscadGc (C2p) unguauUfAfgggu gasasa	1095 TTTCACCTAAATTCAAGGCT TTA	-
AD-1183949	cusucug (Ghd) AfuUfAfafacacuu ususa	741 VPusAfscadGu (G2p) ugguuaAfufcfcg agsasa	1096 TTCTCTGGATTAAACACACTT TC	-

TABLE 3 -continued

Modified Sense and Antisense Strand Coronavirus dsRNA Sequences							Strand of the Viral RNA Targeted by the Agent
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:	
AD-1183950	csusucu (Chd) AfuUAFAfguacuu asasa	742	VPusUfsuadAa (G2p) uacuuAfuGfaga agsusg	1097	CACTTCCTAAAGTACTTTA TC	1452	-
AD-1183951	ascscuu (Uhd) CfuuUFCfuucacau csasa	743	VPusUfsqsdTu (G2p) ugaagaAfAfaga gususu	1098	AAACTCTTCTTCTCACAAATC AC	1453	-
AD-1183952	ususuu (Uhd) AfaAfAfCfuuacugg csasa	744	VPusUfsqsdCa (G2p) uaaguuUfuAfaau aascsc	1099	GTTATTAAAACTTACTGA CAA	1454	+
AD-1183953	ususucu (Ahd) CfAcAfAfAcucuu asasa	745	VPusUfsuudAa (G2p) aguuugUfuGuaga uascsu	1100	AGTATCTACACAAACTCTTA AAG	1455	-
AD-1183954	asutcuu (Ghd) UfuUfUfCfuugunic asasa	746	VPusUfsqsdAa (G2p) agggaaAfAcfaaga usgsa	1101	TCATCTGTGTTTCCTGTCA AC	1456	-
AD-1183955	csascuu (Uhd) UfaUfCfAfccucuu usasa	747	VPusUfsaadGa (G2p) aggugaUfuAfaag ugusua	1102	TACACTTTTATCACCTCTCTT AA	1457	-
AD-1183956	uscsuccu (Ghd) AfAfAfAfguaguug asasa	748	VPusUfsuadCa (G2p) uacuuUfuCfaga gascsu	1103	AGTCCTGTGAAAGTAGTGG AAA	1458	+
AD-1183957	uscsuga (Ahd) GfaAfGFUfuguggaa asasa	749	VPusUfsuudTc (G2p) acuacuUfuUfucag asqsa	1104	TCTCTGAAGAAGTAGTGGAA AAT	1459	+
AD-1183958	cisusgaa (Ghd) AfAfGUfAfguuggaaa asusa	750	VPusUfsuadTu (G2p) cacuacUfuCfuuca gsasg	1105	CTCTGAGAAGTAGTGGAAA ATC	1460	+
AD-1183959	asggugg (Ahd) AfAfAfUfCfuuaccuu ascsa	751	VPusUfsuadTg (G2p) uaggauUfuUfucc cusasc	1106	GTAGTGAAAATCCCTACCAT ACA	1461	+
AD-1183960	gesusgg (Ahd) AfAfUffCfuuaccuu csasa	752	VPusUfsquduu (G2p) guaggauUfuUfucc acsusa	1107	TAGTGGAAAATCCCTACCAT CAG	1462	+
AD-1183961	gssscuu (Uhd) CfuuAfAfccucuu asasa	753	VPusUfsuadAa (G2p) agguuuAfAfaga gcsusu	1108	AAGCTCTTCTAAACCTCAT AAA	1463	-
AD-1183962	asusgg (Uhd) CfAcCcAfucuggng ususa	754	VPusUfsacdAc (G2p) agaugugUfuAfacc aususg	1109	CAATGGTTACCCATCTGGTG TTT	1464	+
AD-1183963	csasugu (Ghd) GfuAfGUfugugguu uususa	755	VPusUfsaadAc (G2p) aacacuAfCfacc gsassa	1110	TTCATGTGGTAGTGTGGTT TA	1465	+
AD-1183964	csasguc (Ahd) UfaAfUfCfuuuguna asasa	756	VPusUfsuudAa (G2p) auagauUfuUfgac ugsusb	1111	CACAGTCATAATCTATGTTA AAA	1466	-

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1183965	ususuug (Ahd) UfguUffGfuuagacc asasa	757 VPusUfsuudGu (C2p) uaacaaAfcauu asggg	1112 CCTTTGATGTGTTAGACA ATG	1467	+
AD-1183966	asusggu (Ahd) AfugfcfUfuuagauc asaaa	758 VPusUfsugdAu (C2p) uaaaagcAfauFacc ausasa	1113 TTATGGTAATGCTTGTAGATC AAG	1468	+
AD-1183967	gscsuag (Ahd) UfucfcfCfuuaagagu gsasa	759 VPusUfscadCu (C2p) uuaggAAfauFcua gcscc	1114 GGGCTAGATTCCCTAAGAGT GAT	1469	+
AD-1183968	ascsaac (Ahd) UfcuFFAfacaacau sasa	760 VPusUfsaadTu (C2p) ugguuaAfauFguu gusgsu	1115 ACACACATCTAACACAT TAG	1470	-
AD-1183969	usasaga (Uhd) GfuUffGfuuacaca csasa	761 VPusUfsugdGu (C2p) uacacaAfcaFu usasc	1116 GTTAAGATGTTGTTACACA CAC	1471	+
AD-1183970	asgsaug (Uhd) UfgeffGFUfacacaca csusa	762 VPusUfsacdGu (C2p) ugquacacAfcau cususa	1117 TAAGATGTTGTTACACA CTG	1472	+
AD-1183971	gsgsugu (Ghd) UfAcAfFcfaacug usasa	763 VPusUfsacdCa (C2p) ugugugAfcaFa acsuu	1118 ATGTTGTTGACACACTGG TAC	1473	+
AD-1183972	csasggc (Ahd) CfUaFGFUfacugaug uscsa	764 VPusUfsacdAu (C2p) aguacauAfguFgcc ugusbg	1119 CACAGGCACTAGTACTGATG TCG	1474	+
AD-1183973	cscguc (Uhd) AfuUfcfUfaacuu asasa	765 VPusUfsuudAu (C2p) uuuuagaAfuaFgac ggussg	1120 CACCGTCTATCTAACTTA AAG	1475	-
AD-1183974	ususuua (Ahd) AfuAUfUFUfgggauca gsasa	766 VPusUfsuudGa (Tgn) ccccaaauAfuuuu asusa	1121 TATTTTAAATATTGGGATCA GAC	1476	+
AD-1183975	ususuua (Ahd) UfauUffGfggaucag ascsa	767 VPusUfsuclTg (Agn) ucccaaAfauuu asasu	1122 ATTTTAAATATTGGGATCA ACA	1477	+
AD-1183976	csasccu (Ahd) CfAfGfFuuggac csasa	768 VPusUfsggdTc (C2p) aaaaacuUfguFagg ugsggg	1123 CCCACCTACAAGTTGGAC CAC	1478	+
AD-1183977	asasuuca (Ghd) GfauUffUfaacuu csasa	769 VPusUfsugdAu (C2p) uuuuacaUfcaFu uusuuu	1124 ATAATCAGGATGTAACTTA CAT	1479	+
AD-1183978	asqsgau (Ghd) UfaAfAfFcfuuacaua gscsa	770 VPusUfsuudAu (C2p) uaagguuAfcaFu cusgsa	1125 TCAGGATGTTAACTTACATA GCT	1480	+
AD-1183979	ascsaau (Ghd) UfugfcfUfuuuu csusa	771 VPusUfsugdTu (C2p) aaaaagcAfcaFu gususa	1126 TAACAATGTTGCTTTCAA CTG	1481	+

TABLE 3 -continued

Modified Sense and Antisense Strand Coronavirus dsRNA Sequences							Strand of the Viral RNA Targeted by the Agent
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO: 5' to 3'	Antisense Strand Sequence	SEQ ID NO: 5' to 3'	mRNA Target Sequence	SEQ ID NO:	
AD-1183980	usgsuug (Chd) UfuUFUFCfaaacuguaasaaa	772	VPUstFsgadca (G2p) uuugaaAfAgfcaa casbu	1127	AATGTGCTTTCAAACTGTCAA	1482	+
AD-1183981	ususgcu (Uhd) UfuCfAfAfacugucaaaa	773	VPUstFsuudGa (C2p) aguuugAfAfagcaasaaa	1128	TGTTGCTTTTCAAAACGTGTCAAAC	1483	+
AD-1183982	gscsuuu (Uhd) CfAaAfFcugucaaa	774	VPUstFsgudTu (G2p) acaguuUfGafaaagcsaaa	1129	TTGCCTTTCAAAACTGTCAAACCCC	1484	+
AD-1183983	usasuga (Chd) UfuUffGfcfugugucuasaaa	775	VPUstFsuadGa (C2p) acagcaAfAgfucauasgsa	1130	TCTATGACTTTGCTGTGTCATAAG	1485	+
AD-1183984	gsusuuc (Uhd) UfuAfAfGfgaaggaa	776	VPUstFscudTC (C2p) uuuccuAfAffgaa	1131	GGTTTCTTAAGGAGGAA	1486	+
AD-1183985	ususucu (Uhd) UfaAfGffGfaaggaa	777	VPUstFscadTu (C2p) cuuuccuAfAfagaa	1132	GGTTCTTTAAGGAAGGAG	1487	+
AD-1183986	asggaa (Chd) GFaAfGFfufcugung	778	VPUstFscudDa (C2p) agaaacuUfcfuuccususa	1133	TAAGGAGGAGGTCTGTG	1488	+
AD-1183987	asascac (Uhd) UfcUfUffCfuuugguc	779	VPUstFsgudAg (C2p) aaagaAfAfagug	1134	AAAACACTCTCTTGTCAGG	1489	+
AD-1183988	ascsuuc (Uhd) UfcUfUfUfgeucagg	780	VPUstFscudCu (G2p) agccaaAfAfgaa	1135	ACACTCTCTCTTGTCAGG	1490	+
AD-1183989	asasugu (Chd) UfGafUfAfucagaca	781	VPUstFsuudGu (C2p) ugauauAfAcfacaa	1136	ACAATGTGTATACAGACA	1491	+
AD-1183990	cscsauu (Uhd) AfauAfAfauugggu	782	VPUstFsuadCC (C2p) cauuauUfAfauuu	1137	TTCCATTAAATAATGGGT	1492	+
AD-1183991	ccssaug (Ahd) GfuUfAfUfUfaggaucaasaaa	783	VPUstFsgudAu (C2p) cucauaAfAfufcau	1138	TTCAATGAGTTATGGGATC	1493	+
AD-1183992	usgscaa (Ahd) GfaAfUfAfagagcucg	784	VPUstFsgcdCa (G2p) cucuaufUfcUfuug	1139	AGTGCAGGAAATAGAGCTC	1494	+
AD-1183993	gscsaaa (Ghd) AfauAfAfagcucgc	785	VPUstFsgudCg (Agn) gcucaUfUfcuuu	1140	GTGCAAGGAATAGAGCTCGC	1495	+
AD-1183994	csasaaag (Ahd) AfuAfAfAfgeucgc	786	VPUstFsgudCc (G2p) agcucuAfUfcuuu	1141	TGCAAAGGAAATAGAGCTCGC	1496	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1183995	asasaga (Ahd) UfAGfAfGfcucgcac csgsa	787 VPusUfsggdTg (C2p) gagcucUfuFaucu ussgc	1142 GCAAAGAAATAGAGCTGGCA CGGT	1497	+
AD-1183996	usgsucu (Chd) UfauFcUFuguauc usasa	788 VPusUfsagdTa (C2p) uacagaUfAgfagac ascsc	1143 GGTGTCCTATCTGTAGTAC TAT	1498	+
AD-1183997	csuscu (Uhd) CfugFuAfguacuu gsasa	789 VPusUfscadTa (G2p) uacuacAfAgfauuga gsasc	1144 GTCTCTATCTGTAGTACTAT GAC	1499	+
AD-1183998	uscsacc (Uhd) UfaUFFGFguugggg ususa	790 VPusUfsaudCc (C2p) aacccaUfaAfggug asgsg	1145 CCTCACCTATGGTTGGGA TTA	1500	+
AD-1183999	csasccu (Uhd) AfuGffGfuugggau usasa	791 VPusUfsaadTc (C2p) caaacctAfuaFafagu gsasg	1146 CTCACCTTATGGTTGGGAT TAT	1501	+
AD-1184000	ascscuu (Ahd) UfggFFFUfugggau ususa	792 VPusUfsaudAu (C2p) ccaaccctAuFaagg usgsa	1147 TCACCTTATGGTTGGGATT ATC	1502	+
AD-1184001	cscuuua (Uhd) CfGGFUfUfugggaua uscsa	793 VPusUfsaudAa (Tgn) cccaaacctAfauag gsusg	1148 CACCTTATGGTTGGGATTA TCC	1503	+
AD-1184002	ascsuug (Uhd) UfcUfUFgfucgccaa ascsc	794 VPusUfsuudTg (C2p) gagccaaGfAfcaag usgsa	1149 TCACITGTTCTTGCTCGCAA ACA	1504	+
AD-1184003	csusegu (Uhd) CfuuUfGfcucgaaa csasa	795 VPusUfsqudTu (G2p) cgagccaAfAfaca agsug	1150 CACTGTTCTTGCTCGCAA CAT	1505	+
AD-1184004	csascaa (Chd) UfgcFuFuAuugcuua usasa	796 VPusUfsaudTa (G2p) cauaaggfAfguug usgscc	1151 GCCACACATGCTTATGCTAA TAG	1506	+
AD-1184005	usgsagu (Ghd) UfcUfUFuauagaaa usasa	797 VPusUfsaudTu (C2p) uaauagAfAcfauc ususa	1152 TATGAGTGTCTATAGAAA TAG	1507	+
AD-1184006	usgsagc (Uhd) GfAgfAfCfugaccuu ascsc	798 VPusUfsuadAg (G2p) ucaguguUfcafguc casasc	1153 GTTGGACTGAGACTGACCTT ACT	1508	+
AD-1184007	ususacc (Chd) AfGAfUFCfcauaga asasa	799 VPusUfsuadTu (G2p) auggauUfugfggua assg	1154 CCTTACCCAGATCCCATCAG AAT	1509	+
AD-1184008	gsasugg (Uhd) AfCAFfCfufuaugau gsasa	800 VPusUfscadAu (C2p) auaaaguUfAfccaa ucsubg	1155 CAGATGGTACACTTATGATT GAA	1510	+
AD-1184009	assasaca (Uhd) CfCuFFAfucaggaa usasa	801 VPusUfsacdTc (C2p) ugauuaGfAgfugu usasg	1156 CTAACACATCCCTAATCAGGAG TAT	1511	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184010	asascau (Chd) CfUAfAUfcaggagn asasa	802 VPusAf suadGu (G2p) cugauuAfGgfaug ususua	1157 TAAACATCTAATCAGGAT ATG	1512	+
AD-1184011	asggag (Uhd) AfuGfCfUfgaugucu ususa	803 VPusAf saadGa (G2p) aucagAf uAf cucc usgsa	1158 TCAGGGATATGCTGAATGTC TTC	1513	+
AD-1184012	cscsuga (Ghd) UfuUfUFafugaggcu asusa	804 VPusAf suadGc (G2p) ucauaAf aFcucag gsusu	1159 AACCTGAGTTTATGAGGT ATG	1514	+
AD-1184013	gscsagc (Ahd) Gf aAfAfCf gcucaa gscsa	805 VPusAf scudTu (G2p) agcguaUf ouf gcu gcsaaa	1160 TTGCAGCAGAAAACGCTCAA GCT	1515	+
AD-1184014	cscuugg (Uhd) Af cuUfGf guaagagn cscsa	806 VPusAf sgadGu (G2p) uuaccaAf uAf fcc ggsssg	1161 CACCTGGTACTGGTAGAGT CAT	1516	+
AD-1184015	usasuag (Ahd) UfaAfAfUfguaguag asasa	807 VPusAf sucdTa (G2p) uacauuUf auFcuaau asgsq	1162 CCTATAGATAAAATGTTAGTAG AAT	1517	+
AD-1184016	csusegu (Ghd) Af aAfUfUfguugaca cscsa	808 VPusAf sgudGu (G2p) aacaaUf uFcagc agsgsa	1163 TCCCTGCTGAAAATTGTTGACA CTG	1518	+
AD-1184017	gscsuga (Ahd) AfuUfGfUfgugacacu gsusa	809 VPusAf scadGu (G2p) ucaacaAf uFuca qcsasq	1164 CTGCTGAAATGTTGACACT GTG	1519	+
AD-1184018	usgsaaa (Uhd) Uf gUfUfGf acacu gsasa	810 VPusAf scadCa (G2p) ugucaaAf aFuuu casgsc	1165 GCTGAAATGTTGACACTGT GAG	1520	+
AD-1184019	asasauu (Ghd) Uf ugAfAfCf acuug genua	811 VPusAf scudCa (G2p) agugucAf aFcfaau uuscsa	1166 TGAATTTGTTGACACTGTGA GTG	1521	+
AD-1184020	usgsuug (Ahd) CfAcFUfGfugagug ususa	812 VPusAf sgddCa (G2p) ucacagUf gUf caac asasu	1167 ATTTGTTGACACTGTGA TTT	1522	+
AD-1184021	gscsaug (Ahd) Uf gUfUfUf caucug asasa	813 VPusAf sgadCa (G2p) augaaaCf auFc gcsgsu	1168 AGGGATGTTGTTCAATCTGC AAT	1523	+
AD-1184022	ususcac (Chd) UfuAfUfAf auucaca gsasa	814 VPusAf scudGu (G2p) aauuuAf aFgug aasabu	1169 ATTTCACCTTATAATTCCACA GAA	1524	+
AD-1184022	ususcac (Chd) UfuAfUfAf auucaca gsasa	814 VPusAf scudGu (G2p) aauuuAf aFgug aasabu	1169 ATTTCACCTTATAATTCCACA GAA	1524	+
AD-1184023	uscsacc (Uhd) Uf auAfAf auucaca asasa	815 VPusAf sgddTg (Tgn) gaauuuAf aFggu gasasa	1170 TTTCACCTTATAATTCCACAG AAT	1525	+

TABLE 3 -continued

Modified Sense and Antisense Strand Coronavirus dsRNA Sequences							Strand of the Viral RNA Targeted by the Agent
Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	SEQ ID NO:	
AD-1184024	asccuu (Ahd) UfaAfUfUfcacaga <u>a</u> usgsa	816 VPusAfssaudTc (Tgn) gugaaufaufaagg usgsa	816 VPusAfssaudTc (Tgn) gugaaufaufaagg usgsa	1171 TCACCTTATAATTCAACAGAA TGC	1526	+	
AD-1184025	cscsuua (Uhd) AfauUfCfacagaa <u>u</u> gscsa	817 VPusGfscadTu (C2p) ugugaaufaufaaua ggusgg	817 VPusGfscadTu (C2p) ugugaaufaufaaua ggusgg	1172 CACCTTATAATTCAACAGAA GCT	1527	+	
AD-1184025	cscsuua (Uhd) AfauUfCfacagaa <u>u</u> gscsa	817 VPusGfscadTu (C2p) ugugaaufaufaaua ggusgg	817 VPusGfscadTu (C2p) ugugaaufaufaaua ggusgg	1172 CACCTTATAATTCAACAGAA GCT	1527	+	
AD-1184026	usasuaa (Uhd) UfcAfCfAfgaau <u>gc</u> gsusa	818 VPusAfssaudCc (Agn) uucugufafauua usasbg	818 VPusAfssaudCc (Agn) uucugufafauua usasbg	1173 CTTATTAATTCAACAGATGCT GTA	1528	+	
AD-1184027	asascug (Uhd) UfgAfUfUfcacaca <u>a</u> gsgsa	819 VPusAfscudGu (G2p) augaaufcaAfca <u>g</u> ususgg	819 VPusAfscudGu (G2p) augaaufcaAfca <u>g</u> ususgg	1174 CAAACTGTGATTCACTACA GGG	1529	+	
AD-1184028	gsasaua (Uhd) GFACfUfAfugucaua <u>a</u> ususa	820 VPusAfssaudAu (G2p) acauaugufcafuau ucusgg	820 VPusAfssaudAu (G2p) acauaugufcafuau ucusgg	1175 CAGAAATGACTATGTCATA TTC	1530	+	
AD-1184029	csusug (Chd) AfuAfAfAggu <u>cu</u> asusa	821 VPusAfssaudGa (G2p) accuuufufgfa <u>ca</u> agsusu	821 VPusAfssaudGa (G2p) accuuufufgfa <u>ca</u> agsusu	1176 AACTTGTCATAAAGGTCTCT ATC	1531	-	
AD-1184030	cuscau (Chd) UfcUfAfugugg <u>gu</u> ususa	822 VPusAfssaudCc (C2p) aucauafafga <u>fu</u> ga gsus <u>c</u>	822 VPusAfssaudCc (C2p) aucauafafga <u>fu</u> ga gsus <u>c</u>	1177 GACTCATCTATGATGGGT TTT	1532	+	
AD-1184031	asgguc (Chd) UfaUfUfu <u>ca</u> aaa <u>a</u> asusa	823 VPusAfssaudTu (G2p) ugaaaaufafgfa <u>ca</u> cusgsa	823 VPusAfssaudTu (G2p) ugaaaaufafgfa <u>ca</u> cusgsa	1178 TCAGGTCCTATTTACAAA ATA	1533	-	
AD-1184032	usu <u>uac</u> (Ahd) AfacAfAfuuu <u>gu</u> csula	824 VPusAfssqudu (C2p) aaaauugufu <u>uf</u> gu <u>a</u> aascsc	824 VPusAfssqudu (C2p) aaaauugufu <u>uf</u> gu <u>a</u> aascsc	1179 GGTTTACAAA <u>CAATTGATA</u> CTT	1534	+	
AD-1184033	asusua (Chd) UfcAfAf <u>cg</u> ugu <u>ca</u> asusa	825 VPusAfssaudGa (C2p) acaguufafguau aususu	825 VPusAfssaudGa (C2p) acaguufafguau aususu	1180 AAATATACCTCAACTGTGTC ATA	1535	+	
AD-1184034	usasguu (Chd) UfuUf <u>cf</u> fuuu <u>gu</u> <u>ac</u> ususa	826 VPusAfssqudu (C2p) aaaagaafafgu <u>ac</u> ascsu	826 VPusAfssqudu (C2p) aaaagaafafgu <u>ac</u> ascsu	1181 AGTAGTACTTCTTTGA <u>ACT</u> TC	1536	+	
AD-1184035	ussg <u>guu</u> (Ahd) Cf <u>Ac</u> FuAfau <u>gu</u> <u>aa</u> asasa	827 VPusUfssaudTa (C2p) uauuagufgu <u>uac</u> cascsa	827 VPusUfssaudTa (C2p) uauuagufgu <u>uac</u> cascsa	1182 TGTGGTAACACTAATAGTAA AAT	1537	-	
AD-1184036	csasaua (Chd) Cf <u>au</u> FuAf <u>fa</u> acc <u>uu</u> sasa	828 VPusUfssaudTa (C2p) gguuuauufggfuau ugsgsa	828 VPusUfssaudTa (C2p) gguuuauufggfuau ugsgsa	1183 TCCAATACCATAA <u>ACCTAT</u> AAG	1538	-	
AD-1184037	asasug <u>u</u> (Uhd) Cf <u>uc</u> FuAf <u>fu</u> gag <u>aa</u> csasa	829 VPusUfssggdTu (C2p) ucau <u>uag</u> A <u>fg</u> A <u>fa</u> uuscsu	829 VPusUfssggdTu (C2p) ucau <u>uag</u> A <u>fg</u> A <u>fa</u> uuscsu	1184 AGAATGTTCTCTATGAGAAC CAA	1539	+	

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184038	ususcug (Chd) UfauFFCfuuggcgg usasa	830 VPusUfsagdCa (G2p) caagauFufgfcaga asgsc	1185 GCTTCGTATACTTGCTGCT	1540	+
AD-1184039	csusgcu (Ahd) AfuCFUFUfcugcuu csusa	831 VPusAfsgudAg (C2p) agcaagAfufuAgc agsasa	1186 TTCTGCTATACTTGCTGCTAC TA	1541	+
AD-1184040	asuscau (Ahd) CfauFCFaFccagau ususa	832 VPusAfscadAu (C2p) ugugauFufguau gausuc	1187 GAATCATACATCACAGATG TTG	1542	+
AD-1184041	gsuscaa (Ahd) UfuAfcffAfuuacaca usasa	833 VPusUfsaudGu (G2p) uaauguAfauFuug acusuc	1188 GAGTCAAATTACATACACA TAA	1543	+
AD-1184042	ascsgac (Chd) AfrcuFFCfuqcguy cscsa	834 VPusUfsqcdAc (G2p) cuquauFufcfcguc guscsq	1189 CGACCGAGACTACTAGCGTGT CCT	1544	+
AD-1184043	csgsacg (Ahd) CfuaAfcfufuAgcggc cscsa	835 VPusAfsggdCa (C2p) gcuuaguAfufcgu cgsusuc	1190 GACGAGCAGACTACTAGCGTGC CTT	1545	+
AD-1184044	ascsgac (Und) AfrcuFFAfcfcqgcuu ususa	836 VPusAfssadAg (C2p) acqcuauFufgfcguc guscsq	1191 CGACGAGACTACTAGCGTGCCT TTG	1546	+
AD-1184045	csgsacu (Ahd) CfuaAfcfufuAgcggc usgsa	837 VPusCfssadAg (G2p) cacgcuAfufguagu cgsusuc	1192 GACGAGACTACTAGCGTGCCT TGT	1547	+
AD-1184046	gsasguu (Chd) GFaaFFCfuuaguac uscsa	838 VPusUfsagdTa (C2p) auaaquFufcguacu usasuu	1193 ATGAGTAGCAGAACTTATGTAC TCA	1548	+
AD-1184047	usascga (Ahd) CfuuFFUfuuacuca ususa	839 VPusAfssadGa (G2p) uacauauFufguug uascsa	1194 AGTACCAACTTATGTACTA TTC	1549	+
AD-1184048	usascuc (Ahd) UfucFFUfuuucggaa gsasa	840 VPusUfscludTc (C2p) gaaaacAfauFgagu ascscs	1195 TGTACTCATTCGTTGGAA GAG	1550	+
AD-1184049	usseguu (Ahd) AfuAfcfufuacuuc ususa	841 VPusAfssagDa (G2p) uacguauFufuAAC ususu	1196 ATAGTTTATAGCGTACTTC TTT	1551	+
AD-1184050	ususcuu (Ghd) CfuuFFUfcfgugguau uscsa	842 VPusUfsagdTa (C2p) cacgaaAfufcfaaga asasaa	1197 TTTCTTGCTTTCTGCTGTATT CT	1552	+
AD-1184051	ususcgua (Ghd) GFuAUFUfcuugcuu genusa	843 VPusAfscudAg (C2p) aagaaauAfufcfaaga asasgg	1198 CTTTCGTGTTTCTGCTGTATT TT	1553	+
AD-1184052	usasgcc (Ahd) UfcccFUfuuacugcgc ususa	844 VPusUfsaggCg (C2p) aquaaggAfauFggc usasgu	1199 ACTAGGCCATCCCTTACTGCGC TTC	1554	+

TABLE 3 -continued

Modified Sense and Antisense Strand Coronavirus dsRNA Sequences							Strand of the Viral RNA Targeted by the Agent
Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent	
AD-1184053	asggccca (Uhd) Cf <u>cu</u> U <u>f</u> Afcugcgcu uscsa	845 VPusGfsaadGc (G2p) caguuaAf <u>g</u> Afugg cusabg	845 VPusGfsaadGc (G2p) caguuaAf <u>g</u> Afugg cusabg	1200 CTAGCCATCCTTACTGGCT TCG	1555	+	
AD-1184054	gscscau (Chd) Cf <u>uu</u> F <u>c</u> fugcgcu csgsa	846 VPusGfsag <u>d</u> g (C2p) gcaguuaAf <u>g</u> Gf <a>ug</a> gcsusa	846 VPusGfsag <u>d</u> g (C2p) gcaguuaAf <u>g</u> Gf <a>ug</a> gcsusa	1201 TAGCCATCCTTACTGGCTT CGA	1556	+	
AD-1184055	cscsauc (Chd) U <u>f</u> uAf <u>C</u> fugcgcuu c gsasa	847 VPusGfscdAa (G2p) cgagu <u>A</u> fa <u>g</u> fgau 9gsbu	847 VPusGfscdAa (G2p) cgagu <u>A</u> fa <u>g</u> fgau 9gsbu	1202 AGCCATCCTTACTGGCTC GAT	1557	+	
AD-1184056	ascsguc (Ghd) Cf <u>u</u> U <u>f</u> cf <u>g</u> fa <u>u</u> ugugu gscsa	848 VPusGfscadCa (C2p) aaucga <u>A</u> fg <u>fg</u> cag usasa	848 VPusGfscadCa (C2p) aaucga <u>A</u> fg <u>fg</u> cag usasa	1203 TTACTGCCTC <u>G</u> A <u>T</u> GTGT GCG	1558	+	
AD-1184057	usgsccg (Uhd) U <u>f</u> cG <u>f</u> A <u>f</u> u <u>u</u> ugugc gssua	849 VPusAfscdCa (C2p) aca <u>a</u> u <u>G</u> fa <u>A</u> fg <u>gc</u> c asgsu	849 VPusAfscdCa (C2p) aca <u>a</u> u <u>G</u> fa <u>A</u> fg <u>gc</u> c asgsu	1204 ACTGCGCTTC <u>G</u> A <u>T</u> GTGT GCA	1559	+	
AD-1184058	csgscuu (Chd) GF <u>a</u> U <u>f</u> U <u>f</u> fgugugc gscsa	850 VPusGfsuadCg (C2p) acaca <u>A</u> uC <u>g</u> fa <u>g</u> ac gscsa	850 VPusGfsuadCg (C2p) acaca <u>A</u> uC <u>g</u> fa <u>g</u> ac gscsa	1205 TGCGTTTC <u>G</u> A <u>T</u> GTGT GCT ACT	1560	+	
AD-1184059	gscsuuc (Ghd) Af <u>u</u> U <u>f</u> U <u>f</u> fgugcgua csusa	851 VPusAfs <u>g</u> uadAc (G2p) cacaca <u>A</u> uC <u>g</u> fa <u>g</u> aa gcspsc	851 VPusAfs <u>g</u> uadAc (G2p) cacaca <u>A</u> uC <u>g</u> fa <u>g</u> aa gcspsc	1206 GCGCTT <u>G</u> A <u>T</u> GTGT GCTA CTG	1561	+	
AD-1184060	gsusucc (Uhd) GF <u>a</u> U <u>f</u> U <u>f</u> fguggguc usasa	852 VPusGfsaggAc (C2p) agaa <u>a</u> u <u>C</u> fa <u>f</u> gga acusbc	852 VPusGfsaggAc (C2p) agaa <u>a</u> u <u>C</u> fa <u>f</u> gga acusbc	1207 GAGTTC <u>C</u> T <u>G</u> A <u>T</u> CTGGCT AA	1562	+	
AD-1184061	ususccu (Ghd) Af <u>u</u> U <u>f</u> U <u>f</u> fgugguu asasa	853 VPusGfsuadG <u>a</u> (C2p) caga <u>a</u> u <u>C</u> u <u>f</u> cgagg aascu	853 VPusGfsuadG <u>a</u> (C2p) caga <u>a</u> u <u>C</u> u <u>f</u> cgagg aascu	1208 AGTTCC <u>T</u> G <u>A</u> CTTC <u>T</u> GGCTAA AA	1563	+	
AD-1184062	cscsuga (Uhd) Cf <u>u</u> U <u>f</u> U <u>f</u> fgggcuua ascua	854 VPusGfsuudTa (G2p) acc <u>g</u> aa <u>A</u> fg <u>fu</u> ca ggssua	854 VPusGfsuudTa (G2p) acc <u>g</u> aa <u>A</u> fg <u>fu</u> ca ggssua	1209 TTCC <u>T</u> G <u>A</u> TC <u>T</u> CTGGCTAAA CG	1564	+	
AD-1184063	uscsuuc (Uhd) GF <u>g</u> u <u>f</u> U <u>f</u> faaacgaa cnsua	855 VPusAfs <u>g</u> uadTc (G2p) uu <u>u</u> u <u>u</u> u <u>A</u> fa <u>g</u> aa gasusc	855 VPusAfs <u>g</u> uadTc (G2p) uu <u>u</u> u <u>u</u> u <u>A</u> fa <u>g</u> aa gasusc	1210 GATCTTC <u>T</u> GGCTAA <u>A</u> CGAA CTA	1565	+	
AD-1184064	cnsuucu (Ghd) GF <u>u</u> U <u>f</u> U <u>f</u> faaacgaa usasa	856 VPusGfs <u>g</u> uadTu (C2p) guuu <u>u</u> u <u>u</u> u <u>A</u> fc <u>u</u> fa <u>g</u> aa agsasu	856 VPusGfs <u>g</u> uadTu (C2p) guuu <u>u</u> u <u>u</u> u <u>A</u> fc <u>u</u> fa <u>g</u> aa agsasu	1211 ATCTTC <u>T</u> GGCTAA <u>A</u> CGAAC TAA	1566	+	
AD-1184065	gsgaaac (Chd) U <u>f</u> af <u>U</u> U <u>f</u> faauagguu uscsa	857 VPusGfsaadGc (C2p) uauu <u>u</u> u <u>u</u> u <u>A</u> fg <u>gu</u> u ccsa	857 VPusGfsaadGc (C2p) uauu <u>u</u> u <u>u</u> u <u>A</u> fg <u>gu</u> u ccsa	1212 ATGGAA <u>AC</u> CTAGTA <u>A</u> TAGTT TCC	1567	+	
AD-1184066	usgsca (Chd) Af <u>u</u> U <u>f</u> U <u>f</u> fgaa <u>ac</u> gcu ususa	858 VPusAfsaadGc (G2p) uu <u>u</u> u <u>u</u> u <u>A</u> fg <u>fu</u> g <u>u</u> casabc	858 VPusAfsaadGc (G2p) uu <u>u</u> u <u>u</u> u <u>A</u> fg <u>fu</u> g <u>u</u> casabc	1213 GTTG <u>C</u> T <u>A</u> CA <u>T</u> AC <u>G</u> AA <u>C</u> GCT TTC	1568	+	
AD-1184067	gscsuac (Ahd) U <u>f</u> ca <u>f</u> U <u>f</u> fgfa <u>ac</u> gcu uscsa	859 VPusGfs <u>g</u> uadDg (C2p) guuc <u>u</u> u <u>u</u> u <u>A</u> fg <u>gu</u> u gcsasa	859 VPusGfs <u>g</u> uadDg (C2p) guuc <u>u</u> u <u>u</u> u <u>A</u> fg <u>gu</u> u gcsasa	1214 TTGCT <u>A</u> CA <u>T</u> AC <u>G</u> AA <u>C</u> GCTT TCT	1569	+	

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184068	csusaca (Uhd) CfAcGfAfacgcuu csusa	860 VPUsAfsgadAa (G2p) cguucgfuAfugu agsca	1215 TGCTACATCACGAACGCTT CTT	1570	+
AD-1184069	ascsgcu (Uhd) UfcUfUffAfuuacaa ususa	861 VPUsAfsgdTu (G2p) uauuaGfAfagc gususc	1216 GAACGCTTTCTTATTACAAA TTG	1571	+
AD-1184070	usgsuac (Ahd) GFuAfffGfugacaac asgaa	862 VPUsUfsugdTu (G2p) ucacuuAfcuFguu casasg	1217 CTTGTAACGTAAGTGAAC AGA	1572	+
AD-1184071	asasgug (Ahd) CfAfffAfgauguu csasa	863 VPUsUfsugdAa (G2p) aucugufguFcac ususac	1218 GAAAGTGCACACAGATGTT CAT	1573	+
AD-1184072	csutacu (Chd) UfaAfUfAfuccau usasa	864 VPUsUfsaadAu (G2p) quauauUfAgagu agsgsa	1219 TCCTACTCTATAAACATT AG	1574	-
AD-1184073	cscscca (Ahd) GfguUfUFuaccuu sasa	865 VPUsUfsugdTu (G2p) gguaaaacfoufugg ggscsc	1220 GGCCCCAAGGTTTACCCAAAT AAT	1575	+
AD-1184074	usasccc (Ahd) AfuAfffAfucugcgu c-susa	866 VPUsAfsgadCq (G2p) aguuauAfUfFggg usasaa	1221 TTACCCATAATACTGGCT CTT	1576	+
AD-1184075	gsasuga (Chd) CfAfffAfugguac usasa	867 VPUsUfsagdTa (G2p) ccaauuUfGfucu ucsusg	1222 CAGATGACCAAATTGGCTAC TAC	1577	+
AD-1184076	gscsuac (Uhd) AfccGfAfagaguca cscsa	868 VPUsUfsqudAg (G2p) ucuucgfuAfugu gcsca	1223 TGGCTACTACCGAAGGCTA CCA	1578	+
AD-1184077	uscegug (Chd) UfAcfafAfucucc asasa	869 VPUsUfsugdAg (G2p) aaggugUfAgfcac gasusu	1224 AATCGTGCTACACTTCCTCA AAG	1579	+
AD-1184078	csgsugc (Uhd) AfcaAfAfciuccu asgaa	870 VPUsUfsuudGa (G2p) gaaguuUfAfgcac cgssuu	1225 ATCGTGCTACACTTCCTCA AGG	1580	+
AD-1184079	usgcuac (Chd) AfAcUfUfuccuaag gsasa	871 VPUsUfscsdTu (G2p) aggaaagUfUfugu cascsg	1226 CGTGTACAACTTCCTCAAG GAA	1581	+
AD-1184080	usascaa (Chd) UfUcUfUfcaaggaaac sasa	872 VPUsUfsqudTc (G2p) uugaggAfAgfugu uasgsc	1227 GCTACAACTTCCTCAAGGAA CAA	1582	+
AD-1184081	ascsaac (Uhd) UfcCfUfCfaaggaaa sasa	873 VPUsUfsugdTu (G2p) cuugaggAfAfugu gusasg	1228 CTACAACCTCCCTCAAGGAA AAC	1583	+
AD-1184082	ascsuuc (Chd) UfcAfffGfgaacaaca susa	874 VPUsAfsgdTu (G2p) uuccuuUfAfGfaga gususb	1229 CAACTTCCTCAAGGAAAC ATT	1584	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184083	uscsuc (Ahd) AfgffAfccacauu gscsa	875 VPusUfscadAu (G2p) uuguucUfuUfagg gaaagg	1230 CTTCCCTCAAGAACACATTC GCC	1585	+
AD-1184084	csasagg (Ahd) AfcaAfCfaauugccaa asaaa	876 VPusUfsuudCg (G2p) aauguuUfuUfcuu ugsaag	1231 CTCAGGAACACATTGCCA AAA	1586	+
AD-1184085	asasgg (Ahd) CfAfAfFafuuugccaa asaaa	877 VPusUfsuudTg (G2p) caauguUfuUfucc uusgsa	1232 TCAAGGAACACATTC AAG	1587	+
AD-1184086	ascsaau (Ghd) CfCAFAfAfaggcunc usaaa	878 VPusUfsagdAa (G2p) cccuuuUfGcfau guusbg	1233 CAACATGGCAAAGGCTTC TAC	1588	+
AD-1184087	gsascag (Ahd) UfuGfAfAfccagguu gsasa	879 VPusUfscadAg (G2p) ugguuAfaufcug ucsaaa	1234 TTGACAGATGAAACCAAGCTT GAG	1589	+
AD-1184088	csasaac (Uhd) GFUfAfFcfaaagaaau scsaa	880 VPusUfsaudTu (G2p) uuaguUfcafguu ugsgsc	1235 GCCAAACTGTCACTAAAGAA TCT	1590	+
AD-1184089	gsusecca (Ghd) AfAcAfAfacccaa gsasa	881 VPusUfscdTu (G2p) ggguuugUfuUfugg acsaaa	1236 TGGTCAGAACAAACCCAG GAA	1591	+
AD-1184090	gsgsccg (Chd) AfAfUfUfUfgcacaau ususa	882 VPusUfsaadTu (G2p) ugcaauUfuUfgcgg ccsaaa	1237 TTGGCGCAAATTGCACAAAT TTG	1592	+
AD-1184091	gscsaug (Ghd) AfAgfUfUfaccuuu cgsaa	883 VPusUfsagdAg (G2p) ugugactUfuUfcuu gcscsa	1238 TGGCATGGAAAGTCACACTT CGG	1593	+
AD-1184092	usasuag (Uhd) CfUaUfCfUfuUgugc asgaa	884 VPusUfsugdCa (G2p) aagaguAfgafcua ususua	1239 TATATAGTCTACTCTTGTC AGA	1594	+
AD-1184093	usasegc (Uhd) AfCuUfUfugugcag asasa	885 VPusUfsuudTg (G2p) acaagaAfUfagcu asusa	1240 TATAGTCTACTCTTGTCAG AAT	1595	+
AD-1184094	agsgsucu (Ahd) CfUcUfUfugugcaga asusa	886 VPusUfsuudCu (G2p) cacaaggAfUfaga cususa	1241 ATAGTCTACTCTTGTCAGA ATG	1596	+
AD-1184095	uscsuac (Uhd) CfUfUfUfugcagaau gsasa	887 VPusUfscadTu (G2p) ugcaacaAfUfagua gascsu	1242 AGTCTACTCTTGTCAGAAT GAA	1597	+
AD-1184096	cnsuccu (Ghd) UfGCFAfGfaauugaa uscsa	888 VPusUfsaadTu (G2p) auucugCfAcfaaga gsusa	1243 TACTCTTGTCAGAATGAAT TCT	1598	+
AD-1184097	usasguu (Ahd) AfCuUfUfaaucucca csasa	889 VPusUfsugdGa (G2p) auuuaaGfuUfaac uascsa	1244 TGTAGTTAACTTTAACTCTCA CAT	1599	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent	
					Strand of the Viral RNA	Targeted by the Agent
AD-1184098	usasacu (Uhd) UfaAfUfcuacaua gscsa	890 VPusGfscudAu (G2p) ugagauUfaAfagu usasc	1245 GTTAACTTATCTCACATA GCA	1600	+ +	
AD-1184099	ususuaa (Uhd) CfUcFcAfCuauagcaa uscsa	891 VPusGfsaudTg (C2p) uaugugAfAfauua aasgu	1246 ACTTTAAATCTCACATAGCAA TCT	1601	+ +	
AD-1184100	ususaa (Chd) UfcAfcFafuagcaau ccsusa	892 VPusAfsgadTu (G2p) cuauugAfAfagu aasag	1247 CTTAAATCTCACATAGCAAAT CTT	1602	+ +	
AD-1184101	gsgsgag (Ghd) AfCUfUffGfaaagagc csasa	893 VPusUfsggdCu (C2p) uuuccaAfUcfucuccusa	1248 TAGGGAGGACTTGAAAGAG CCAC	1603	+ +	
AD-1184102	gsusaga (Uhd) CfUgFUfUfcucaaa csgsa	894 VPusUfsguuufaggaaacAfAfucuacs a	1249 TTGTAGATCTGTTCTCTAA CGA	1604	+ +	
AD-1184103	asgsauc (Uhd) GfuUfUfUfcuuaaacg asasa	895 VPusUfsgucgfuuauagaaAfcaAfgaucusas c	1250 GTAGATCTGTTCTCTAAACG AAC	1605	+ +	
AD-1184104	ususucu (Uhd) AfAfCfGfaacuua asasa	896 VPusUfssuuuAfagqucquUfaAfjagaaacs a	1251 TGTTCTCTAAACGAACCTTA AAA	1606	+ +	
AD-1184105	uscsucu (Ahd) AfAcAfGFAfacuuua asasa	897 VPusUfssuuuAfagaauucgUfuUfagagasas c	1252 GTTCCTCTAAACGAACCTTAA AAT	1607	+ +	
AD-1184106	cisusaaa (Chd) GFaAfCcFuuuuuuauccusus	898 VPusAfsgauUfuuuuuuauqUfcfuuuags g	1253 CTCTAAACGAACCTTAAAT CTG	1608	+ +	
AD-1184107	usaaac (Ghd) AfAcFuFuuaaaaucc usgsa	899 VPusCfsgauUfuuuuuuagUfUfcguuusas a	1254 TCTAAACGAACCTTAAATC TGT	1609	+ +	
AD-1184108	asasacg (Ahd) AfCUfUfUfaaaaucc gsusa	900 VPusAfscagAfuuuuuuuagUfUfcguuusas g	1255 CTAACCGAACCTTAAATCT GTG	1610	+ +	
AD-1184109	ascgaa (Chd) UfuUfAfAfauucugu gensa	901 VPusAfscacAfgaauuuuafAfjucguus u	1256 AACGGAACTTTAAATCTGT GTG	1611	+ +	
AD-1184110	gscsugc (Uhd) UfaCfGfGuuuucguc csgsa	902 VPusCfsgggacfgaaaaaccgUfaAfjcgccscs u	1257 AGGCTGCTTACGGTTTCGTC CGT	1612	+ +	
AD-1184111	usgsuu (Ahd) CfGfFUfUfugucgg usgsa	903 VPusCfscacGfagaaaccfGUfaagcgscc	1258 GCTGCTTACGGTTTCGTC CGT	1613	+ +	
AD-1184112	gscsuua (Chd) GFgGUfUfUfegucguu gsusa	904 VPusAfscacGfagaaaccfGUfaagcgsas g	1259 CTGCTTACGGTTTCGTC CGT	1614	+ +	

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184113	cusuac (Ghd) GfuUfUfcguccug ususa	905 a VPusufsacacfgggacaaafcfcguagscs	1260 TG TGCTTACGGTTTCGTCCGGTGT	1615	+
AD-1184114	ususacg (Ghd) UFUUFUfcguccug usgsa	906 c VPusufsacacfccggacgaaafcfcguags	1261 GC GCTTACGGTTTCGTCCGGTGT	1616	+
AD-1184115	usgsuga (Chd) CfgaAfAfAgguuaaga usgsa	907 c VPusufsauUfuacuuucfgGfucacascsc	1262 ATGG GGTGTGACCGAAAGGTAAG	1617	+
AD-1184116	gsasccg (Ahd) AfagfGUfaagaugg asgsa	908 c VPusufsucuafucuuaccufuUfcggucusas	1263 GAGA GTGACCGAAAGGTAAGATG	1618	+
AD-1184117	asasaac (Ahd) CfacGfGUfUcaacuca sgsa	909 c VPusufsaaacfuggaguugGfacfugugusus	1264 AGTA AGAAAACACACGTCACACTC	1619	+
AD-1184118	csascac (Ghd) UFCCAfAfucacagu usgsa	910 u VPusufsaaacfuggaguugGfacfugugusus	1265 TGC AACACACGTCACACTCAGTT	1620	+
AD-1184119	asacac (Uhd) CfCAFAfFcfcuaguu gscsa	911 u VPusufscaaAffcuaguuGfAfegugusgs	1266 GCC ACACACGTCACACTCAGTT	1621	+
AD-1184120	csascgu (Chd) CfAfcffUfcaguug cscsa	912 g VPusufssgcaAfacuugaguUfgfegacguusus	1267 CCT CACACGTCACACTCAGTTG	1622	+
AD-1184121	ascgcuc (Chd) AfacffUfcaguug cnsua	913 u VPusufsggcAfaaeguagUfuUfgfegacguus	1268 CTG ACACGTCACACTCAGTTG	1623	+
AD-1184122	csgsuucc (Ahd) AfcuUffAfguuugcc usgsa	914 g VPusufsaggcfaaaacuugaGfuUfgfegacguus	1269 TGT CACACGTCACACTCAGTTGCC	1624	+
AD-1184123	gsusucu (Uhd) CfuuUfcGuuagaacc gsgsa	915 u VPusufsccguUfuacuacgAfgafaagaacs	1270 GGT AGGTCTTCTTCGTAAGAAC	1625	+
AD-1184124	ususcuu (Chd) UfufcGUfaagaaccy gsusa	916 c VPusufsccguUfuacuacgAfgafaagaacs	1271 GTA GGTTCTTCTTCGTAAGAACG	1626	+
AD-1184125	ususcuu (Uhd) UfUcGUfaagaaccy ususa	917 c VPusufsccguUfuacuacGfafaagausas	1272 TAA GTTCCTTCTTCGTCCTCT	1627	+
AD-1184126	asuscuu (Chd) UfUcGUfUfcuucuc ususa	918 g VPusufsagaAfsgaaggAfafaagausas	1273 TC CAATCTTCTTCGTCCTCT	1628	-
AD-1184127	gsguuua (Uhd) UfUAAfAfacuuacu gsasa	919 c VPusufsagufaaguuuuAfafaaccas	1274 GAC GTGGTTATTTAAACTTACT	1629	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent	
					Strand of the Viral RNA Targeted by the Agent	Strand of the Viral RNA Targeted by the Agent
AD-1184128	uscsuac (Ahd) CfAAfFcfcuuuaaa gsaaa	920 VPusUfsccuUfaaggauUfugfuguagus a	TATCTACACAAACTCTTAA GAA	1630	-	-
AD-1184129	asasgaa (Ghd) UfaGfUffGfgaaaauc csusa	921 VPusUfsggauUuuuccacUfciuuuucs a	TGAAGAGTAGTGGAAAAAT CCTA	1631	+	
AD-1184130	ascsaau (Uhd) GFUGFUfAfccuuuuc usaaa	922 VPusUfsaguafaaaguacAfcafuuagus g	CTACAAATTGTTGACTTTTACT AG	1632	+	
AD-1184131	ascscacu (Chd) UfuAFAfFcfcaguauuc ususa	923 VPusUfsagaAfuaucuguuAfafGfagugus g	CGACACTCTAACAGTATTC TTT	1633	-	
AD-1184132	asutsgua (Chd) AfAcFUfAfutguuua usgsa	924 VPusUfsauuAfaccuuuagufuGuacauus c	GAATGTACAACATTTGTTAA TGG	1634	+	
AD-1184133	usgsuac (Ahd) AfFcUfAfUFuguuau gsgsa	925 VPusUfsccauUfaacaaauaGfuUfuguacaus u	AATGTACAACATTTGTTAA GGT	1635	+	
AD-1184134	cscsagg (Ahd) GFUUfUFUfcuguguu gsusa	926 VPusUfscccfacagaaaAfCUfccuggus a	TACCAAGGTTTCTGTGTT GTA	1636	+	
AD-1184135	uscsaug (Uhd) GfGufAfFfuguugg uuussa	927 VPusUfsaacFaacacuacFcAfcaugasasc	GTTCATGTTAGTGTGTT TTT	1637	+	
AD-1184136	cscscug (Uhd) AfCAFfGUfcuuuaau gsusa	928 VPusUfsccauUuuuagacuGuAfcaugsgs c	GCCACTGTACAGTCTAAAT GTC	1638	+	
AD-1184137	ascscug (Ahd) CfAgFUfFcfcuuuau uscsa	929 VPusUfsacaUfuuuagacUfGuAfcaugsgs g	CCACTGTACAGTCTAAATG TCA	1639	+	
AD-1184138	ususuga (Ahd) UfGUfFGfGfcuuuau usgsa	930 VPusUfsccauUuuuagccacFuUfucaaaags a	TCTTTGAATGTGGCTAAATC TGA	1640	+	
AD-1184139	ascaaac (Chd) UfaAAfFUfAgaggua usgsa	931 VPusUfsccauUfaccucuuUfuUfegguusgs u	AMACAACTTAAATAGGGT ATGG	1641	+	
AD-1184140	asasccu (Ahd) AfauUfAfGfagguaung gsusa	932 VPusUfsccauUfaccucuuUfuUfegguusgs c	ACAACCTTAAATAGGGTATG GTA	1642	+	
AD-1184141	uscsauc (Chd) AfAAfUfFcfcuaagg asusa	933 VPusUfsccgadfcgguaAfAfcccgug u	GATCATCCAAATCCTAAAGG ATT	1643	+	
AD-1184142	csasccag (Uhd) CfUGfUfAfcccgug csgsa	934 VPusUfsccgadfcgguaAfAfcccgug u	AACACAGTCTGTACCGTCGT CGG	1644	+	

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184143	asgggg (Ahd) UfugfUffguagua <u>gsa</u>	934 VPus <u>UfscuUfacaccgchAfcocguus</u> <u>u</u>	1289 AAACGGGTTCGGGTTAAC <u>TGC</u>	1645	+
AD-1184144	asggca (Chd) UfagfUafcgugau <u>gsa</u>	935 VPus <u>CfsgacAfucaguacUafgugccus</u> <u>u</u>	1290 ACAGGCCACTAGTACTGATGT <u>CGT</u>	1646	+
AD-1184145	ususcuu (Ahd) CfuuUffguuu <u>gsa</u>	936 VPus <u>UfscuuAfacucaaAfgufagaas</u> <u>c</u>	1291 GATTCTTACTTGTAGTTAA <u>GAG</u>	1647	+
AD-1184146	csuscua (Ahd) CfUaffCfaacaug <u>gsa</u>	937 VPus <u>CfuuAfuguguAfgufuagags</u> <u>sa</u>	1292 TTCTCTAACTACCAAAGATA <u>AGA</u>	1648	+
AD-1184147	ususug (Ahd) UfgAfuffGfauuu <u>ucsaa</u>	938 VPus <u>UfsgaaAfuuaucaUfcacaacs</u> <u>sa</u>	1293 TGGTGTGATGATGATTTC <u>AA</u>	1649	+
AD-1184148	usgsuga (Ahd) GFauffGfauuu <u>asaa</u>	939 VPus <u>UfsugaAfauuucaUfcufucas</u> <u>c</u>	1294 GTTGTGATGATGATTTC <u>AAT</u>	1650	+
AD-1184149	asuscag (Chd) AfugfUfafacuu <u>asaa</u>	940 VPus <u>AfsugAfayuuuacAfucfuganus</u> <u>a</u>	1295 TAATCAGGATTAACTTAC <u>ATA</u>	1651	+
AD-1184150	usasaca (Ahd) UfguUffGfcuuuu <u>asaa</u>	9 VPus <u>UfuuuAfaaaggcaacAfufuguuas</u> <u>u</u>	10 ACTAACATGTTGCTTTCA <u>AAC</u>	1652	+
AD-1184151	usuucc (Ahd) AfacffGfuu <u>cgss</u>	941 VPus <u>CfsgggUfuugacagUfuUfgaaa</u> <u>cg</u>	1296 GCTTTCAAACTGTCAACCC <u>CGG</u>	1653	+
AD-1184152	ascsuqu (Chd) Afafcfccfgguuu <u>usua</u>	942 VPus <u>AfsaaufaccggguluFuGfucag</u> <u>us</u>	1297 AAACGTCAAAACCCGGTAA <u>TTT</u>	1654	+
AD-1184153	csusuua (Ahd) GFgAfAfGfaga <u>gsa</u>	943 VPus <u>CfsgaaAfucuuuucfUfutaaags</u> <u>a</u>	1298 TTCTTTAAGGAAGGAGTC <u>TGT</u>	1655	+
AD-1184154	ususuaa (Ghd) GfafaGffGfaagu <u>gsa</u>	944 VPus <u>AfscaGfacaucuUfcfuuaags</u> <u>a</u>	1299 TCTTTAAGGAAGGAA <u>GTTCT</u> <u>GTT</u>	1656	+
AD-1184155	ususaag (Ghd) AfagfGfAgau <u>usua</u>	945 VPus <u>AfsacGfaacuuuccUfcfuuaas</u> <u>g</u>	1300 CTTTAAGGAAGGAA <u>GTTCT</u> <u>TGA</u>	1657	+
AD-1184156	usasagg (Ahd) AfgGfAfAgucu <u>usgsa</u>	946 VPus <u>CfssaacAfgaacuuuccfuUfcuuas</u> <u>a</u>	1301 TTTAAGGAAGGAA <u>GTTCT</u> <u>CA</u>	1658	+
AD-1184157	assaaac (Ahd) CfuuUffUfuu <u>uscsa</u>	947 VPus <u>CfsgaaAgaaagaaAfgufiuuuuas</u> <u>a</u>	1302 TTAACACACTCTCTTTGCT	1659	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
Modified Sense and Antisense Strand Coronavirus dsRNA Sequences									
AD-1184158	gsgsuua (Ghd) GfCUUAFGfacuuua usgsa	948	VPusUfsauAfaaguguauGfcfuuacscs c	1303	GGGTAAAGGTAGACTTTAT TAT	1660	+ + +		
AD-1184159	gsusaag (Ghd) CfUAfGffAfccuuauu asgsa	949	VPusUfsuuUfaaaguguauAfGfcfuuacscs c	1304	GGGTAAAGGTAGACTTTATT ATG	1661	+ + +		
AD-1184160	gsasucu (Ahd) GFauGFCfacuuuuc gscsa	950	VPusGfscgaaFaaguguauFcufuaguacscs u	1305	AGGATAAAGATGCACTTTTC GCA	1662	+ + +		
AD-1184161	usasgcu (Ghd) GfuGffFcfcuuaucu gsusa	951	VPusUfsccagAfuuagagacAfCcfcguacscs g	1306	CGTAGCTGGTGTCTATCT GTA	1663	+ + +		
AD-1184162	gsguugu (Chd) UfcUfAfufcuguagn asgsa	952	VPusGfssuactfaccguauGfcacccsas g	1307	CTGGTATCTCTATCTGTAGT ACT	1664	+ + +		
AD-1184163	uscsucu (Ahd) UfcUfGfUFfaguacua usgsa	953	VPusUfsauaGfuuacuacGfaUfagagacscs a	1308	TGTCCTATCTGTAGTACTAT GA	1665	+ + +		
AD-1184164	ususguu (Chd) UfuGfCfUFfcqcaac asusa	954	VPusUfsuguluFggcgacAfGfaacaaags u	1309	ACTTGTTCTTGCTCGAAAC ATA	1666	+ + +		
AD-1184165	ususcac (Uhd) AfuAfUffGfuuaaac asgsa	955	VPusUfssugguuuuacauAfuAfuguacscs c	1310	GTTTCACATATGTTAACCC AGG	1667	+ + +		
AD-1184166	ascsaac (Uhd) GfCUUAFGfcuuaau asgsa	956	VPusUfsuuuUfaggcauaAfGfcfuguugus g	1311	CCACAACCTGCTTATGCTAAT AGT	1668	+ + +		
AD-1184167	csasacu (Ghd) CfUuAfUfGfcuuaaua gsusa	957	VPusUfsuuuUfaggcauaAfGfcfuguugus g	1312	CACAACCTGCTTATGCTAATA GTG	1669	+ + +		
AD-1184168	asascug (Chd) UfuAfUfGfcuuaauag usgsa	958	VPusUfsacuAfuuuagcauAfGfcaguugus u	1313	ACAACCTGCTTATGCTAATAG TGT	1670	+ + +		
AD-1184169	ascuugc (Uhd) UfuAfGfcuuaauagu gensa	959	VPusUfsacuAfuuuagcauAfGfcaguugus g	1314	CAACCTGCTTATGCTAATAGT GTT	1671	+ + +		
AD-1184170	csascuc (Ahd) UfaAfAfGfcuugugu usgsa	960	VPusUfsaaAcAfccagacuuuUfAgagugus c	1315	GACACTCATAAAGTCGTGT TGT	1672	- - -		
AD-1184171	gsasgug (Uhd) CfUcFUAfugaaau asgsa	961	VPusUfsuuuUfuctuuuagAfGfcacuas u	1316	ATGAGTGTCTCTATGAAAT AGA	1673	+ + +		
AD-1184172	ascsguga (Ghd) AfCuUfGfAfccuuacu asasa	962	VPusUfsuuuUfaggguuacGfUfctuaguugus c	1317	GGACTGAGACTGACCTTACT AAA	1674	+ + +		

TABLE 3 -continued

Modified Sense and Antisense Strand Coronavirus dsRNA Sequences										Strand of the Viral RNA
Duplex Name	Sense Strand Sequence 5' to 3'	SEQ ID NO:	Antisense Strand Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:	Strand of the Viral RNA	
AD-1184173	csasuuac (Ahd) AfuGfCfUfaguuaaa csasa	963	vPusufsguuUfaacuagchAfufguauugus u	1318	AACATACAAAGCTAGTTAAA CAG	1675	+ +	+ +	Targeted by the Agent	
AD-1184174	ascsgaa (Uhd) GFgutAfCfacuuuug asusa	964	vPusufsguuUfaaiguuactcAfucugus u	1319	AAACAGATGGTACACTTATG ATT	1676	+ +	+ +	Viral RNA	
AD-1184175	csasgau (Ghd) GfuAfCcAfcuuauug ususa	965	vPusufsguuAfuaaguAfcCfaucugus u	1320	AAACAGATGGTACACTTATGA TTG	1677	+ +	+ +	Targeted by the Agent	
AD-1184176	asggag (Ahd) GFuAfcfAfccuuuugg asasa	966	vPusufsguuAfaaagguguAfcufcuccus u	1321	ATAGGGAGGTACACCTTTGA AAA	1678	+ +	+ +	Viral RNA	
AD-1184177	usasuuu (Chd) AfGAfUffGfaguuuuc usasa	967	vPusufsgaaAfacuacuAfugfagauus u	1322	AAATATCTCAGATGAGTTTC TAG	1679	+ +	+ +	Targeted by the Agent	
AD-1184178	asuscuc (Ahd) GFauGFAfguuuuuc asgsa	968	vPuscfsguAgfaaacucaufcufqagauas u	1323	ATATCTCAGATGAGTTTC AGC	1680	+ +	+ +	Viral RNA	
AD-1184179	asusuu (Ghd) CfAAfAfufuaucaa asgsa	969	vPuscfsguuUfgauauUfgcfacauus g	1324	CAATGTTGCAAAATTATCAA AGG	1681	+ +	+ +	Targeted by the Agent	
AD-1184180	gsusugc (Ahd) AfauUfAfufucaaag gsusa	970	vPuscfscuuUfuugauauaAfufqcaacs u	1325	ATGTTGCAAAATTATCAAAG GTT	1682	+ +	+ +	Viral RNA	
AD-1184181	gsusacu (Ghd) GfuAfAfGfagucuu ususa	971	vPusafsgaaaUfgaeeuuUfcCfaguacscs a	1326	TGGTACTGGTAAGAGTCATT TTG	1683	+ +	+ +	Targeted by the Agent	
AD-1184182	usascug (Ghd) UfaAfCcAfgucauuu usgsa	972	vPuscfsgaaaAfuggacucaufcfcaguacs c	1327	GGTACTGGTAAGAGTCATT TGC	1684	+ +	+ +	Viral RNA	
AD-1184183	gsusaga (Ghd) UfgufUfufguauaa ususa	973	vPusufsguuUfaaaaaAfacfcuacsc asc	1328	GTGTAGAGTGTGTTGATAAA TTC	1685	+ +	+ +	Targeted by the Agent	
AD-1184184	asgsagu (Ghd) UfuUfUfGfauuuuu csasa	974	vPusufsgaaUfuuuuuAfacfcacuus c	1329	GTAGAGTGTGTTGATAAAATT CAA	1686	+ +	+ +	Viral RNA	
AD-1184185	gsusguu (Uhd) UfGAFUfAfauuuuu asgsa	975	vPuscfsguuUfgauuuAfafacac c	1330	GAGTGTGTTGATAAAATTCAA AGT	1687	+ +	+ +	Targeted by the Agent	
AD-1184186	gsusuuu (Ghd) AfuAfAfAfuuuuuu usgsa	976	vPuscfscuuUfgauuuAfucfaaaacs c	1331	GTGTTTGATAAAATTCAAAG TGA	1688	+ +	+ +	Viral RNA	
AD-1184187	csacac (Uhd) AfGAAfCcfcagauuu ususa	977	vPusufsguuUfucuguuUfcuAfuguguc sc	1332	GGCACACTAGACCCGAAAT ATT	1689	+ +	+ +	Viral RNA	

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184188	ascacu (Ahd) GfAAfCfCfagaauau usgsa	978 VPusIAfsaaufuuucgguufcuagugug Sc	GCACACTAGAACAGATAT TTC	1690	+
AD-1184189	gsasau (Uhd) GfuUfGfAfcaugug asgsa	979 VPusCFsucacfagugucafafuuuucs g	CTGAAATTGTTGACACTGTG AGT	1691	+
AD-1184190	cscscug (Chd) UfugfGfAfagaaggc usgsa	980 VPusCFsagecfuuucccafagfagggs u	AACCCUTGCTTGAGAAAAGC TGT	1692	+
AD-1184191	cusuau (Ahd) AfuUfCfAfcaagaug csusa	981 VPusAFsgcaUfucugugafuUfuaags u	ACCTTATAATTACAGAAATG CTG	1693	+
AD-1184191	csusuau (Ahd) AfuUfCfAfcaugaug csusa	981 VPusAFsgcaUfucugugafuUfuaags u	ACCTTATAATTACAGAAATG CTG	1693	+
AD-1184192	ususaua (Ahd) UfucfafCfagaauugc usgsa	982 VPusCFsagCAFuuucugugafuUfuaausgs g	CCTTATAATTACAGAAATG TGT	1694	+
AD-1184193	assasau (Ghd) AfCUfAfUfgucaau uscsa	983 VPusGFsaaufugicaauGfUfcaauuscs u	AGAATATGACTATGTCAAT TCA	1695	+
AD-1184194	asusaug (Ahd) CfUfUffGfcauaau csasa	984 VPusUFsgaaUFaugacauAfUfcauaus c	GAATATGACTATGTCAATT CAC	1696	+
AD-1184195	usasuga (Chd) UfaUffGfcauaauc ascsa	985 VPusGFsugaaufuaugacaufafgucaus u	AATATGACTATGTCAATT ACT	1697	+
AD-1184196	asasgac (Uhd) CfauFCfUfcaugaau gsgsa	986 VPusCFscacufcauagagAfUfcaugucus u	AGAAGACTCATCTCTGAT GGG	1698	+
AD-1184197	asqscacu (Chd) AfuCFUfCfuaugaug gsgsa	987 VPusCFscacufcauagagAfUfcaugucus c	GAAGACTCATCTCTGATG GGT	1699	+
AD-1184198	usscaga (Ghd) UfuUfAfGfaaauug gsgsa	988 VPusCFscacAfuuuucuafafcuugugas g	CTTCAGAGTTAGAAATGT GGC	1700	+
AD-1184199	ascscacu (Chd) AfacFUfUfucuuaua asusa	989 VPusAfssuuaufaagaaagufuUfcaugguggs u	ACACCATCAACTTCTTATA ATA	1701	-
AD-1184200	csuscca (Uhd) AfAAfCfGfauaugguu csgsa	990 VPusCFsgaaCfauaucguufuUfcauggag u	ATCTCCATAAACGATATGTT CGA	1702	-
AD-1184201	csasuag (Ghd) AfauUfAfAfaaucunc usasa	991 VPusUFsgaaAfgaauuuuufuUfcauggug a	TCCATAGGAAATAAAATCTTC TAA	1703	-

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184202	cscsuua (Uhd) AfuUffCfaaacuug usgsa	992 VPusCfscacAfguuuquaAfufuaggss a	1347 TTCCCTAAATTACAAAACITG TGC	1704	+
AD-1184203	gscsuug (Uhd) UfaAfFcfaacuuag ccsusa	993 VPusAfsccuAfaguuguuAfacaaggcsgs u	1348 ACGCTTGTTAAACAACTTAG CTC	1705	+
AD-1184204	cusuug (Uhd) AfafAfCcfaacuuagc uscsa	994 VPusGfsaggUFaaggugUfuAfacaagscs g	1349 CGCTTGTTAAACAACTTAGC TCC	1706	+
AD-1184205	csusugc (Uhd) GFcUFfAfcfuuuagg uscsa	995 VPusGfscacUfuuuaguacGfcafgcaagsas u	1350 ATCTTGCTGCTACTAAATG TCA	1707	+
AD-1184206	ascsuua (Uhd) GfgAfUfUfuguuuu gsasa	996 VPusUfscauAfaaacaaucfcAfuaagusus c	1351 GAACTTATGGATTGTTTAT GAG	1708	+
AD-1184207	csgsacg (Ahd) CfGAFFfUfacuagcg usgsa	997 VPusCfscacgfuaquaguUfGUfCguccgsgs u	1352 ACCGACGGAGCTACTAGCG TGC	1709	+
AD-1184208	gsasoga (Chd) CfAcfUfAfcaugcy gscsa	998 VPusGfscacGfcaaguaguUfCfugccgsgs g	1353 CGGACGACGACTACTAGCGT GCC	1710	
AD-1184209	asusggag (Uhd) AfccGfAfAfcauuuug ascsa	999 VPusGfsuacAfuaaguuccGfuAfcaucusus a	1354 TGATGAGTAGGAACTTATGT ACT	1711	+
AD-1184210	csgaaac (Uhd) UfaUfGUfAfcauuu csgsa	1000 VPusCfsgaaUfagaquuAcAfguucgus a	1355 TAGGAACTTATGTACTCATTT CGT	1712	+
AD-1184211	gsasacu (Uhd) AfuGfUfAfcauuuic gsua	1001 VPusAfscgaaAfuggaguacAfuaaguusgs u	1356 ACGAACTTATGTACTCATTC GTT	1713	+
AD-1184212	asasuu (Ahd) UfGUfAfFcfaauucg ususa	1002 VPusAfsacgAfauaguacAfuaaguuscs g	1357 CGAACTTATGTACTCATTCG TTT	1714	+
AD-1184213	ascsuua (Uhd) GFuAfFcfaauucgcu ususa	1003 VPusAfsaacGfaauugaguAfcafuauagus c	1358 GAACTTATGTACTCATTCGT TTC	1715	+
AD-1184214	csusuuu (Ghd) UfaCfUfFcfaauucg uscsa	1004 VPusGfssaaAcFgaaauugaguAfcafuauagus u	1359 AACTTATGTACTCATTCGTTT CG	1716	+
AD-1184215	ususaug (Uhd) AfcaUfCfAfufucgusu csgsa	1005 VPusCfsgaaAfccgaauugaguAfcauauagss u	1360 ACTTATGTACTCATTCGTTTC GG	1717	+
AD-1184216	usasugu (Ahd) CfUcEAFUfufucguuu csgsa	1006 VPusCfscgaaAfccgaauugaguAfcauauas s g	1361 CTTATGTACTCATTCGTTTCG GA	1718	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184217	asusguu (Chd) UEcAUFUfcguuuucg gsaaa	1007 VPusUfscccGAfaacgaaauGfaguacausas a	1362 TTATGTACTCATTCGTTTCGG AA	1719	+
AD-1184218	usgsuac (Uhd) CfauUffCfguuuucg asasa	1008 VPusUfsuccGfaaacgaaauGfaguacaus a	1363 TATGTACTCATTCGTTTCGG AAG	1720	+
AD-1184219	gsusacu (Chd) AFuUfcfGfuuucgg asgaa	1009 VPusUfsuuccGfaaacgaaauGfaguacaus u	1364 ATGTACTCATTCGTTTCGG AGA	1721	+
AD-1184220	csggu (Ahd) CfguUffAfauaguua asusa	1010 VPusUfsuuaAfcuuuaauaCfguUfaccugs c	1365 GACAGGTA CGTTAAATAGTTA ATA	1722	+
AD-1184221	asgguu (Chd) GfuUffAfauaguua usaaa	1011 VPusUfsuauAfcauuuaAfGfuuaccugs u	1366 ACAGGTACGTTAAATAGTTAA TAG	1723	+
AD-1184222	usasaua (Ghd) UfuAfffUfagcqauc ususa	1012 VPusUfsaguUfcgcuuuuAfcauuuasas c	1367 GTTAATAGTTAAATAGCGTAC TTC	1724	+
AD-1184223	uscsuug (Chd) UfuUffCfGUgguaau csusa	1013 VPusUfsagaauUfaccaccaGfaAfGcaag a	1368 TTCTCTGCTTTGTTGTTTC TT	1725	+
AD-1184224	csusugc (Uhd) UfucfGfUfGUgguaau ususa	1014 VPusUfsagaAUfuacaccacGfaAfGcaags a	1369 TTCTTGCTTTCGTTGTTATCT TG	1726	+
AD-1184225	ususgcu (Uhd) UfcGUffGfGUuuuu usgsa	1015 VPusUfsaagAfauaccacGfaAfGcaasgs a	1370 TCTTGCTTTGTTGTTATTCTT GC	1727	+
AD-1184226	usgcuu (Uhd) CfguUffGfGUuuuu gcsca	1016 VPusUfscaaGfaauaccacGfaAfGcaags a	1371 CTTGCTTTGTTGTTATTCTT CT	1728	+
AD-1184227	gcsuuu (Chd) GfGUffGfUauucung csusa	1017 VPusUfsgcaAfguauaccAcGfcaagg a	1372 TTGCTTTGTTGTTATTCTTGC TA	1729	+
AD-1184228	ususucg (Uhd) GfGUffUfuucung usgsa	1018 VPusUfsuagCfaaggaaauAfcafgaaasgs a	1373 GCTTTCGTTGTTATTCTTGC GT	1730	+
AD-1184229	cussgcg (Chd) UfucfGfAfuuugung csgsa	1019 VPusUfsgcadfaccuuauGfcaGcag a	1374 TACTGGCTTCGATTGTGTG CGT	1731	+
AD-1184230	gsusacu (Ghd) CfugfcfAfauuuugu usasa	1020 VPusUfsaacAfauuuugcAfGcfaguac c	1375 GCGTACTGCTGCAAAATTGT TAA	1732	+
AD-1184231	csusgcu (Ghd) CfAfUffAfuuuuua csgsa	1021 VPusUfsguuAfaccuuauUfGfagcag a	1376 TACTGCTGCAAAATTGTAA CGT	1733	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184232	usgscug (Chd) AfAfAfUfuguuacu gsusa	1022 VPusAfscguUfaacaauaUfuGfagcaegs u	ACTGCTGCAATATTGTAAAC GTG	1734	+
AD-1184233	gscsugc (Ahd) AfAfUfUfuguuacg usgsa	1023 VPusCfscguUfaacaauaUfuUfqaggcsas g	CTGCTGCATAATTGTAAACG TGA	1735	+
AD-1184234	csusgca (Ahd) UfaUfUffguuacgu gsasa	1024 VPusUfsacGfuuaacaauaUfuUgcagscs a	TGCTGCATAATTGTAAACGT GAG	1736	+
AD-1184235	asgsagu (Uhd) CfCuUfGfAfucuucg gsusa	1025 VPusAfsccgfaaqaucaGfAgfacucusas g	CTAGAGTTCCGATCUTCTG GTC	1737	+
AD-1184236	cusugau (Chd) UfucUfUffguuacaa csgsa	1026 VPusUfsquuUfagaccaggAfAgfaucagsgs a	TCCTGATCTCTGGCTAAAA CGA	1738	+
AD-1184237	gsasucu (Uhd) CfUfGfGUfucuaaacg asasa	1027 VPusUfsucguUuuagaccAfAgfaucuas g	CTGATCTCTGGCTAAACG AAC	1739	+
AD-1184238	ascsaaau (Chd) CfAAfAfCfCuGuauuu asgsa	1028 VPusCfscuaUfcautaggUfUfcauugus c	GAAACATGAACTCTAGTAAT AGG	1740	+
AD-1184239	csasaug (Chd) AfAcCcFfUfAguaauaa gsgsa	1029 VPusUfscuaufuaucuauaggUfUfcuuugus u	AACAATGGAACTCTAGTAATA GGT	1741	+
AD-1184240	asasugg (Ahd) AfCcCUfAfguuaauag gsusa	1030 VPusAfsccuUfuuaucuagGfuUfcuuugus u	ACAATGGAACTCTAGTAATAAG GTT	1742	+
AD-1184241	asusgg (Ahd) CfCuUfAfGfuuaauagg ususa	1031 VPusAfscuccuauacuaGfGuUfuccausus g	CAATGGAACTCTAGTAATAAGG TTT	1743	+
AD-1184242	asasccu (Ahd) GfuAfAfUfaguuuuc cnsua	1032 VPusAfsggaAfaccuuuAfcUfagguscs c	GGAACCTAGTAATAAGGTTTC CTA	1744	+
AD-1184243	ascscua (Chd) UfaAfUfAfgeguucc ususa	1033 VPusUfsaggAfaaaccuuuUfcauaggusus c	GAACCTAGTAATAAGGTTTC TAT	1745	+
AD-1184244	usasccau (Chd) AfCfAfAfAfgeguucc ususa	1034 VPusAfsgaaAfaggguucGfuGfaguuaeegs c	GCTACATCACGAAACGCTTTC TTA	1746	+
AD-1184245	ascscauc (Ahd) CfGAfAfCfgeguucc ususa	1035 VPusUfsaagAfaaqcgwuUfUfaguugusas g	CTACATCACGAAACGCTTTC TAT	1747	+
AD-1184246	csasuca (Chd) GfAfAfCfGeuuuccu asusa	1036 VPusAfssuaGfaaaagcgwuUfcGfaguugus a	TACATCACGAAACGCTTTC ATT	1748	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184247	asuscac (Ghd) AfacGfCfuuucuna ususa	1037 u VPusUfsauaAfgaaaaggcgUFufgugausgs	1392 ACATACGAAAGCTTCTTA	1749	+
AD-1184248	uscsacg (Ahd) AfFcGfCfuuucuuau usasa	1038 g VPusUfsauaAfagaaaaggcgUFufgugausgs	1393 CATACGAAAGCTTCTTAT	1750	+
AD-1184249	csascga (Ahd) CfGcfufufuucuuau ascga	1039 u VPusUfsauaAfagaaaaggcgUFufgugausgs	1394 ATCACGAAAGCTTCTUATT	1751	+
AD-1184250	ascsgaa (Chd) GfcUfUfUfuuuuuu csasa	1040 a VPusUfsquaAfuaaaaadGfcGfufuugusgs	1395 TCACGAAAGCTTCTTATTA	1752	+
AD-1184251	csgaac (Ghd) CfUufUfCfuuauuac asasa	1041 g VPusUfsugnAfauaaaaAfgcGfufuugusgs	1396 CACGAAAGCTTCTTATTAC	1753	+
AD-1184252	gsusaag (Uhd) GfacAfAfcaagaugu ususa	1042 g VPusUfsaacAfufucuugugUfCaFuuacsus	1397 CAGTAAGTGACAACAGATGT	1754	+
AD-1184253	ususagc (Chd) UfUffUfCfuuauuic c-susa	1043 a VPusUfsggaaAfuaadjcagaAfafgjcuuasas	1398 TTTAGCCCTTCGCTTATTC	1755	+
AD-1184254	usaegcc (Uhd) UfucfUffGfcuuauucc ususa	1044 a VPusUfsaggAfauagcagaaAfaggcuuasas	1399 TTAGGCCTTCGCTTATTCCT	1756	+
AD-1184255	asgscsu (Uhd) UfcUffGfcuuauucc usgsaa	1045 a VPusUfsaagdfauuaggcdafafaggcuuas	1400 TTAGCCCTTCGCTTATTCCTT	1757	+
AD-1184256	cscsuu (Chd) Ufgcfufuccuug ususa	1046 u VPusUfsaacAfggauuagcAfggaaaggcs	1401 AGCCTTCTGCTTATTCCTGT	1758	+
AD-1184257	cusuuc (Uhd) GFcUfAfufuccuug ususa	1047 c VPusUfsaacAfaggaaauAfggaaaggss	1402 GCCTTCTGCTTATTCCTGTT	1759	+
AD-1184258	ususuu (Ghd) CfUafUfUfuuuguu ususa	1048 g VPusUfsaaAfcaaggaaauAfggaaaggss	1403 CCTTCTGCTTATTCCTGTT	1760	+
AD-1184259	ususcug (Chd) UfaUfUfCfuuuguu usasa	1049 g VPusUfsaaaAfcaaggaaauAfggaaaggss	1404 CTTTCTGCTTATTCCTGTT	1761	+
AD-1184260	uscaugc (Uhd) AfUffCfuuugguu usasa	1050 a VPusUfsaaAfcaaggaaauAfggaaaggss	1405 TTCTGCTTATTCCTGTT	1762	+
AD-1184261	cussgcu (Ahd) UfUfCfUfufuguuua ususa	1051 a VPusUfsuuuAfaaacaaggAfauffgagss	1406 TTCTGCTTATTCCTGTTAA	1763	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184262	cscsaag (Ghd) UfuUfAfFcfcuuaua usgsa	1052 VPusUfsauuAfungguuAfAcfcuuggsg sg	1407 CCCAAAGGTTTACCCAAATAA TAC	1764	+
AD-1184263	asgsuu (Uhd) UfAcFcFcfaauaauc susua	1053 VPusAfsguaufuuuuggouAfaccuuusgs g	1408 CCAAGGTTAACCAAATAA CTG	1765	+
AD-1184264	asgsuu (Uhd) AfFcFcFaauaauc usgsa	1054 VPusCfsaguAfuuauuggfufaccusus g	1409 CAAGGTTAACCAAATAAATAC TGC	1766	+
AD-1184265	asccca (Ahd) UfAAfUfAfugcgc ususa	1055 VPusAfsgaAfccaguauUfugguusas a	1410 TTACCGAAATAACTCGGTG TTG	1767	+
AD-1184266	asgucc (Ahd) GfauUfAfccaaauu gsgsa	1056 VPusCfscaaUfuugcuuAfUfugacuss c	1411 GCAGTCAGATGACCAAAATT GGC	1768	+
AD-1184267	gsucca (Ghd) AfuGfAfFcfaaung gscsa	1057 VPusGFsccaaFuuggucAfucfuggacss g	1412 CAGTCCAGATGACCAAAATG GCT	1769	+
AD-1184268	asusgg (Chd) AfAAfAfGfgeuuuca csgsa	1058 VPusCfsquaAfsgaaggccuufugfgecausgs u	1413 ACATTCGCCAAAAGGTTCTTA CGC	1770	+
AD-1184269	ususgcc (Ahd) AfAAfGfGfceuucuac gscsa	1059 VPusCfsquAfsgaaggccuufugfgecausus g	1414 CATTGCCAAAAGGTTCTAC GCA	1771	+
AD-1184270	gsgscag (Uhd) CfAAfGfFcfcuuu csgsa	1060 VPusCfsagafagggcuUfugfugcsgs c	1415 GGGCAGTCAAGCCTCTCT CGT	1772	+
AD-1184271	asascug (Uhd) CfAcFUfAfagaaau usgsa	1061 VPusCfsagauuuuaggufgAfcaaguus g	1416 CAAACTGTCACTAAGAAATC TGC	1773	+
AD-1184272	usgsuca (Chd) UfAAfGfAfauuc usgsa	1062 VPusCfsagAfsgauuuuAfgtigacags u	1417 ACTGTCAGTAAAGAAATCTGC TGC	1774	+
AD-1184273	asascug (Uhd) GfAcFUfFcfcuuu usgsa	1063 VPusCfsaggAfaggaaagufcAfcaaguus g	1418 CAAACTGTGACTCTCTCCCT GC	1775	+
AD-1184274	uscsuug (Uhd) GfCaGfAfauuaau cscsa	1064 VPusAfsgaaUfuccuuuGfcAfcaagags u	1419 ACTCTTGTCAGAATGAAATT CTC	1776	+
AD-1184275	cnsuug (Ghd) CfAgAfAfugaaunc uscsa	1065 VPusGfsagafuuaucuUfGfcacaags g	1420 CTCTTGTCAGAATGAAATT TCG	1777	+
AD-1184276	ususugug (Chd) AfGAAfAfUfugaaau csgsa	1066 VPusCfsagafauuaucuUfGfcacaags a	1421 TCTTGTCAGAATGAAATT CGT	1778	+

TABLE 3 -continued

Duplex Name	Sense Strand Sequence 5' to 3'	Antisense Strand Sequence SEQ ID NO: 5' to 3'	mRNA Target Sequence SEQ ID NO: 5' to 3'	SEQ ID NO:	Strand of the Viral RNA Targeted by the Agent
AD-1184277	usgsugc (Ahd) GFAAfUFGfaauucu gssua	1067 VPusIAfsccgAGfaauucauUfcUfgcacas g	1422 CTTGTCAGATGAATTCTC GTA	1779	+
AD-1184278	gsusgca (Ghd) AfAUfGfAfauucucg usasa	1068 VPusIufsacgAGfaauucauUfcUfgcacas a	1423 TTGTGCAGGAATGAATTCTCG TAA	1780	+
AD-1184279	usgscag (Ahd) AFUGfAfAfuuucucg asasa	1069 VPusIufsacGfAgaaucAfUfUfgcacas a	1424 TGTGCAGAAATGAATTCTGTT AAC	1781	+
AD-1184280	gscsaga (Ahd) UfgAAfAfUfUfucugua ascsa	1070 VPusGfsuuuCfAgaaucFaUfUfgcgs c	1425 GTGCAGAAATGAATTCTCGTA ACT	1782	+
AD-1184281	csagcaa (Uhd) GFAAfUfUfucugua csusa	1071 VPusIAfsquuAfCggaaauUfcAfUfucugcs a	1426 TGCAAGATGATTCTCGTAA CTA	1783	+
AD-1184282	usasauc (Uhd) CfAcAfAfUfagcaauc ususa	1072 VPusIAfsagaUfUfgcuauugUfgAfgaauuas a	1427 TTTAAATCTCACATAGCAATC TTT	1784	+
AD-1184283	uscsuca (Chd) AfUfAfUfucuuu asasa	1073 VPusIufsuaAfAgauugcuaUfUfgcagasus u	1428 AATCTGACATAGCAATCTTT AAT	1785	+
AD-1184284	cusucac (Ahd) UfAgfAfAfauuuua asusa	1074 VPusIAfsuuuAfAgauugcuaUfUfgugagaa u	1429 ATCTCACATAGCAATCTTTA ATC	1786	+
AD-1184285	uscsaca (Uhd) AfAgfAfAfucuuua uscsa	1075 VPusGfsauuAfAgauugcuaUfUfgugagss a	1430 TCTCACATAGCAATCTTTAA TCA	1787	+
AD-1184286	csascau (Ahd) GfCafAfAfUfuuuuu csasa	1076 VPusIufsauUfuuacacauUfaGfgcucus g	1431 CTCACATAGCAATCTTTAAT CAG	1788	+
AD-1184287	gsasgcc (Chd) UfAAfUfGfuguaaaa ususa	1077 VPusIAfsauuAfUfuuacacauUfaGfgcucus u	1432 AAGAGCCCTAAATGTGTAAA TTA	1789	+
AD-1184288	gscscuu (Ahd) AfUfUfGfuuuuuu asasa	1078 VPusIufsuaUfuuacacauUfuUfaggcs c	1433 GAGGCCCTAAATGTGTAAAATT AAT	1790	+
AD-1184289	cscscua (Ahd) UfGUfGfUfuuuuuu asusa	1079 VPusIAfsuuuAfUuuuacacauUfuUfaggcs u	1434 AGCCCCCTAAATGTGTAAAATT ATT	1791	+
AD-1184290	cscscuaa (Uhd) GFUGfUFfAfaauua ususa	1080 VPusIAfsauuAfauuuacAcAfUfuUggs c	1435 GCCCTAAATGTGTAAAATTAA TTT	1792	+
AD-1184291	cscsccau (Ghd) UfGAfUfUfuuuuu csusa	1081 VPusIAfsgruAfuuuuuuuucFaCfUsugggs a	1436 TCCCCATGTGTGTTAAATAG CTT	1793	+

TABLE 4  
Unmodified Sense and Antisense Strand Coronavirus\_dsrNA Sequences

Duplex Id	Sense Sequence 5' to 3'	Antisense Sequence 5' to 3'	BetaCoV_Wuhan-Hu-1/2019 EPI_ISL_402125	Start in BetaCoV_Wuhan-Hu-1/2019 EPI_ISL_402125	End in BetaCoV_Wuhan-Hu-1/2019 EPI_ISL_402125	Targets SARS? Targets MERS?	Targets SARS? Targets MERS?	Strand of the Viral RNA targeted by the Agent
AD-1231467	UACUCAUUCGUUUCCGAGAA (SEQ ID NO: 1794)	UUCUUCGGAAACGAUGAGUACA (SEQ ID NO: 1834)		26246	26268	TRUE	FALSE	+
AD-1231468	CUCUCGCUAACAAACUAA (SEQ ID NO: 1795)	UAGAUGUGUAGACCAGAGAU (SEQ ID NO: 1835)		26439	26481	TRUE	FALSE	+
AD-1231469	UUCUUCGUUCUGGUUAUCA (SEQ ID NO: 1796)	UGAAUACCAGAACGAAAGAAA (SEQ ID NO: 1836)		26301	26323	TRUE	FALSE	+
AD-1231470	UUAUUCUCAUCAGUAUCA (SEQ ID NO: 1797)	UAGAUACUAUGUGAGAUAAAG (SEQ ID NO: 1837)		29639	29681	TRUE	TRUE	+
AD-1231471	UAAUCUUAUUCUCAUAUAGCA (SEQ ID NO: 1798)	UGCUCAUUAUGAGAUAAAGUAC (SEQ ID NO: 1838)		29654	29676	TRUE	TRUE	+
AD-1231472	CCUGAUCCUUCGGUUAAGA (SEQ ID NO: 1799)	UGUUUAACCGAAAGAUCAAGAA (SEQ ID NO: 1839)		26453	26475	TRUE	TRUE	+
AD-1231473	UGUAGAUAGUGUACAGA (SEQ ID NO: 1800)	UCUGUUAUCUUAUCGUOCAG (SEQ ID NO: 1840)		27180	27202	TRUE	TRUE	+
AD-1231474	UCCUGAUCCUUCGGUCUAA (SEQ ID NO: 143)	UUUAGACCAAGAGAUCAAGAACU (SEQ ID NO: 498)		26451	26473	TRUE	TRUE	+
AD-1231475	UAUGAUACUACUUCGUUCGGA (SEQ ID NO: 296)	UCCGAACGAAUGGUACAUAG (SEQ ID NO: 651)		26242	26264	TRUE	TRUE	+
AD-1231476	ACUGUACAGUCUAAAUGUCA (SEQ ID NO: 7)	UGACAUUUUAGACGUACAGUG (SEQ ID NO: 8)		11832	11854	TRUE	TRUE	+
AD-1231477	CCCAUGUGAUUUAAUAGCUA (SEQ ID NO: 1801)	UAGCUAUUUAAAUCACAUAGGGA (SEQ ID NO: 1841)		29834	29856	TRUE	TRUE	+
AD-1231478	UCCUGGUAAUCUACUAGUA (SEQ ID NO: 1802)	UACUAGUAAGAAUACCAAGAAAG (SEQ ID NO: 1842)		26309	26331	TRUE	TRUE	+
AD-1231479	UCUUCUGGUAAAUGAACUA (SEQ ID NO: 1803)	UAGGUCAUTUAGACCGAGAAUC (SEQ ID NO: 1843)		26458	26480	TRUE	TRUE	+
AD-1231480	GUACUGUGCAAUAGUUA (SEQ ID NO: 310)	UUAACAAUAUUGCAGCAUAGC (SEQ ID NO: 665)		26365	26387	TRUE	TRUE	+

TABLE 4-continued

Duplex Id	Sense	Sense Sequence 5' to 3'	Antisense Sequence 5' to 3'	Start in BetaCoV/Wuhan-Hu-1/2019 EP1_ISL_402125	End in BetaCoV/Wuhan-Hu-1/2019 EP1_ISL_402125	Targets SARS?	Targets SARS2?	Strand of the Viral RNA	Targeted by the Agent	
AD-1231481	UUAAAUCUCACAUAGCAAUC	(SEQ ID NO : 1804)	UGAUUUCUAUGUGAGAUAAAUGU (SEQ ID NO : 1844)	29658	29680	TRUE	TRUE	FALSE	FALSE	+
AD-1231482	UACAAUCCUCCAAAGAACAA	(SEQ ID NO : 162)	UGUCCUCUAGGGAGGUUGUGC (SEQ ID NO : 517)	28747	28769	TRUE	TRUE	FALSE	FALSE	+
AD-1231483	CUGCUAUCCUUGUUUAAA	(SEQ ID NO : 1805)	UAUUAAAACAAAGGAUAGCAGAA (SEQ ID NO : 1845)	27802	27824	TRUE	TRUE	FALSE	FALSE	+
AD-1231484	CUCACUAGGAAUCUTUAAA	(SEQ ID NO : 1806)	UATUAAAAGAUGCUAUGUGAGAU (SEQ ID NO : 1846)	29664	29686	TRUE	TRUE	FALSE	FALSE	+
AD-1231485	UCGUGUACAACTUUCUCAAA	(SEQ ID NO : 1807)	UTUGAGAAAUGUUGHAGCAGAU (SEQ ID NO : 1847)	28741	28763	TRUE	TRUE	FALSE	FALSE	+
AD-1231486	CAGAUGGUACACUTUAGAUAA	(SEQ ID NO : 1808)	UAAUCAAAAGGUACAUCAUCUGU (SEQ ID NO : 1848)	15937	16009	TRUE	TRUE	FALSE	FALSE	+
AD-1231487	UAACACAUUGUGCUUUCUCAAA	(SEQ ID NO : 1809)	UUUGAAAAGGAAACAUUGUAGU (SEQ ID NO : 1849)	14644	14666	TRUE	TRUE	FALSE	FALSE	+
AD-1231488	UAUAUAGUAAAAGGUACUTUA	(SEQ ID NO : 1810)	UAAGUACGUAAUAAACUAAAC (SEQ ID NO : 1850)	26277	26299	TRUE	TRUE	FALSE	FALSE	+
AD-1231489	CAUACAAUGCUAGGUAAACZA	(SEQ ID NO : 1811)	UGUUUAAACUAGCAUUGUAGUU (SEQ ID NO : 1851)	15884	15906	TRUE	TRUE	FALSE	FALSE	+
AD-1231490	UUUUCAAACUGUCAACCCGA	(SEQ ID NO : 1812)	UCCGGUUGUGAGGUUGAAAAAGC (SEQ ID NO : 1852)	14656	14678	TRUE	TRUE	FALSE	FALSE	+
AD-1231491	CUUAGUACUACUUGUUUCA	(SEQ ID NO : 1813)	UGAACCGAAUGGAGCAUAGUU (SEQ ID NO : 1853)	26240	26262	TRUE	TRUE	FALSE	FALSE	+
AD-1231492	GUUGUGUACACACAUGGUAA	(SEQ ID NO : 1814)	UUACCAAUGUGUGUACACACAU (SEQ ID NO : 1854)	13154	13176	TRUE	TRUE	FALSE	FALSE	+
AD-1231493	AACUUAUGUACUACUGUUA	(SEQ ID NO : 1815)	UAACCAAUGGAGUAUAAGUUCG (SEQ ID NO : 1855)	26238	26260	TRUE	TRUE	FALSE	FALSE	+
AD-1231494	CUGCUCAAUAAUUGGUAAACGA	(SEQ ID NO : 1816)	UCCGUUACAAUAAUUGCAGGAGUA (SEQ ID NO : 1856)	26368	26390	TRUE	TRUE	FALSE	FALSE	+

TABLE 4-continued

Duplex Id	Sense Sequence 5' to 3'	Antisense Sequence 5' to 3'	Start in Betacov/Wuhan-Hu-1/2019 EP1_ISL_402125	End in Betacov/Wuhan-Hu-1/2019 EP1_ISL_402125	Targets SARS? Targets SARS? Targets SARS? Targets SARS?	Strand of the Viral RNA	Targeted by the Agent
AD-1231495	UUCUUGUAAGAACGGUAAA (SEQ ID NO: 27)	UAUUACCGGUUCUACGAAAGA (SEQ ID NO: 382)	628	650	TRUE	FALSE	+
AD-1231496	CGUGCUACAACUUUCUCAAGA (SEQ ID NO: 1817)	UCUUGAAGAAGUGUAGCAGAU (SEQ ID NO: 1857)	28742	28764	TRUE	TRUE	+
AD-1231497	UGAAAATGGUGACAUUGUGAA (SEQ ID NO: 1818)	UUCAGAAUGUCAAAGAAUUTCAGC (SEQ ID NO: 1858)	17572	17594	TRUE	TRUE	+
AD-1231498	ACAAUUGUUGCUUUUUAACUA (SEQ ID NO: 1819)	UAGUUUUAAAAGCAACAUUGUUA (SEQ ID NO: 1859)	14646	14668	TRUE	TRUE	+
AD-1231499	AAAUUUGUGACACUAGUGUA (SEQ ID NO: 1820)	UACUGUAUGUGCAACAAUUCUA (SEQ ID NO: 1860)	17574	17596	TRUE	TRUE	+
AD-1231500	UCUUCGUAAAGAACGUAAUZA (SEQ ID NO: 28)	UUAUUACCCGUUCUACGAGAG (SEQ ID NO: 383)	629	651	TRUE	TRUE	+
AD-1231501	CUGCAAUATUGUUAACGUGUA (SEQ ID NO: 1821)	UUCAGGUUAAACAAUUAUGCGAGA (SEQ ID NO: 1861)	26371	26393	TRUE	TRUE	+
AD-1231502	GCUGGAAUUGUGACUGUGUA (SEQ ID NO: 1822)	UACAGGUUAUCAACAAUUCGGAG (SEQ ID NO: 1862)	17570	17592	TRUE	TRUE	+
AD-1231503	CUGCGAAAATGGUGACACTUA (SEQ ID NO: 1823)	UAGUGUCAAACAAUUCAGCAGGA (SEQ ID NO: 1863)	17568	17590	TRUE	TRUE	+
AD-1231504	UUGUGGAUGAUGAUAUUCCAA (SEQ ID NO: 228)	UUGAAAUAUCAUCAUCAACA (SEQ ID NO: 583)	17578	17600	TRUE	TRUE	+
AD-1231505	UGUUGACACUGUGAAUGCUTA (SEQ ID NO: 1824)	UAGGAUUCACAGUGUCAACAU (SEQ ID NO: 1864)	26288	26290	TRUE	TRUE	+
AD-1231506	CAGGUACGUAAUAGUUAUA (SEQ ID NO: 300)	UAUUAZCUAUAAAGUACCGUC (SEQ ID NO: 655)	28767	28789	TRUE	TRUE	+
AD-1231507	ACAUUCCCCAAAGGUUCUUA (SEQ ID NO: 1825)	UAGAAAACCUUUGCCAAGUG (SEQ ID NO: 1865)	26370	26392	TRUE	TRUE	+
AD-1231508	GCUGGAUUAUUGUUAACGUGA (SEQ ID NO: 313)	UCACGUUAAACAAUAUUGCGAG (SEQ ID NO: 668)	29688	TRUE	TRUE	FALSE	+

TABLE 4-continued

Duplex Id	Sense Sequence 5' to 3'	Antisense Sequence 5' to 3'	Start in BetaCoV/Wuhan-Hu-1/2019 EP1_ISL_402125	End in BetaCoV/Wuhan-Hu-1/2019 EP1_ISL_402125	Targets SARS?	Targets Targets MERS?	Strand of the Viral RNA	Targeted by the Agent
AD-1231509	CACAUAGCAAAUCUUTUAUCUA (SEQ ID NO : 1862)	UGAUAAAAGAUUGCUAUGUGAG (SEQ ID NO : 1866)	14824	14846	TRUE	TRUE	FALSE	+
AD-1231510	AAUGUGUGAUAAUCAGAACAA (SEQ ID NO : 1827)	UGGUUCUGUGAUAGCACACAUUG (SEQ ID NO : 1867)	26451	26473	TRUE	TRUE	FALSE	+
AD-1231511	GUUCCUGAUUCUUCUGGUCAUA (SEQ ID NO : 142)	UUAGACCAGAAAGAUCAAGAACUC (SEQ ID NO : 497)	26450	26472	TRUE	TRUE	FALSE	+
AD-1231512	UGGCCAAAAGCCUUUACGCA (SEQ ID NO : 349)	UGCCGTAAGACCUUUGGGAAUG (SEQ ID NO : 704)	28770	28792	TRUE	TRUE	FALSE	+
AD-1231513	UUCUGCUAAUCUUGUUGGUCAUA (SEQ ID NO : 1828)	UUAGCAACAAAGAUUAGCAGAAC (SEQ ID NO : 1868)	24620	24642	TRUE	TRUE	FALSE	+
AD-1231514	ACCUACUAAUAGGUTUCCUAA (SEQ ID NO : 1829)	UUAGGAACCAUAAUACUAGGUUC (SEQ ID NO : 1869)	26552	26604	TRUE	TRUE	FALSE	+
AD-1231515	CUGCUAAUCUUGGUCAUACUA (SEQ ID NO : 121)	UAGUAGCAGCAAGAUUAGCAGAA (SEQ ID NO : 476)	24622	24644	TRUE	TRUE	FALSE	+
AD-1231516	CACUCUAAAGUCUGUGUGA (SEQ ID NO : 1830)	UCAACAGACGUUUAUCCUUAUGA (SEQ ID NO : 1870)	15609	15631	TRUE	FALSE	FALSE	-
AD-1231517	CAUAGGAUAAAACUUCUZA (SEQ ID NO : 281)	UAGAAGAUUUUAUCCUUAUGA (SEQ ID NO : 636)	20413	20435	TRUE	FALSE	FALSE	-
AD-1231518	UCUACACAAACUCUUTAAAGAA (SEQ ID NO : 210)	UUCUUAAGGUUGUGUAGUA (SEQ ID NO : 555)	3745	3767	TRUE	FALSE	FALSE	-
AD-1231519	AUCUUGUUUUCUUAUCUAA (SEQ ID NO : 1831)	UUUGAUAGGAAACAGAUGA (SEQ ID NO : 1871)	3929	3951	TRUE	FALSE	FALSE	-
AD-1231520	CAGUCUAAUCUUAUAAA (SEQ ID NO : 1832)	UUUUAAUAGAUUAGACUGUG (SEQ ID NO : 1872)	10501	10523	TRUE	FALSE	FALSE	-
AD-1231521	UGGUACACUAAUAAA (SEQ ID NO : 1833)	UUUUAAUAGGUUACCA (SEQ ID NO : 1873)	23712	23734	TRUE	FALSE	FALSE	-

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TABLE 5

Modified Sense and Antisense Strand dsRNA Sequences Targeting COVID-19				
Duplex Id	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:
AD-1231467	usascuca (Uhd) uCfGfUfuucggaaagsasa	1874	VPUsUfscudTc (Cgn) gaaacgAfaUfgaguasca	1925
AD-1231468	csusuc (Uhd) gGfuCfUfAfaacaaacusa	1875	VPUsUfsagdTudTguuuagAfcCfagaagsasu	1926
AD-1231469	ususcuugCfuUfUfCfugg (Uhd) auuscsa	1876	VPUsGfsaadTa (Cgn) cacgaaAfgCfaagaasasa	1927
AD-1231470	ususaau (Chd) UfcAfCfAfuaquaaucsusa	1877	VPUsAfsgadTudAcuauguGfaGfauuaasag	1928
AD-1231471	usasacu (Uhd) UfaAfUfCfucauauagscsa	1878	VPUsGfscudAudAugagauUfaAfaguuaasc	1929
AD-1231472	cscsuga (Uhd) CfufifCfUfguuuaaascsa	1879	VPUsGfsuudTadAaccagaAfgAfucaggsasa	1930
AD-1231473	usgsua (Chd) aGfuAfAfGfugauaacasgsa	1880	VPUsCfsugdTudAucacuuAfcUfguacasasg	1931
AD-1231474	ususccugAfuCfUfUfcugg (Uhd) cuasasa	1881	VPUsUfsuadGa (Cgn) cagaagAfuCfaggaascu	1932
AD-1231475	usasuguaCfuCfAfUfucgu (Uhd) ucgsgsa	1882	VPUsCfscgaAfacgaaugAfgUfacauasasg	1361
AD-1231476	ascsguua (Chd) aGfUfCfuaaaauguscsa	1883	VPUsGfsacaUfuuuagacUfgUfacagusgsg	12
AD-1231477	cscscaugUfgAfUfUfuua (Uhd) agcsusa	1884	VPUsAfsgcuAfuuuuuuauCfaCfaugggsgsa	1436
AD-1231478	ususcgugGfuAfUfUfcuua (Chd) uagsusa	1885	VPUsAfscudAgdTaaauAfcCfacgaasasg	1933
AD-1231479	uscsuuuc (Uhd) GfgUfCfUfaauaugacsusa	1886	VPUsAfsgudTcdAuuuagaCfcAfgaagasc	1934
AD-1231480	gsusacugCfuGfCfAfauau (Uhd) guusasa	1887	VPUsUfsaacAfauuuugcAfgCfaguacsgsc	1375
AD-1231481	ususuaa (Uhd) CfufCfAfCfauagcaauscsa	891	VPUsGfsaudTg (Cgn) uaugugAfgAfuuuaasgsu	1935
AD-1231482	usascaa (Chd) UfuCfCfUfcaaggaaacsasa	872	VPUsUfsugdTc (Cgn) uuaggAfaGfuguugasgsc	1936
AD-1231483	csusgcuaUfuCfCfUfuguu (Uhd) uaasusa	1888	VPUsAfsuuuAfaacaaggAfaUfagcagsasa	1406
AD-1231484	csuscacaUfaGfCfAfauu (Uhd) uaasusa	1889	VPUsAfsuuuAfaaguugcUfaUfugugagsasu	1429
AD-1231485	uscsugug (Chd) UfaCfAfAfuuucucasasa	1890	VPUsUfsugdAgdAaauugUfaGfcacgasusu	1937
AD-1231486	csasgaugGfuAfCfAfcuua (Uhd) gaususa	1891	VPUsAfsaucAfuaaguguAfcCfaucugsusu	1320
AD-1231487	usasacaaUfgUfUfGfcuuu (Uhd) caasasa	1892	VPUsUfsuugAfaaagcaaCfaUfuguuasgsu	10
AD-1231488	usasauagUfuAfAfUfagcg (Uhd) acususa	1893	VPUsAfsaguAfccgcuuuAfaCfauuuasasc	1367
AD-1231489	csasua (Chd) aAfuGfCfUfaguuaacsasa	1894	VPUsUfsguuUfaacuagcAfuUfuguugususu	1318
AD-1231490	ususuu (Chd) aAfaCfUfGfucuaacccsgsa	1895	VPUsCfsuggUfuugacagUfuUfgaaaasgsc	1296
AD-1231491	csusuaug (Uhd) aCfUfCfauuucguuuscsa	1896	VPUsGfsaaaCfgaauugAfaCfauuaagsusu	1359
AD-1231492	gsusugugUfaCfAfCfacau (Uhd) ggusasa	1897	VPUsUfsacdCadAugugugUfaCfacaacsasu	1938
AD-1231493	asascuuaUfgUfAfCfucau (Uhd) cgususa	1898	VPUsAfsacgAfaugaguaCfaUfaaguuscsq	1357
AD-1231494	csusgcugCfaAfUfAfuuugu (Uhd) aacsgsa	1899	VPUsCfsguuAfacaauauUfgCfagcagsusa	1376
AD-1231495	ususcuu (Chd) GfuAfAfGfaacgguaasusa	737	VPUsAfsuudAc (Cgn) guucuuAfcGfaagaasgsa	1939
AD-1231496	csgsugc (Uhd) AfcAfAfCfuuucaasgsa	1900	VPUsCfsuudGadAgaaguuGfuAfcacgsasu	1940
AD-1231497	usgsaaa (Uhd) UfgUfUfGfacaauugugsasa	1901	VPUsUfscadCadAugucaaCfaAfuuuasgsc	1941
AD-1231498	ascsaau (Uhd) uGfCfUfuuuuaacsusa	1902	VPUsAfsgudTudAaaaagcAfaCfauugususa	1942
AD-1231499	asasauugUfuGfAfCfacua (Uhd) gagsusa	1903	VPUsAfscudCadTagugucAfaCfaauuuscsa	1943
AD-1231500	uscsuuucGfaAfGfAfacgg (Uhd) aausasa	1904	VPUsUfsaudTa (Cgn) cguucuuUfaCfagaagasasg	1944
AD-1231501	csusgcaaUfaUfUfGfuua (Chd) gugsasa	1905	VPUsUfscacGfuuuacaaUfaUfugcagcsa	1379
AD-1231502	gscsugaaUfuUfGfUfugaua (Chd) ugsusa	1906	VPUsAfscadGudAucaacaAfuUfucagcsasg	1945
AD-1231503	csusgc (Uhd) gAfaAfUfUfuguugacacsusa	1907	VPUsAfsgudGu (Cgn) aacaauUfuCfagcagsgsa	1946
AD-1231504	ususgugaUfgAfUfGfaaua (Uhd) uucsasa	1908	VPUsUfsgaaAfuaaucauCfaUfcacaacsca	1293

TABLE 5-continued

Modified Sense and Antisense Strand dsRNA Sequences Targeting COVID-19				
Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:
AD-1231505	usgsuugaCfaCfUfGfugaa (Uhd) gcususa	1909	VPUsAfsagdCadTucacagUfgUfcacatasu	1947
AD-1231506	csasgguaCfUfUfAfauag (Uhd) uaasusa	1910	VPUsAfsuuuAfcuuuuuaCfUfaccugsusc	1365
AD-1231507	ascscuuugCfcAfAfAfaggu (Uhd) ucusasa	1911	VPUsUfsagdAadAccuuuuGfgCfaaugususg	1948
AD-1231508	gscsug (Chd) aAfuAfUfUfguuaacgusgsa	1912	VPUsCfsacgUfuaacaauAfuUfgcagcsasg	1378
AD-1231509	csasca (Uhd) aGfcAfAfUfcuuuuaucsasa	1913	VPUsUfsagdUfaaagauuGfcUfaugugsasg	1431
AD-1231510	asasugug (Uhd) gAfUfAfucagacaacsca	1914	VPUsGfsuudGu (Cgn) ugauauCfaCfacauusgsu	1949
AD-1231511	gsusucc (Uhd) GfaUfCfUfucuggucusasa	852	VPUsUfsagdAc (Cgn) agaagaUfcAfggaaucsusc	1950
AD-1231512	ususgccaAfaAfGfGfcuuc (Uhd) acgscsa	1915	VPUsGfscguAfgaagccuUfuUfggcaasusg	1414
AD-1231513	ususcug (Chd) UfaAfUfCfuuuugucusasa	1916	VPUsUfsagdCadAcaagauUfaGfcagaasgsc	1951
AD-1231514	ascscuagUfaAfUfAfgguu (Uhd) ccusasa	1917	VPUsUfsaggAfaaccuuauUfaCfuaggususc	1388
AD-1231515	csusgcuaAfuCfUfUfgcug (Chd) uacsasa	1918	VPUsAfsgudAg (Cgn) agcaagAfuUfagcagsasa	1952
AD-1231516	csascucaUfaAfAfGfucug (Uhd) guusgsa	1919	VPUsCfsaacAfcagacuuUfaUfgagugsusc	1315
AD-1231517	csasuaggAfaUfAfAfaauc (Uhd) ucusasa	1920	VPUsUfsagaAfgauuuuaUfuCfcuaugsgsa	1346
AD-1231518	uscsuaca (Chd) aAfAfCfucuuuaagsasa	1921	VPUsUfscuuUfaagaguuUfgUfguagasusa	1275
AD-1231519	asuscuugUfuUfUfCfucua (Uhd) ucusasa	1922	VPUsUfsugdAadTagagaaAfaCfaagausgsa	1953
AD-1231520	csasgucaUfaAfUfCfuua (Uhd) uaasasa	1923	VPUsUfsuudAadTauagauUfaUfgacugsusg	1954
AD-1231521	usgsuuaCfaCfUfAfauaa (Uhd) aaasasa	1924	VPUsUfsuudTadTuauuagUfgUfuaccascsa	1955

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TABLE 6

Single Dose In Vitro Screens in Cos-7 Cells					Single Dose In Vitro Screens in Cos-7 Cells					
Duplex ID	% of Message Remaining- 10 nM Concatenate-02	STDEV	% of Message Remaining- 10 nM Concatenate-21	STDEV	Duplex ID	% of Message Remaining- 10 nM Concatenate-02	STDEV	% of Message Remaining- 10 nM Concatenate-21	STDEV	
AD-1184048.1	2.63	0.37	10.90	2.58	40	AD-1184230.1	7.85	0.71	11.08	1.15
AD-1184130.1	4.52	0.51	15.30	3.51	45	AD-1184099.1	7.94	0.91	1.24	0.61
AD-1184064.1	5.13	2.78	18.41	12.53	AD-1184189.1	7.94	0.98	6.87	1.66	
AD-1184050.1	5.58	2.20	14.85	7.91	AD-1184152.1	8.01	0.63	45.16	29.64	
AD-1184202.1	5.58	2.27	7.20	2.28	AD-1184080.1	8.03	3.13	20.44	9.44	
AD-1184100.1	6.41	1.86	1.63	1.97	AD-1184261.1	8.04	0.33	10.46	5.96	
AD-1184098.1	6.46	0.74	1.51	1.09	AD-1184138.1	8.11	1.81	34.34	17.00	
AD-1184123.1	6.48	0.59	19.79	1.49	AD-1184221.1	8.28	0.89	14.34	3.37	
AD-1184223.1	6.63	0.25	8.39	1.65	50 AD-1184284.1	8.28	0.72	0.55	0.15	
AD-1184219.1	6.66	0.52	6.38	2.51	AD-1184144.1	8.31	0.21	19.46	14.43	
AD-1184062.1	6.67	4.16	4.12	0.32	AD-1184272.1	8.43	0.68	2.04	0.80	
AD-1184070.1	6.72	0.66	16.86	4.27	AD-1184285.1	8.55	2.60	N/A	N/A	
AD-1184061.1	6.78	0.65	10.62	2.56	AD-1184167.1	8.55	0.22	26.83	12.68	
AD-1184216.1	6.82	0.44	11.90	0.70	AD-1184110.1	8.57	0.27	32.02	18.77	
AD-1184255.1	6.88	0.67	2.84	0.96	55 AD-1184113.1	8.67	0.36	42.10	37.37	
AD-1184237.1	6.90	0.16	5.26	0.45	AD-1184141.1	8.67	0.76	32.39	13.05	
AD-1184218.1	7.05	0.15	10.23	0.16	AD-1184226.1	8.70	0.62	10.59	3.78	
AD-1184215.1	7.15	0.17	15.26	3.28	AD-1184077.1	8.72	0.18	16.74	1.13	
AD-1184137.1	7.17	1.30	18.05	4.06	AD-1184175.1	8.79	0.38	17.35	1.43	
AD-1184271.1	7.19	0.52	4.76	2.43	AD-1184053.1	8.85	1.05	26.88	9.12	
AD-1184166.1	7.57	0.13	N/A	N/A	60 AD-1184114.1	8.96	0.95	35.26	15.77	
AD-1184291.1	7.60	0.68	3.12	1.19	AD-1184091.1	9.06	0.96	35.70	15.75	
AD-1184256.1	7.68	2.71	4.95	0.80	AD-1184228.1	9.10	1.23	9.24	4.10	
AD-1184260.1	7.69	1.24	10.95	3.08	AD-1184150.1	9.15	2.15	11.22	2.79	
AD-1184051.1	7.71	0.32	17.00	2.76	AD-1184222.1	9.27	1.29	11.23	2.32	
AD-1184063.1	7.71	3.85	10.87	3.90	AD-1184173.1	9.32	3.48	12.47	5.60	
AD-1184213.1	7.71	0.22	14.68	9.77	65 AD-1184040.1	9.46	3.27	53.64	29.25	
AD-1184124.1	7.85	1.08	18.09	1.81	AD-1184125.1	9.62	2.10	27.24	1.20	

TABLE 6-continued





TABLE 7-continued

Duplex ID	Single Dose In Vitro Screens in Cos-7 Cells					
	10 nM Avg	10 nM STDEV	1 nM Avg	1 nM STDEV	0.1 nM Avg	0.1 nM STDEV
AD-1231477.1	13.7	7.4	36.0	9.5	104.2	12.0
AD-1231515.1	51.9	6.6	79.3	15.4	113.3	24.4
AD-1231503.1	58.9	14.7	91.2	11.9	139.0	7.0
AD-1231479.1	15.4	3.7	50.2	13.1	123.5	24.1
AD-1231498.1	15.5	9.0	17.0	2.8	78.8	22.3
AD-1231483.1	16.7	3.0	31.0	11.8	78.9	2.7
AD-1231484.1	14.7	7.3	28.2	4.7	80.1	19.1
AD-1231506.1	45.8	13.2	52.3	5.1	112.1	14.4
AD-1231495.1	20.4	8.1	51.1	6.8	98.9	25.0
AD-1231516.1	109.2	32.1	129.8	28.9	102.8	22.3
AD-1231508.1	30.6	5.6	65.3	8.9	121.5	8.5
AD-1231475.1	8.7	4.3	14.8	4.0	70.9	12.4
AD-1231490.1	23.2	19.6	32.0	5.9	86.5	11.7
AD-1231494.1	42.3	9.1	89.6	9.6	128.1	16.4
AD-1231473.1	12.1	5.5	35.2	4.6	108.2	18.5
AD-1231496.1	8.5	3.6	51.5	10.9	112.9	11.9
AD-1231491.1	33.4	26.2	38.9	17.4	88.1	4.4
AD-1231469.1	46.2	8.2	37.9	5.2	82.2	14.7
AD-1231476.1	18.3	17.0	34.7	7.4	89.7	21.5
AD-1231481.1	10.6	1.0	36.2	6.6	107.7	6.3
AD-1231512.1	61.1	37.0	63.7	9.3	94.9	11.2
AD-1231471.1	12.1	5.3	26.7	7.9	99.6	24.4
AD-1231510.1	12.5	5.9	49.9	1.8	106.0	19.4
AD-1231472.1	11.3	6.2	29.0	7.1	80.3	19.1
AD-1231480.1	49.7	25.7	73.5	12.6	107.0	19.1
AD-1231492.1	36.8	24.7	73.8	15.3	105.4	40.6
AD-1231507.1	61.0	22.1	73.5	1.5	100.8	10.4
AD-1231517.1	87.4	18.0	99.2	25.5	109.4	25.0
AD-1231511.1	13.7	4.8	39.3	10.6	108.1	7.9
AD-1231513.1	60.8	12.9	70.9	11.0	98.8	13.1
AD-1231514.1	57.8	18.2	86.1	15.6	91.7	11.5
AD-1231468.1	8.9	0.1	46.8	18.4	93.5	19.1
AD-1231500.1	43.4	16.2	50.8	7.8	85.0	16.7
AD-1231497.1	15.1	13.6	24.9	2.8	80.1	18.9
AD-1231501.1	20.7	7.8	65.5	10.7	122.5	5.7
AD-1231467.1	35.9	8.6	62.0	15.1	102.7	10.7
AD-1231518.1	126.4	19.5	131.1	15.7	141.9	22.7
AD-1231504.1	9.6	6.0	29.1	12.9	89.7	16.4
AD-1231509.1	28.9	25.3	44.1	13.6	87.6	13.3
AD-1231482.1	28.0	10.4	54.0	3.5	136.1	31.3
AD-1231489.1	12.9	3.0	21.4	2.0	90.5	9.6
AD-1231474.1	59.0	26.0	66.1	17.5	86.9	19.8
AD-1231519.1	85.2	19.5	107.1	12.6	116.2	24.4
AD-1231485.1	22.8	17.8	42.3	3.9	80.5	21.0
AD-1231520.1	111.6	15.3	103.8	24.6	99.7	15.5
AD-1231487.1	22.5	9.9	51.5	14.2	96.5	17.8
AD-1231521.1	107.1	20.2	100.7	30.3	115.6	24.2

## Example 3. In Vivo Screening of dsRNA Duplexes in Mice

siRNA molecules targeting the coronavirus genome, identified from the above in vitro studies, are evaluated in vivo.

Mice previously infected with a coronavirus, e.g., severe acute respiratory syndrome-2 (SARS-2)-CoV-2, are administered, via pulmonary system or subcutaneous delivery, a dsRNA molecule at a dose of 0.1 mg/kg, 1 mg/kg or 10 mg/kg. Uptake of dsRNA in bronchioles and alveoli and expression level of target gene in whole lung of treated mice are measured. Expression level of coronavirus target genes are further evaluated by in situ hybridization in mice bronchus and bronchiole.

## Example 4. In Vitro SARS-CoV-2 Replication Screening of siRNA Duplexes

## In Vitro screening of siRNAs in SARS-CoV-2 Infection Assay

Vero E6 cells cultured in DMEM supplemented with 10% FBS (VWR) and 1× Penicillin/Streptomycin (Thermo Fisher Scientific) were reverse transfected with siRNAs in white 96-well plates using RNAiMax transfection reagent (Thermo Fisher Scientific) according to the manufacturer's instructions. Twenty-four hours later, cells were infected with SARS-CoV-2 (isolate USA-WA1/2020, passage 2, MOI 0.001) in a BSL-3 facility. The viral inoculum was removed after 4 hours, cells were washed with phosphate-buffered saline (PBS, pH 7.4) and media was replaced. At 48 hours post-infection, the cell supernatant was collected for RNA extraction and RT-qPCR analysis. The cells were fixed for in-cell ELISA analysis (below).

## Quantification of Extracellular SARS-CoV-2 Genomes by RT-qPCR

Viral RNA was extracted from the cell culture supernatant using the NucleoSpin 96 Virus kit (Macherey-Nagel). Quantification of viral genomes was performed using the Luna Universal Probe One-Step RT-qPCR Kit (New England Biolabs) with a primer/probeset binding in the M region (forward: CACTATTCTGACCAGACCGCTTCT (SEQ ID NO: 1956), reverse: CCTGCTACACGCTGCGAAG (SEQ ID NO: 1957), probe: TCACGAACGCTTCTT (SEQ ID NO: 1958))). A standard curve of defined dilutions of a synthetic SARS-CoV-2 RNA (Twist Bioscience) was used for normalization.

## Quantification of Intracellular Viral Nucleocapsid Protein by In-Cell ELISA

Cells were fixed with 4% paraformaldehyde for 30 minutes, followed by two PBS (pH 7.4) washes and permeabilization with 0.125% Triton X-100 in PBS for 30 min. After blocking in 2% milk powder/PBS for 30 minutes, cells were incubated with a primary antibody targeting SARS-CoV-2 nucleocapsid protein (Sino Biological, cat. 40143-R001) at a 1:3000 dilution for 1 hour. After washing and incubation with a secondary HRP-labeled antibody for 1 hour, Super-Signal ELISA Pico Chemiluminescent Substrate (Thermo Fisher Scientific) was added to the cells and luminescence signal was read on an Envision plate reader (Perkin-Elmer). After subtraction of background (uninfected) controls, all signals were normalized to the mock transfected controls.

## Results

The RT-qPCR assay quantifying viral genome copy number based on the M (membrane) ORF, identified 47 siRNAs capable of reducing viral RNA  $\geq 2\log_{10}$ s at 10 nM, with 10 siRNAs reducing viral RNA  $\geq 2\log_{10}$ s at 0.1 nM. Reduction in viral RNA correlated with reduction in intracellular nucleocapsid protein. A total of 11 siRNAs had >80% reduction of viral nucleocapsid at a 0.1 nM dose. As expected, the control siRNA (targeting firefly luciferase transcripts) had no significant effect on SARS-CoV2 viral replication. The results of these assays are provided in Table 8 and FIG. 3.

TABLE 8

Single Dose In Vitro SARS-CoV-2 Replication Screens							
Duplex ID	RT-qPCR (% mock transfected)			in-cell ELISA (% mock transfected)			
	10 nM	1 nM	0.1 nM	10 nM	1 nM	0.1 nM	Target
AD-1184106.1	0.12	0.21	3.46	8.5	8.6	24.0	
AD-1184102.1	0.13	0.17	2.65	8.5	8.4	25.0	
AD-1184136.1	0.17	41.04	25.26	9.6	77.7	54.9	
AD-1184151.1	0.05	0.10	16.96	10.5	10.0	33.8	
AD-1184130.1	0.14	0.05	36.95	11.0	9.5	63.4	
AD-1184137.1	0.06	0.04	0.03	10.2	10.6	10.2	ORF1ab
AD-1184144.1	0.30	0.26	66.10	9.9	9.4	118.1	
AD-1184189.1	0.05	0.06	33.02	7.7	7.6	84.5	
AD-1184123.1	0.13	0.80	81.37	6.3	13.2	95.6	
AD-1184168.1	0.08	0.08	33.20	8.4	7.5	70.2	
AD-1184124.1	0.06	0.07	174.39	9.0	9.2	110.3	
AD-1184131.1	18.05	45.93	48.79	47.1	78.8	81.0	(-)strand
AD-1184147.1	5.74	0.03	0.04	26.7	10.2	10.2	ORF1ab
AD-1184170.1	26.55	38.87	150.04	74.2	66.1	123.1	(-)strand
AD-1184199.1	12.44	38.26	185.16	47.2	91.5	119.0	(-)strand
AD-1184126.1	8.75	103.16	32.55	42.9	120.5	80.3	(-)strand
AD-1184148.1	0.08	0.08	27.76	8.8	9.4	74.0	
AD-1184200.1	15.87	75.29	120.16	51.7	101.5	105.0	(-)strand
AD-1184128.1	26.30	93.02	225.36	71.9	94.9	112.0	(-)strand
AD-1184150.1	0.05	0.07	0.20	10.3	10.2	10.0	ORF1ab
AD-1184173.1	0.95	3.84	166.25	8.9	9.4	119.1	
AD-1184202.1	0.74	30.76	51.06	10.7	61.0	87.7	
AD-1184210.1	0.09	0.10	2.41	9.7	8.1	25.5	ORF3AE
AD-1184218.1	0.07	0.71	79.43	11.9	15.5	98.8	
AD-1184232.1	0.29	0.10	22.09	9.1	10.5	46.1	
siLuc	24.50	79.00	351.04	73.3	98.0	131.0	
mock tr	116.89	35.49	79.73	102.3	72.8	116.8	
mock tr	118.33	83.41	166.15	118.5	81.5	108.1	
AD-1184255.1	5.15	33.33	50.18	47.0	87.9	88.6	
AD-1184270.1	0.23	2.32	0.03	9.1	22.6	88.9	N
AD-1184211.1	0.09	0.39	28.21	10.1	13.9	89.8	
AD-1184219.1	12.94	1.54	75.97	82.3	19.9	96.7	
AD-1184226.1	0.06	0.60	22.51	9.3	14.4	81.1	
AD-1184233.1	1.04	5.11	0.72	37.5	27.9	10.6	E
AD-1184256.1	89.78	45.86	31.97	148.0	76.4	83.1	
AD-1184271.1	0.03	0.02	1.26	7.5	8.0	22.5	N
AD-1184286.1	0.26	2.20	38.59	9.3	19.5	86.2	
AD-1184212.1	0.07	0.57	3.56	8.5	14.9	22.1	ORF3AE
AD-1184234.1	0.18	1.01	27.60	12.9	19.2	72.6	
AD-1184213.1	0.04	0.04	10.47	7.4	8.8	55.0	
AD-1184220.1	0.06	1.47	35.19	8.7	17.9	70.4	
AD-1184227.1	0.10	1.02	29.57	7.8	13.4	80.7	
AD-1184235.1	0.16	0.09	110.96	9.3	8.6	108.8	
AD-1184272.1	0.04	0.03	4.82	7.7	7.6	50.5	
AD-1184221.1	0.06	0.09	23.30	12.3	9.2	68.5	
AD-1184228.1	0.10	0.56	1.75	7.3	15.6	15.4	E
AD-1184259.1	11.19	11.00	43.81	50.6	45.4	92.3	
AD-1184215.1	0.09	0.81	15.71	9.8	24.5	59.9	
AD-1184229.1	0.07	0.20	8.25	9.2	9.6	65.3	
AD-1184237.1	0.04	0.07	37.98	8.5	8.8	88.0	
AD-1184252.1	1.63	9.54	45.25	38.0	82.0	111.9	
AD-1184260.1	53.62	25.57	6.91	117.5	65.9	119.8	
AD-1184282.1	0.10	0.04	48.94	8.9	6.9	99.7	
siLuc	6.59	8.32	72.62	45.3	32.0	104.8	
mock tr	1.98	50.59	65.01	12.4	65.0	99.3	
mock tr	132.78	85.04	166.58	114.7	103.5	117.6	
AD-1184216.1	20.99	0.27	9.84	52.2	7.4	48.0	
AD-1184223.1	0.38	0.02	16.14	8.4	10.1	32.1	E
AD-1184261.1	323.03	96.87	107.35	178.0	98.1	92.5	
AD-1184268.1	88.37	no result	95.18	112.9	31.9	83.7	
AD-1184283.1	0.09	3.19	99.85	8.3	17.7	93.3	
AD-1184209.1	15.92	60.57	138.32	78.1	92.9	92.0	
AD-1184217.1	0.18	1.82	38.03	12.6	14.0	79.4	
AD-1184224.1	0.52	2.86	257.68	7.6	20.8	95.8	
AD-1184254.1	156.78	31.46	109.25	121.2	45.3	83.7	
AD-1184269.1	1.67	3.94	31.99	16.6	26.5	71.1	
AD-1184284.1	0.36	0.07	25.81	7.1	7.1	42.5	
AD-1231467.1	0.19	0.12	21.93	12.7	7.7	52.6	
AD-1231475.1	0.06	no result	37.33	8.4	13.3	73.6	
AD-1231482.1	0.11	no result	44.60	10.3	9.8	78.7	
AD-1231490.1	0.14	0.07	0.06	7.6	7.5	6.3	
AD-1231512.1	0.23	4.74	241.32	8.5	25.2	90.0	
AD-1231520.1	113.26	146.18	54.93	107.1	90.5	58.9	

TABLE 8-continued

Duplex ID	Single Dose In Vitro SARS-CoV-2 Replication Screens						
	RT-qPCR (% mock transfected)			in-cell ELISA (% mock transfected)			
	10 nM	1 nM	0.1 nM	10 nM	1 nM	0.1 nM	Target
AD-1231468.1	1.29	18.06	161.56	23.3	56.2	84.8	
AD-1231476.1	0.22	0.23	75.68	8.8	7.6	57.7	
AD-1231491.1	0.39	0.92	16.39	8.9	10.2	40.8	
AD-1231506.1	0.45	1.96	194.85	13.0	16.6	104.6	
AD-1231513.1	0.10	1.12	1.76	8.5	8.7	9.4	
AD-1231521.1	130.20	106.72	399.69	114.6	85.9	101.9	
AD-1231469.1	12.77	21.10	66.09	50.1	44.0	63.3	
AD-1231484.1	0.08	0.11	72.20	7.2	9.1	107.4	
siLuc	55.81	27.22	143.92	117.5	52.2	95.6	
mock tr	102.03	78.63	199.25	88.9	95.0	126.0	
mock tr	66.37	55.42	98.31	80.1	89.1	120.9	
AD-1231492.1	0.28	0.78	70.62	9.4	11.0	86.6	
AD-1231514.1	0.01	132.16	79.46	39.0	116.7	84.5	
AD-1231485.1	0.16	no result	0.50	11.3	11.5	9.4	
AD-1231500.1	56.30	85.87	10.97	108.2	108.1	42.2	
AD-1231507.1	0.62	0.23	2.89	8.8	9.5	20.2	
AD-1231471.1	0.13	0.22	0.16	8.1	8.0	8.3	
AD-1231494.1	0.14	0.17	1.98	10.1	11.0	100.5	
AD-1231501.1	0.11	no result	53.02	11.7	26.2	72.7	
AD-1231508.1	0.25	2.32	no result	9.5	21.7	58.9	
AD-1231516.1	32.57	50.07	119.43	50.4	77.9	86.8	
AD-1231472.1	0.23	1.00	53.86	10.2	17.6	81.8	
AD-1231480.1	0.18	12.95	52.14	12.2	60.2	90.8	
AD-1231487.1	0.13	0.14	8.03	8.4	8.1	24.8	
AD-1231495.1	10.79	no result	109.05	44.8	8.1	94.1	
AD-1231509.1	0.58	2.36	46.14	9.7	16.1	61.0	
AD-1231517.1	50.31	51.27	42.30	105.6	82.7	69.1	
AD-1231473.1	0.46	20.26	55.45	19.6	48.4	73.3	
AD-1231496.1	0.23	0.19	0.85	8.4	9.2	10.8	
AD-1231510.1	0.15	12.10	57.03	10.3	41.1	70.3	
AD-1231518.1	49.92	92.40	57.36	122.1	103.1	69.1	
AD-1231474.1	no result	59.84	42.40	105.4	70.6	88.3	
AD-1231497.1	0.19	0.24	0.16	5.4	7.7	8.5	
AD-1231504.1	1.71	0.15	41.15	8.3	6.4	60.3	
AD-1231511.1	no result	0.48	12.27	8.6	9.0	27.4	
AD-1231519.1	23.98	24.46	113.17	76.6	78.7	124.1	
siLuc	35.83	46.93	121.44	89.0	74.5	115.7	
mock tr	112.40	0.16	60.57	84.8	4.8	79.7	
mock tr	116.06	99.56	111.85	107.6	105.2	117.5	

#### Example 5. Evaluation of siRNA Duplex Against Resistance Mutants

Because of their high mutation rates, viruses, such as SARS-CoV-2, have the potential to elude host defense systems as well as antiviral drugs and vaccines.

Accordingly, in order to identify duplexes, or combinations or duplexes, that are able to evade or delay the emergence of antiviral resistance, a resistance selection analysis was performed and, subsequently, agents targeting the coronavirus genome were assessed for their ability to inhibit expression and inhibit infection of host cells and infectious virus particles in a focus-forming assay using these resistant cells.

The materials and methods for this example are described below.

##### Resistance Selection Using Fixed Concentrations

The selection of variants in the presence of fixed concentrations of AD-1184150 or a combination of AD-1184150 with AD-1184137 was conducted in VeroE6 cells cultured in DMEM supplemented with 10% FBS (VWR) and 1× Penicillin/Streptomycin (Thermo Fisher Scientific).  $1.2 \times 10^5$  VeroE6 cells per well in a 24-well plate were reverse transfected with 5×, 10× or 20× EC<sub>50</sub> of AD-1184150 (330 pM, 660 pM or 1320 pM, respectively) or of an equimolar mixture of AD-1184150 and AD-1184137 at the same com-

bined total concentrations. As non-targeting control, VeroE6 cells were reverse transfected with the highest concentration (1320 pM) of an siRNA targeting the luciferase gene. All transfections used RNAiMax transfection reagent (Thermo Fisher Scientific) according to the manufacturer's instructions. Six hours post reverse transfection, cells were incubated with SARS-CoV-2 (isolate USA-WA1/2020, passage 2) at an MOI (multiplicity of infection) of 0.01 in infection medium (DMEM, 10% FBS) for 1 hour at 37° C. After viral adsorption, cells were washed with DMEM and overlaid with infection media. For each condition, three independent wells were transfected and infected, and the supernatants were pooled together at the time of harvest. Infected cells were monitored visually for cytopathic effect (CPE) daily. When the cells in the luciferase-targeting control wells exhibited >50% CPE, the culture supernatants were harvested, diluted 1:10 and added to fresh VeroE6 cells in 24-well plates that had been reverse-transfected with the equivalent amounts of siRNA(s) as used for the initial passage. Selection continued for a total of 5 passages. At each passage, supernatant was aliquoted and frozen at -80° C for further analyses.

##### Determination of Viral Titer by Focus-Forming Assay

Viral titers were determined using a focus-forming assay (FFA) on VeroE6 cells. One day prior to infection,  $1.5 \times 10^4$  VeroE6 cells were plated in black-walled, clear bottomed

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96-well plates. The next day, undiluted or 4-point 10-fold serially diluted virus samples using 10% FBS-containing media were adsorbed onto VeroE6 cells for one hour at 37° C. The cells were washed once and overlaid with 1% methylcellulose (Sigma-Aldrich) in serum-containing medium. At 24 hours post-infection, the methylcellulose overlay was removed and cells were washed with PBS. Cells were fixed with 4% PFA, incubated for 30 minutes at room temperature, then washed with PBS to remove residual PFA. The cells were permeabilized with 100 µL of 0.25% Triton X-100 (Sigma-Aldrich) in PBS for 30 minutes at room temperature. The Triton X-100 was removed, cells were washed twice with PBS, and incubated with 50 µL of SARS-CoV-2 nucleocapsid (N) antibody (Sino Biological) at 1:2,000 in blocking buffer (2% milk powder/PBS) for 1 hour at room temperature. Plates were washed three times with PBS and then incubated for 1 hour at room temperature with 50 µL/well of goat anti-rabbit-Alexa647 (Thermo Fisher Scientific) secondary antibody at 1:1,000 in blocking buffer along with 1 µg/ml Hoechst33342 (Thermo Fisher Scientific). After washing three times with PBS, plates were imaged on a Cyvation5 (BioTek) plate reader (12 images at 4x magnification) with fluorescence detected in DAPI (377, 447 nm) and Cy5 (628,685 nm) channels. Nucleocapsid-positive foci were counted from images and used to determine focus-forming units/mL supernatant (FFU/mL).

#### Evaluation of Antiviral Activity Against Selected Virus

Cell supernatants from viral passages containing detectable virus as determined by FFA were evaluated for a shift in EC<sub>50</sub> values in an siRNA antiviral activity assay. 7-point 5-fold serial dilutions of AD-1184150 and AD-1184137 were prepared in PBS and VeroE6 cells were reverse transfected in 96-well plates with each dilution in duplicates (range: 41250 to 3 pM final concentration). Twenty-four hours later, cells were infected with 20 FFUs of the virus-containing cell supernatants generated during passaging. The viral inoculum was removed after 1 hour and media was replaced. At 24 hours post-infection, the cells were fixed with 4% PFA and viral nucleocapsid protein was immunostained as described above. For automated image acquisition and quantification, cells were imaged on a Cyvation 5 Cell Imaging reader with 12 images per well to cover the complete well. Nuclei and AlexaFluor647-positive cells were counted using the manufacturer's provided software. After subtraction of background (uninfected) controls, all signals were normalized to the mock transfected controls.

#### Sequencing of siRNA Binding Sites within the SARS-CoV-2 Genome

To isolate nucleic acid from the supernatant of viral passages, 300 µL of cell supernatant was added to 900 µL of Trizol and stored at -80° C. for further analysis. Trizol collected samples were subjected to RNA isolation using PureLink RNA Mini Kit with the incorporation of on-column PureLink DNase Treatment, following manufacturer's instructions. Reverse transcription reactions were performed with 6 µL of purified RNA and random hexamer primers using the NEB ProtoScript II First Strand cDNA Synthesis kit, according to manufacturer's instructions. The resulting cDNA was used as a template for PCR amplification of the siRNA binding sites, two primer pairs per site, using KapaBiosystems polymerase (KAPA HiFi HotStart ReadyMix) with primers, 5'-acgctgcctctggtaatc-3' (SEQ ID NO: 1959) plus 5'-agaaacccttagacacagc-3' (SEQ ID NO:

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1960), and 5'-ctagataaacgcactacgtg-3' (SEQ ID NO: 1961) and 5'-cctgagcaagaagaagtg-3' (SEQ ID NO: 1962) for the AD-1184150 binding site, and 5'-agatgcctcaaactcaac-3' (SEQ ID NO: 1963) plus 5'-ttctactctgagttgtgc-3' (SEQ ID NO: 1964), and 5'-tgggtggcaaaccttgtate-3' (SEQ ID NO: 1965) plus 5'-tgtgttaactggcacatcg-3' (SEQ ID NO: 1966) for the AD-1184137 binding site. Each PCR with a primer pair was carried out independently, then PCR products from each treatment were pooled for purification and subsequent library preparation. Amplification conditions included an initial 3 minutes at 95° C., followed by 24 cycles with 20 seconds at 98° C., 15 seconds at 60° C. and 72° C. for 15 seconds, with a final 1 minute at 72° C. Pooled PCR products were purified using AMPure XP beads following manufacturer's instructions. The size of the amplicon was confirmed by analyzing 2 µL of PCR products using the Agilent D1000 ScreenTape System. Products were quantified by analyzing 1 µL with the Quant-iT dsDNA High-Sensitivity Assay Kit. Fifty ng of purified PCR product was used as input for library construction using the NEBNext Ultra II DNA Library Prep kit following manufacturer's instructions. NEBNext Multiplex Oligos for Illumina Dual Index Primer Set 1 was used for library construction, with a total of 4 PCR cycles. Libraries size was determined using the Agilent D1000 ScreenTape System and quantified with the Quant-iT dsDNA High-Sensitivity Assay Kit. Equal amounts of each library were pooled together for multiplexing and 'Protocol A: Standard Normalization Method' of the Illumina library preparation guide was used to prepare 8 pM final multiplexed library with 1% PhiX spike-in for sequencing. The MiSeq Reagent Kit v3 (600-cycle) was used for sequencing the libraries on the Illumina MiSeq platform, with 150 cycles for Read 1, 150 cycles for Read 2, 8 cycles for Index 1, and 8 cycles for Index 2.

#### Sequence Analysis of siRNA Binding Sites

Paired-end reads were trimmed to 2×150 upon inspection with FastQC to retain segments of high quality (>Q30). Illumina adapters were clipped using Trimmomatic. Read alignment to SARS-CoV-2 Wuhan-Hu-1 reference (NCBI: NC\_045512.2) was performed with Burrows-Wheeler Aligner (BWA). Variants were called with LoFreq\* upon indel realignment and base quality recalibration, using a frequency threshold of 1%. Primers were excluded from variant calling. A consensus sequence was generated, mapped back to reference sequence coordinates and used to align reads a second time. The incorporation of variants from the first mapping iteration into a consensus sequence facilitates read alignment in case of mismatches with the reference. Variants were called again against the reference sequence from reads mapped to the consensus sequence. A third iteration of consensus generation read alignment and variant calling was performed. The variant call set from this last iteration was retained as final. Nucleotide variants were annotated with SnpEff to generate amino acid variants. Extensive QC's were performed at read, alignment and variant level using FastQC, samtools, picard, mosdepth, bcftools and MultiQC. An end-to-end workflow was automated using NextFlow. All programs are available through the Bioconda Initiative ([bioconda.github.io](https://bioconda.github.io)).

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Quantification of Extracellular SARS-CoV-2 Genomes by RT-qPCR

Viral RNA was extracted from the cell culture supernatant using the NucleoSpin 96 Virus kit (Macherey-Nagel). Quantification of viral genomes was performed using the Luna Universal Probe One-Step RT-qPCR Kit (New England Biolabs) with a primer/probeset binding in the orflab region (forward: CCCTGTGGGTTTACACTTAA (SEQ ID NO: 1967), reverse: ACGATTGTGCATCAGCTGA (SEQ ID NO: 1968), probe: CCGTCTCGGGTATGTGGAAAGGT-TATGG (SEQ ID NO: 1969)). A standard curve of defined dilutions of a synthetic SARS-CoV-2 RNA (Twist Bioscience) was used for normalization.

Results

Duplexes AD-1184137; AD-1184150; AD-1184151; AD-1184284; AD-1184212; AD-1231490; and the combinations of duplexes AD-1184137 and AD-1184150; AD-1184137 and AD-1184151; and AD-1184137, AD-1184150, AD-1184284, and AD-1184212 were assessed for their ability to inhibit coronavirus genome expression and focus formation in resistance selected cells.

As depicted in FIG. 4, all of the duplexes and duplex combinations inhibited expression of the SARS-CoV2 genome in the resistance selected cells and, as depicted in FIG. 5, all of the duplexes and duplex combinations inhibited SARS-CoV2 cell infection of the resistance selected cells. FIG. 6 is an exemplary immunofluorescence assay confirming the results of the q-PCR and focus-forming assays that the duplexes inhibit formation of viral particles in resistance selected cells. The duplexes that were most effective were AD-1184137 and AD-1184150, as was the combination of duplexes AD-1184137 and AD-1184150 (see Table 9 below and FIGS. 4 and 5).

TABLE 9

siRNA	EC <sub>50</sub> EC <sub>95</sub> (pM; PCR)	EC <sub>50</sub> EC <sub>95</sub> (pM; IFA)	Genome Reactivity* (0 mm)	Genome Reactivity* (1 mm)
AD-1184150	42	66	99.91%	100.00%
	1183	763		
AD-1184137	86	118	99.89%	99.98%
	702	608		

\*N = 4386 genomes analyzed

Example 6. Intranasal Delivery of siRNA Duplexes Prevents Coronavirus Infection

Experimental Design

To determine the efficacy of dsRNA agents administered intranasally, fifty-four (54) Male Syrian Golden hamsters, approximately 6-8 weeks of age were divided among seven groups, according to Table 10, below, in groups of 6 animals. Group 1 was a control group administered PBS via intranasal (IN) dosing on day -7 pre-challenge. Group 2 was a control group administered a dsRNA agent targeting luciferase via intranasal (IN) dosing on day -7 pre-challenge. Groups 3-6 were administered either a combination of AD-1184150 and AD-1184137, both targeting COVID-19, or an iRNA agent targeting ACE2, (see Table 10) via intranasal (IN) dosing on day -7 pre-challenge. Group 7 was administered a combination of AD-1184150 and AD-1184137, via subcutaneous (SQ) dosing on day -7 pre-challenge.

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Animals were challenged on study day 0 with SARS-CoV-2 via the intranasal route. Animals were monitored to Day 7 post-challenge. Oral swabs were collected in the post-challenge period, days 1, 3, and 5. Terminal oral swabs, blood, and tissue collection occurred on day 7 post-challenge.

TABLE 10

Experimental Design						
Group	N	Treatment	Route	Dose at each Treatment	Treatment	Days
1	6	PBS	IN	0 mg/kg	SD	-7
2	6	iRNA agent targeting Luciferase	IN	30 mg/kg	SD	-7
3	6	AD-1184150 + AD-1184137	IN	30 mg/kg	SD	-7
4	6	iRNA agent targeting ACE2	IN	30 mg/kg	SD	-7
5	6	AD-1184150 + AD-1184137	IN	10 mg/kg	SD	-7
6	6	AD-1184150 + AD-1184137	IN	1 mg/kg	SD	-7
7	5	AD-1184150 + AD-1184137	SQ	30 mg/kg	SD	-7

For animals receiving a combination of AD-1184150 and AD-1184137, the two duplexes were mixed together and the weight administered to each animal, as indicated in Table 10, is the total weight of the mixture of the two duplexes.

Each animal received a dose volume for IN dosing of 100  $\mu$ l per animal (50  $\mu$ l per nostril) or 200  $\mu$ l per animal for SQ dosing.

Virus Challenge with SARS-CoV-2

The intranasal inoculation (IN) was performed on Ketamine/Xylazine anesthetized hamsters. Administration of virus was conducted as follows: using a calibrated P200 pipettor, 50  $\mu$ L of the viral inoculum was administered dropwise into each nostril, for a total of 100  $\mu$ L per animal. Anesthetized animals were held upright such that the nostrils of the hamster were pointing towards the ceiling. The tip of the syringe was placed into the first nostril and virus inoculum was slowly injecting into the nasal passage, and then removed. This was repeated for the second nostril. The animal's head was tilted back for about 20 seconds and then returned to its housing unit and monitored until fully recovered.

Body weights were determined each day post-challenge through Day 7 post-challenge to assess the effectiveness of the duplexes as assessed by the weight of the animals.

The results are provided in FIGS. 7 and 8 and demonstrate that intranasal administration of a single 10 mg/kg dose or 50 30 mg/kg dose of the combination of AD-1184137 and AD-1184150 prevents SARS-CoV-2 infection as demonstrated by the maintenance of the weights of the hamsters (FIG. 7) and that intranasal administration of a single 30 mg/kg dose of the combination of AD-1184137 and 55 AD-1184150 is superior to subcutaneous administration of a single 30 mg/kg dose of the combination of AD-1184137 and AD-1184150 in preventing SARS-CoV-2 infection (FIG. 8).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

## SEQUENCE LISTING

The patent contains a lengthy sequence listing. A copy of the sequence listing is available in electronic form from the USPTO web site (<https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US12391945B2>). An electronic copy of the sequence listing will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

We claim:

1. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of a coronavirus genome in a cell, or a salt thereof,  
wherein the dsRNA agent, or a salt thereof, comprises a sense strand and an antisense strand forming a double stranded region,  
wherein the antisense strand comprises a nucleotide sequence differing by no more than three bases from any one of the antisense strand nucleotide sequences selected from the group consisting of  
(a) 5'-CCGGGUUUGACAGUUUGAAAAGC-3' of SEQ ID NO: 586;  
(b) 5'-GAUUAAAGAUUGCUALUGUGAGAU-3' of SEQ ID NO: 719; and  
(c) 5'-UCGGGUUUGACAGUUUGAAAAGC-3' of SEQ ID NO: 1852.
2. An isolated cell containing the dsRNA agent, or a salt thereof, of claim 1.
3. A pharmaceutical composition for inhibiting expression of a coronavirus genome, comprising the dsRNA agent, or a salt thereof, of claim 1.
4. The dsRNA agent, or a salt thereof, of claim 1, wherein the sense strand is conjugated to one or more lipophilic moieties.
5. The dsRNA agent, or a salt thereof, of claim 4, wherein the one or more lipophilic moieties is selected from the group consisting of lipid, cholesterol, retinoic acid, cholic acid, adamantanone acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-bis-O (hexadecyl) glycerol, geranylloxyhexanol, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, 03-(oleoyl) lithocholic acid, 03-(oleoyl) cholenic acid, dimethoxytrityl, or phenoxazine.
6. The dsRNA agent, or a salt thereof, of claim 5, wherein the one or more lipophilic moieties is an aliphatic, alicyclic, or polycyclic compound.
7. The dsRNA agent, or a salt thereof, of claim 6, wherein the one or more lipophilic moieties contains a saturated or unsaturated C4-C30 hydrocarbon chain.
8. The dsRNA agent, or a salt thereof, of claim 7, wherein the one or more lipophilic moieties contains a saturated or unsaturated C16 hydrocarbon chain.
9. The dsRNA agent, or a salt thereof, of claim 8, wherein the saturated or unsaturated C16 hydrocarbon chain is conjugated to position 6, counting from the 5'-end of the strand.
10. The dsRNA agent, or a salt thereof, of claim 9, wherein the saturated or unsaturated C16 hydrocarbon chain is conjugated to a nucleobase, a sugar moiety, or an internucleoside linkage.
11. The dsRNA agent, or a salt thereof, of claim 10, wherein the saturated or unsaturated C16 hydrocarbon chain comprises a 2'-O-hexadecyl-adenosine-3'-phosphate nucleotide.
12. The dsRNA agent, or a salt thereof, of claim 1, wherein all of the nucleotides of sense strand and all of the nucleotides of the antisense strand comprise a nucleotide modification.
13. The dsRNA agent, or a salt thereof, of claim 1, wherein the dsRNA agent, or a salt thereof, further comprises at least one phosphorothioate internucleotide linkage.
14. The dsRNA agent, or a salt thereof, of claim 1, wherein the dsRNA agent, or a salt thereof, further comprises a phosphate or phosphate mimic at the 5'-end of the antisense strand.
15. The dsRNA agent, or a salt thereof, of claim 14, wherein the phosphate mimic is a 5'-vinyl phosphonate (VP).
16. The dsRNA agent, or a salt thereof, of claim 1, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.
17. The dsRNA agent, or a salt thereof, of claim 1, wherein the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-UUUCAACUGUCAAACCCGG-3' of SEQ ID NO: 231 and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-CCGGGUUUGACAGUUUGAAAAGC-3' of SEQ ID NO: 586.
18. The dsRNA agent, or a salt thereof, of claim 1, wherein the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-CUCACAUAGCAAUCUUUAUC-3' of SEQ ID NO: 364 and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-GAUUAAGAUUGCUALUGUGAGAU-3' of SEQ ID NO: 719.
19. The dsRNA agent, or a salt thereof, of claim 1, wherein the nucleotide sequence of the sense strand differs by no more than 3 bases from the nucleotide sequence 5'-UUUCAACUGUCAAACCCGA-3' of SEQ ID NO: 1812 and the nucleotide sequence of the antisense strand differs by no more than 3 bases from the nucleotide sequence 5'-UCGGGUUUGACAGUUUGAAAAGC-3' SEQ ID NO: 1852.
20. The dsRNA agent, or a salt thereof, of claim 1, wherein the sense strand comprises the nucleotide sequence 5'-ususu(Ahd)AfaCfUfGfucaaaccsgsa-3' of SEQ ID NO:941 and the antisense strand comprises the nucleotide sequence 5'-VPusCfsgggUfuugacagUfuUfgaaaasgsc-3' of SEQ ID NO:1296,  
wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexadecyl-adenosine-3'-phosphate; and VP is Vinyl-phosphonate.

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**21.** The dsRNA agent, or a salt thereof, of claim 1, wherein the sense strand comprises the nucleotide sequence 5'-csuscac(Ahd)UfaGfCfAfaucuuuaasusa-3' of SEQ ID NO: 1074 and the antisense strand comprises the nucleotide sequence 5'-VPusAfsuuuaAfagauugcUfaUfgugagsasu-3' of 5 SEQ ID NO:1429,

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Ahd) is 2'-O-hexa-decyl-adenosine-3'-phosphate; and VP is Vinyl-phos- 10 phonate.

**22.** The dsRNA agent, or a salt thereof, of claim 1, wherein the sense strand comprises the nucleotide sequence 5'-ususuu(Chd)aAfaCfUfGfucaaaccsgsa-3' of SEQ ID NO: 1895 and the antisense strand comprises the nucleotide 15 sequence 5'-VPusCfsgggUfuugacagUfuUfgaaaasgsc-3' of SEQ ID NO:1296

wherein a, g, c and u are 2'-O-methyl (2'-OMe) A, G, C, and U; Af, Gf, Cf and Uf are 2'-fluoro A, G, C and U; s is a phosphorothioate linkage; (Chd) is 2'-O-hexa- 20 decyl-cytidine-3'-phosphate; and VP is Vinyl-phospho-nate.

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