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(71) Applicant: **IONIS PHARMACEUTICALS, INC.** [US/US]; 2855 Gazelle Court, Carlsbad, CA 92010 (US).

(72) Inventor: **BUI, Huynh-Hoa**; 2855 Gazelle Ct., Carlsbad, CA 92010 (US).

(74) Agent: **LIU, Jing** et al.; Sheppard Mullin Richter & Hampton LLP, 650 Town Center Drive, 10th Floor, Costa Mesa, CA 92626 (US).

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(54) Title: COMPOUNDS FOR MODULATING CHMP7

(57) Abstract: Provided are compounds and pharmaceutical compositions for reducing the amount or activity of Charged Multivesicular Body Protein 7 (CHMP7) RNA in a cell or subject, and in certain instances reducing the amount of CHMP7 protein in a cell or subject. Such compounds and pharmaceutical compositions are useful to ameliorate diseases or conditions associated with aberrant activation of Endosomal Sorting Complexes Required for Transport-III proteins.

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COMPOUNDS FOR MODULATING CHMP7

Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0405WOSEQ_ST25.txt, created on September 28, 2021, which is 124 Kb in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

Field

Provided are compounds and pharmaceutical compositions for reducing the amount or activity of Charged Multivesicular Body Protein 7 (CHMP7) RNA in a cell or subject, and in certain instances reducing the amount of CHMP7 protein in a cell or subject. Such compounds and pharmaceutical compositions are useful to ameliorate diseases or conditions associated with aberrant activation of Endosomal Sorting Complexes Required for Transport-III proteins.

Background

The nuclear envelope has an important role in maintaining the separation between the nucleus and cytoplasm of eukaryotic cells. Defective nuclear envelopes can cause cell death, losses in genome integrity, and disease. These defects can involve either inefficient sealing of the nuclear membrane and/or inappropriate assembly of nuclear pore complexes. (Thaller, D.J., et al., bioRxiv, 2020, 2020.2005.2004.074880, doi:10.1101/2020.05.05.074880).

During eukaryotic cell division, the nuclear envelope is broken down and reformed using a complex process involving Endosomal Sorting Complexes Required for Transport-III (ESCRT-III) proteins. These ESCRT-III proteins have been implicated in sealing holes in the nuclear envelope in mammals and ensuring quality control of nuclear pore complexes (NPCs). Charged Multivesicular Body Protein 7 (CHMP7) is an ESCRTII/III protein that has been implicated in recruiting additional ESCRT-III proteins to holes in the nuclear membrane, and in sealing nuclear pores to protect the compartmentalization of the nucleus and cytoplasm (Gu, M., et al., Proc. Natl. Acad. Sci. 2017, 114, E2166-e2175, doi:10.1073/pnas.1613916114). Studies in yeast using the CHMP7 ortholog Chm7, indicate that controlling CHMP7 activation is critical to prevent the protein taking on gain-of-function roles at the nuclear envelope. Such over-activation of CHMP7 could lead to inappropriate sealing of nuclear membrane pores, and defects in the assembly of the nuclear pore complex (Thaller, D.J., et al., Elife, 2019, 8, doi:10.7554/eLife.45284; Webster, B.M., et al., EMBO 2016, *25*, 10.15252/embj.201694574). CHMP7 has been identified as a potential therapeutic target for familial and sporadic amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), and possibly other neurodegenerative diseases associated with nucleoporin reduction and TDP-43 pathology (Coyne, A.N., et al., Science Trans. Med., 2021, 13 (604):eabe1923, doi: 10.1126/scitranslmed.abe1923. PMID: 34321318).

Currently there is a lack of acceptable options for treating diseases associated with over-activation of the ESCRT-III proteins, resulting in inappropriate sealing of pores in the nuclear membrane, defective nuclear envelopes, or defective nuclear pore complexes. It is therefore an object herein to provide compounds and pharmaceutical compositions for the treatment of such diseases.

Summary of the Invention

Provided herein are compounds and pharmaceutical compositions for reducing the amount or activity of CHMP7 RNA, and in certain embodiments reducing the amount of CHMP7 protein in a cell or animal. In certain embodiments, the animal has a disease or disorder associated with over-expression of CHMP7. In certain embodiments, the animal has a disease or disorder associated with over-activation of CHMP7 protein activity. In certain embodiments, the animal has a disease or condition associated with defects in the nuclear envelope. In certain embodiments, the defect in the nuclear envelope comprises a defect in nuclear pore closure. In certain embodiments, the animal has a disease or condition associated with a defect in the assembly of the nuclear pore complex. In certain embodiments, compounds are useful for reducing expression of CHMP7 RNA. In certain embodiments, compounds useful for reducing expression of CHMP7 RNA are oligomeric compounds. In certain embodiments, compounds useful for reducing expression of CHMP7 RNA and/or CHMP7 protein are modified oligonucleotides.

Detailed Description of the Invention

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive. Herein, the use of the singular includes the plural unless specifically stated otherwise. As used herein, the use of "or" means "and/or" unless stated otherwise. Furthermore, the use of the term "including" as well as other forms, such as "includes" and "included" is not limiting. Also, terms such as "element" or "component" encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated otherwise.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including, but not limited to, patents, patent applications, articles, books, treatises, and GenBank, ENSEMBL, and NCBI reference sequence records, are hereby expressly incorporated-by-reference for the portions of the document discussed herein, as well as in their entirety.

Definitions

Unless specific definitions are provided, the nomenclature used in connection with, and the procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Where permitted, all patents, applications, published applications and other publications and other data referred to throughout in the disclosure are incorporated by reference herein in their entirety.

Unless otherwise indicated, the following terms have the following meanings:

DEFINITIONS

As used herein, "2'-deoxynucleoside" means a nucleoside comprising a 2'-H(H) deoxyfuranosyl sugar moiety. In certain embodiments, a 2'-deoxynucleoside is a 2'-β-D-deoxynucleoside and comprises a 2'-β-D-deoxyribosyl sugar moiety, which has the β-D ribosyl configuration as found in naturally occurring deoxyribonucleic acids (DNA). In certain embodiments, a 2'-deoxynucleoside may comprise a modified nucleobase or may comprise an RNA nucleobase (uracil).

As used herein, "2'-MOE" means a 2'-$OCH_2CH_2OCH_3$ group in place of the 2'-OH group of a furanosyl sugar moiety. A "2'-MOE modified sugar moiety" means a sugar moiety with a 2'-$OCH_2CH_2OCH_3$ group in place of the 2'-OH group of a furanosyl sugar moiety. Unless otherwise indicated, a 2'-MOE modified sugar moiety is in the β-D-ribosyl configuration. "MOE" means O-methoxyethyl.

As used herein, "2'-MOE nucleoside" means a nucleoside comprising a 2'-MOE modified sugar moiety.

As used herein, "2'-OMe" means a 2'-OCH_3 group in place of the 2'-OH group of a furanosyl sugar moiety. A"2'-O-methyl modified sugar moiety" or "2'-OMe modified sugar moiety" means a sugar moiety with a 2'-OCH_3 group in place of the 2'-OH group of a furanosyl sugar moiety. Unless otherwise indicated, a 2'-OMe modified sugar moiety is in the β-D-ribosyl configuration.

As used herein, "2'-OMe nucleoside" means a nucleoside comprising a 2'-OMe modified sugar moiety.

As used herein, "2'-substituted nucleoside" means a nucleoside comprising a 2'-substituted sugar moiety. As used herein, "2'-substituted" in reference to a sugar moiety means a sugar moiety comprising at least one 2'-substituent group other than H or OH.

As used herein, "5-methyl cytosine" means a cytosine modified with a methyl group attached to the 5 position. A 5-methyl cytosine is a modified nucleobase.

As used herein, "ameliorate" in reference to a disease or condition means improvement in at least one symptom of the disease or condition relative to the same symptom in the absence of the treatment. In certain embodiments, amelioration is the reduction in the severity or frequency of the symptom or the delayed onset or slowing of progression in the severity or frequency of a symptom.

As used herein, "antisense activity" means any detectable and/or measurable change attributable to the hybridization of an antisense compound to its target nucleic acid. In certain embodiments, antisense activity is a decrease in the amount or expression of a target nucleic acid or protein encoded by such target nucleic acid compared to target nucleic acid levels or target protein levels in the absence of the antisense compound.

As used herein, "antisense agent" means an antisense compound and optionally one or more additional features, such as a sense compound.

As used herein, "antisense compound" means an antisense oligonucleotide and optionally one or more additional features, such as a conjugate group. As used herein, "antisense compound" means an oligomeric compound capable of achieving at least one antisense activity.

As used herein, "sense compound" means a sense oligonucleotide and optionally one or more additional features, such as a conjugate group.

As used herein, "antisense oligonucleotide" means an oligonucleotide, including the oligonucleotide portion of an antisense compound, that is capable of hybridizing to a target nucleic acid and is capable of at least one antisense activity. Antisense oligonucleotides include but are not limited to antisense RNAi oligonucleotides and antisense RNase H oligonucleotides.

As used herein, "sense oligonucleotide" means an oligonucleotide, including the oligonucleotide portion of a sense compound, that is capable of hybridizing to an antisense oligonucleotide.

As used herein, "bicyclic nucleoside" or "BNA" means a nucleoside comprising a bicyclic sugar moiety.

As used herein, "bicyclic sugar" or "bicyclic sugar moiety" means a modified sugar moiety comprising two rings, wherein the second ring is formed via a bridge connecting two of the atoms in the first ring thereby forming a

bicyclic structure. In certain embodiments, the first ring of the bicyclic sugar moiety is a furanosyl moiety. In certain embodiments, the furanosyl sugar moiety is a ribosyl moiety. In certain embodiments, the bicyclic sugar moiety does not comprise a furanosyl moiety.

As used herein, “cerebrospinal fluid” or “CSF” means the fluid filling the space around the brain and spinal cord. “Artificial cerebrospinal fluid” or “aCSF” means a prepared or manufactured fluid that has certain properties of cerebrospinal fluid.

As used herein, “cleavable moiety” means a bond or group of atoms that is cleaved under physiological conditions, for example, inside a cell, an animal, or a human.

As used herein, “complementary” in reference to an oligonucleotide means that at least 70% of the nucleobases of the oligonucleotide or one or more portions thereof and the nucleobases of another nucleic acid or one or more portions thereof are capable of hydrogen bonding with one another when the nucleobase sequence of the oligonucleotide and the other nucleic acid are aligned in opposing directions. As used herein, “complementary nucleobases” means nucleobases that are capable of forming hydrogen bonds with one another. Complementary nucleobase pairs include adenine (A) and thymine (T), adenine (A) and uracil (U), cytosine (C) and guanine (G), 5-methyl cytosine (^{m}C) and guanine (G). Complementary oligonucleotides and/or target nucleic acids need not have nucleobase complementarity at each nucleoside. Rather, some mismatches are tolerated. As used herein, “fully complementary” or “100% complementary” in reference to an oligonucleotide, or a portion thereof, means that the oligonucleotide, or portion thereof, is complementary to another oligonucleotide or target nucleic acid at each nucleobase of the shorter of the two oligonucleotides, or at each nucleoside if the oligonucleotides are the same length.

As used herein, “conjugate group” means a group of atoms that is directly or indirectly attached to an oligonucleotide. Conjugate groups include a conjugate moiety and a conjugate linker that attaches the conjugate moiety to the oligonucleotide.

As used herein, “conjugate linker” means a single bond or a group of atoms comprising at least one bond that connects a conjugate moiety to an oligonucleotide.

As used herein, “conjugate moiety” means a group of atoms that is attached to an oligonucleotide via a conjugate linker.

As used herein, "contiguous" in the context of an oligonucleotide refers to nucleosides, nucleobases, sugar moieties, or internucleoside linkages that are immediately adjacent to each other. For example, “contiguous nucleobases” means nucleobases that are immediately adjacent to each other in a sequence.

As used herein, “cEt” means a 4’ to 2’ bridge in place of the 2’OH-group of a ribosyl sugar moiety, wherein the bridge has the formula of 4'-CH(CH_3)-O-2', and wherein the methyl group of the bridge is in the S configuration. A “cEt sugar moiety” is a bicyclic sugar moiety with a 4’ to 2’ bridge in place of the 2’OH-group of a ribosyl sugar moiety, wherein the bridge has the formula of 4'-CH(CH_3)-O-2', and wherein the methyl group of the bridge is in the S configuration. “cEt” means constrained ethyl.

As used herein, “cEt nucleoside” means a nucleoside comprising a cEt sugar moiety.

As used herein, “chirally enriched population” means a plurality of molecules of identical molecular formula, wherein the number or percentage of molecules within the population that contain a particular stereochemical configuration at a particular chiral center is greater than the number or percentage of molecules expected to contain the same particular stereochemical configuration at the same particular chiral center within the population if the particular

chiral center were stereorandom. Chirally enriched populations of molecules having multiple chiral centers within each molecule may contain one or more stereorandom chiral centers. In certain embodiments, the molecules are modified oligonucleotides. In certain embodiments, the molecules are compounds comprising modified oligonucleotides.

As used herein, "chirally controlled" in reference to an internucleoside linkage means chirality at that linkage is enriched for a particular stereochemical configuration.

As used herein, "deoxy region" means a region of 5-12 contiguous nucleotides, wherein at least 70% of the nucleosides are 2'-β-D-deoxynucleosides. In certain embodiments, each nucleoside is selected from a 2'-β-D-deoxynucleoside, a bicyclic nucleoside, and a 2'-substituted nucleoside. In certain embodiments, a deoxy region supports RNase H activity. In certain embodiments, a deoxy region is the gap or internal region of a gapmer.

As used herein, "gapmer" means a modified oligonucleotide comprising an internal region having a plurality of nucleosides that support RNase H cleavage positioned between external regions having one or more nucleosides, wherein the nucleosides comprising the internal region are chemically distinct from the nucleoside or nucleosides comprising the external regions. The internal region may be referred to as the "gap" and the external regions may be referred to as the "wings" or "wing segments." In certain embodiments, the internal region is a deoxy region. The positions of the internal region or gap refer to the order of the nucleosides of the internal region and are counted starting from the 5'-end of the internal region. Unless otherwise indicated, "gapmer" refers to a sugar motif. In certain embodiments, each nucleoside of the gap is a 2'-β-D-deoxynucleoside. In certain embodiments, the gap comprises one 2'-substituted nucleoside at position 1, 2, 3, 4, or 5 of the gap, and the remainder of the nucleosides of the gap are 2'-β-D-deoxynucleosides. As used herein, the term "MOE gapmer" indicates a gapmer having a gap comprising 2'-β-D-deoxynucleosides and wings comprising 2'-MOE nucleosides. As used herein, the term "mixed wing gapmer" indicates a gapmer having wings comprising modified nucleosides comprising at least two different sugar modifications. Unless otherwise indicated, a gapmer may comprise one or more modified internucleoside linkages and/or modified nucleobases and such modifications do not necessarily follow the gapmer pattern of the sugar modifications.

As used herein, "hotspot region" is a range of nucleobases on a target nucleic acid that is amenable to oligomeric compound-mediated reduction of the amount or activity of the target nucleic acid.

As used herein, "hybridization" means the pairing or annealing of complementary oligonucleotides and/or nucleic acids. While not limited to a particular mechanism, the most common mechanism of hybridization involves hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleobases.

As used herein, "internucleoside linkage" means the covalent linkage between contiguous nucleosides in an oligonucleotide. As used herein, "modified internucleoside linkage" means any internucleoside linkage other than a phosphodiester internucleoside linkage. "Phosphorothioate internucleoside linkage or "PS internucleoside linkage" is a modified internucleoside linkage in which one of the non-bridging oxygen atoms of a phosphodiester internucleoside linkage is replaced with a sulfur atom.

As used herein, "linker-nucleoside" means a nucleoside that links, either directly or indirectly, an oligonucleotide to a conjugate moiety. Linker-nucleosides are located within the conjugate linker of an oligomeric compound. Linker-nucleosides are not considered part of the oligonucleotide portion of an oligomeric compound even if they are contiguous with the oligonucleotide.

As used herein, “non-bicyclic modified sugar moiety” means a modified sugar moiety that comprises a modification, such as a substituent, that does not form a bridge between two atoms of the sugar to form a second ring.

As used herein, “mismatch” or “non-complementary” means a nucleobase of a first oligonucleotide that is not complementary with the corresponding nucleobase of a second oligonucleotide or target nucleic acid when the first and second oligonucleotide are aligned.

As used herein, “motif” means the pattern of unmodified and/or modified sugar moieties, nucleobases, and/or internucleoside linkages, in an oligonucleotide.

As used herein, "nucleobase" means an unmodified nucleobase or a modified nucleobase. As used herein an “unmodified nucleobase” is adenine (A), thymine (T), cytosine (C), uracil (U), or guanine (G). As used herein, a “modified nucleobase” is a group of atoms other than unmodified A, T, C, U, or G capable of pairing with at least one unmodified nucleobase. A “5-methyl cytosine” is a modified nucleobase. A universal base is a modified nucleobase that can pair with any one of the five unmodified nucleobases. As used herein, “nucleobase sequence” means the order of contiguous nucleobases in a target nucleic acid or oligonucleotide independent of any sugar or internucleoside linkage modification.

As used herein, “nucleoside” means a compound, or a fragment of a compound, comprising a nucleobase and a sugar moiety. The nucleobase and sugar moiety are each, independently, unmodified or modified. As used herein, “modified nucleoside” means a nucleoside comprising a modified nucleobase and/or a modified sugar moiety. Modified nucleosides include abasic nucleosides, which lack a nucleobase. “Linked nucleosides” are nucleosides that are connected in a contiguous sequence (i.e., no additional nucleosides are presented between those that are linked).

As used herein, "oligomeric compound" means an oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group. An oligomeric compound may be paired with a second oligomeric compound that is complementary to the first oligomeric compound or may be unpaired. A “singled-stranded oligomeric compound” is an unpaired oligomeric compound. The term “oligomeric duplex” means a duplex formed by two oligomeric compounds having complementary nucleobase sequences. Each oligomeric compound of an oligomeric duplex may be referred to as a “duplexed oligomeric compound.”

As used herein, "oligonucleotide" means a strand of linked nucleosides connected via internucleoside linkages, wherein each nucleoside and internucleoside linkage may be modified or unmodified. Unless otherwise indicated, oligonucleotides consist of 8-50 linked nucleosides. As used herein, “modified oligonucleotide” means an oligonucleotide, wherein at least one nucleoside or internucleoside linkage is modified. As used herein, “unmodified oligonucleotide” means an oligonucleotide that does not comprise any nucleoside modifications or internucleoside modifications.

As used herein, “pharmaceutically acceptable carrier or diluent” means any substance suitable for use in administering to a subject. Certain such carriers enable pharmaceutical compositions to be formulated as, for example, tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspension and lozenges for the oral ingestion by a subject. In certain embodiments, a pharmaceutically acceptable carrier or diluent is sterile water, sterile saline, sterile buffer solution or sterile artificial cerebrospinal fluid.

As used herein, “pharmaceutically acceptable salts” means physiologically and pharmaceutically acceptable salts of compounds. Pharmaceutically acceptable salts retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

As used herein, "pharmaceutical composition" means a mixture of substances suitable for administering to a subject. For example, a pharmaceutical composition may comprise an oligomeric compound and a sterile aqueous solution. In certain embodiments, a pharmaceutical composition shows activity in free uptake assay in certain cell lines.

As used herein, "reducing the amount or activity" refers to a reduction or blockade of the transcriptional expression or activity relative to the transcriptional expression or activity in an untreated or control sample and does not necessarily indicate a total elimination of transcriptional expression or activity.

As used herein, "RNA" means an RNA transcript and includes pre-mRNA and mature mRNA unless otherwise specified.

As used herein, "RNAi agent" means an antisense agent that acts, at least in part, through RISC or Ago2 to modulate a target nucleic acid and/or protein encoded by a target nucleic acid. RNAi agents include, but are not limited to double-stranded siRNA, single-stranded RNAi (ssRNAi), and microRNA, including microRNA mimics. RNAi agents may comprise conjugate groups and/or terminal groups. In certain embodiments, an RNAi agent modulates the amount and/or activity, of a target nucleic acid. The term RNAi agent excludes antisense agents that act through RNase H.

As used herein, "RNAi compound" means an antisense compound that acts, at least in part, through RISC or Ago2 to modulate a target nucleic acid and/or protein encoded by a target nucleic acid. RNAi compounds include, but are not limited to double-stranded siRNA, single-stranded RNA (ssRNA), and microRNA, including microRNA mimics. In certain embodiments, an RNAi compound modulates the amount, activity, and/or splicing of a target nucleic acid. The term RNAi compound excludes antisense compounds that act through RNase H.

As used herein, "RNase H agent" means an antisense agent that acts through RNase H to modulate a target nucleic acid and/or protein encoded by a target nucleic acid. In certain embodiments, RNase H agents are single-stranded. In certain embodiments, RNase H agents are double-stranded. RNase H compounds may comprise conjugate groups and/or terminal groups. In certain embodiments, an RNase H agent modulates the amount and/or activity of a target nucleic acid. The term RNase H agent excludes antisense agents that act principally through RISC/Ago2.

As used herein, "self-complementary" in reference to an oligonucleotide means an oligonucleotide that at least partially hybridizes to itself.

As used herein, "standard *in vitro* assay" means the assay described in Example 1 and reasonable variations thereof.

As used herein, "stereorandom chiral center" in the context of a population of molecules of identical molecular formula means a chiral center having a random stereochemical configuration. For example, in a population of molecules comprising a stereorandom chiral center, the number of molecules having the (*S*) configuration of the stereorandom chiral center may be but is not necessarily the same as the number of molecules having the (*R*) configuration of the stereorandom chiral center. The stereochemical configuration of a chiral center is considered random when it is the result of a synthetic method that is not designed to control the stereochemical configuration. In certain embodiments, a stereorandom chiral center is a stereorandom phosphorothioate internucleoside linkage.

As used herein, "subject" means a human or non-human animal. The terms "subject" and "individual" are used interchangeably. In certain embodiments, the subject is human.

As used herein, "sugar moiety" means an unmodified sugar moiety or a modified sugar moiety. As used herein, "unmodified sugar moiety" means a 2'-OH(H) β-D-ribosyl sugar moiety, as found in RNA (an "unmodified RNA sugar moiety"), or a 2'-H(H) β-D-deoxyribosyl sugar moiety, as found in DNA (an "unmodified DNA sugar moiety").

Unmodified sugar moieties have one hydrogen at each of the 1', 3', and 4' positions, an oxygen at the 3' position, and two hydrogens at the 5' position. As used herein, "modified sugar moiety" or "modified sugar" means a modified furanosyl sugar moiety or a sugar surrogate.

As used herein, "sugar surrogate" means a modified sugar moiety having other than a furanosyl moiety that can link a nucleobase to another group, such as an internucleoside linkage, conjugate group, or terminal group in an oligonucleotide. Modified nucleosides comprising sugar surrogates can be incorporated into one or more positions within an oligonucleotide and such oligonucleotides are capable of hybridizing to complementary oligomeric compounds or target nucleic acids.

As used herein, "target nucleic acid" and "target RNA" mean a nucleic acid that an antisense compound is designed to affect. Target RNA means an RNA transcript and includes pre-mRNA and mature mRNA unless otherwise specified.

As used herein, "target region" means a portion of a target nucleic acid to which an oligomeric compound is designed to hybridize.

As used herein, "terminal group" means a chemical group or group of atoms that is covalently linked to a terminus of an oligonucleotide.

CERTAIN EMBODIMENTS

The present disclosure provides the following non-limiting numbered embodiments:

Embodiment 1. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to an equal length portion of a CHMP7 nucleic acid, and wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

Embodiment 2. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or 20 contiguous nucleobases of any of the nucleobases of SEQ ID NOs: 10-477, wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

Embodiment 3. The oligomeric compound of embodiment 2, wherein the modified oligonucleotide has a nucleobase sequence consisting of the nucleobase sequence of any of SEQ ID NOs: 10-477.

Embodiment 4. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 contiguous nucleobases complementary to:

an equal length portion within nucleobases 3950-3983 of SEQ ID NO: 1;
an equal length portion within nucleobases 4242-4266 of SEQ ID NO: 1;
an equal length portion within nucleobases 4480-4525 of SEQ ID NO: 1;
an equal length portion within nucleobases 4534-4566 of SEQ ID NO: 1;
an equal length portion within nucleobases 5205-5232 of SEQ ID NO: 1;
an equal length portion within nucleobases 5404-5430 of SEQ ID NO: 1;

an equal length portion within nucleobases 8323-8344 of SEQ ID NO: 1;
an equal length portion within nucleobases 16927-16950 of SEQ ID NO: 1;
an equal length portion within nucleobases 17298-17340 of SEQ ID NO: 1; or
an equal length portion within nucleobases 18287-18313 of SEQ ID NO: 1;

wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

Embodiment 5. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, or at least 18 contiguous nucleobases of a sequence selected from:

SEQ ID NOs: 220, 302, and 345;
SEQ ID NOs: 21, 131, 191, and 465;
SEQ ID NOs: 34, 116, 184, 242, 257, 340, and 474;
SEQ ID NOs: 55, 118, 202, 267, 372, and 422;
SEQ ID NOs: 73, 136, 197, and 421;
SEQ ID NOs: 79, 160, 168, 230, 313, 331, and 464;
SEQ ID NOs: 157, 186, and 265;
SEQ ID NOs: 128, 182, and 309;
SEQ ID NOs: 44, 76, 153, 206, 283, 363, and 416; or
SEQ ID NOs: 85, 121, 189, 300, and 354;

wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

Embodiment 6. The oligomeric compound of any of embodiments 1-5, wherein the modified oligonucleotide has a nucleobase sequence that is at least 80%, 85%, 90%, 95%, or 100% complementary to the nucleobase sequence of SEQ ID NO: 1 or SEQ ID NO: 2 when measured across the entire nucleobase sequence of the modified oligonucleotide.

Embodiment 7. The oligomeric compound of any of embodiments 1-6, wherein the modified oligonucleotide comprises at least one modified nucleoside.

Embodiment 8. The oligomeric compound of embodiment 7, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a modified sugar moiety.

Embodiment 9. The oligomeric compound of embodiment 8, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety.

Embodiment 10. The oligomeric compound of embodiment 9, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety having a 2'-4' bridge, wherein the 2'-4' bridge is selected from -O-CH_2-; and -O-$CH(CH_3)$-.

Embodiment 11. The oligomeric compound of any of embodiments 7-10, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a non-bicyclic modified sugar moiety.

Embodiment 12. The oligomeric compound of embodiment 11, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a non-bicyclic modified sugar moiety comprising a 2'-MOE modified sugar moiety or a 2'-OMe modified sugar moiety.

Embodiment 13. The oligomeric compound of any of embodiments 7-12, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a sugar surrogate.

Embodiment 14. The oligomeric compound of embodiment 13, wherein the sugar surrogate is selected from any of morpholino, modified morpholino, PNA, THP, and F-HNA.

Embodiment 15. The oligomeric compound of any of embodiments 1-8 or 11-14, wherein the modified oligonucleotide does not comprise a bicyclic modified sugar moiety.

Embodiment 16. The oligomeric compound of any of embodiments 1-15, wherein the modified oligonucleotide is a gapmer.

Embodiment 17. The oligomeric compound of any of embodiments 1-16 wherein the modified oligonucleotide comprises a deoxy region consisting of 5-12 linked 2'-deoxynucleosides.

Embodiment 18. The oligomeric compound of any of embodiments 1-16, wherein the modified oligonucleotide comprises a deoxy region consisting of 5-12 linked 2'-β-D-deoxynucleosides.

Embodiment 19. The oligomeric compound of embodiment 17 or embodiment 18, wherein the deoxy region consists of 6, 7, 8, 9, 10, or 6-10 linked nucleosides.

Embodiment 20. The oligomeric compound of any of embodiments 17-19, wherein each nucleoside immediately adjacent to the deoxy region comprises a modified sugar moiety.

Embodiment 21. The oligomeric compound of any of embodiments 17-20, wherein the deoxy region is flanked on the 5'-side by a 5'-external region consisting of 1-6 linked 5'-external region nucleosides and on the 3'-side by a 3'-external region consisting of 1-6 linked 3'-external region nucleosides; wherein

the 3'-most nucleoside of the 5' external region comprises a modified sugar moiety; and

the 5'-most nucleoside of the 3' external region comprises a modified sugar moiety.

Embodiment 22. The oligomeric compound of embodiment 21, wherein each nucleoside of the 3' external region comprises a modified sugar moiety.

Embodiment 23. The oligomeric compound of embodiment 21 or embodiment 22, wherein each nucleoside of the 5' external region comprises a modified sugar moiety.

Embodiment 24. The oligomeric compound of any of embodiments 1-23, wherein the modified oligonucleotide comprises:

a 5'-region consisting of 1-7 linked 5'-region nucleosides;

a central region consisting of 6-10 linked central region nucleosides; and

a 3'-region consisting of 1-7 linked 3'-region nucleosides; wherein

each of the 5'-region nucleosides and each of the 3'-region nucleosides comprises a modified sugar moiety and each of the central region nucleosides comprises a 2'-β-D-deoxyfuranosyl sugar moiety.

Embodiment 25. The oligomeric compound of embodiment 24, wherein the modified oligonucleotide comprises:

a 5'-region consisting of 5 linked 5'-region nucleosides;

a central region consisting of 10 linked central region nucleosides; and

a 3'-region consisting of 5 linked 3'-region nucleosides; wherein

each of the 5'-region nucleosides and each of the 3'-region nucleosides is a 2'-MOE nucleoside and each of the central region nucleosides is a 2'-β-D-deoxynucleoside.

Embodiment 26. The oligomeric compound of any of embodiments 1-25, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.

Embodiment 27. The oligomeric compound of embodiment 26, wherein each internucleoside linkage of the modified oligonucleotide is a modified internucleoside linkage.

Embodiment 28. The oligomeric compound of embodiment 26 or embodiment 27 wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 29. The oligomeric compound of embodiment 26 or embodiment 28 wherein the modified oligonucleotide comprises at least one phosphodiester internucleoside linkage.

Embodiment 30. The oligomeric compound of any of embodiments 26, 28, or 29, wherein each internucleoside linkage is either a phosphodiester internucleoside linkage or a phosphorothioate internucleoside linkage.

Embodiment 31. The oligomeric compound of embodiment 27, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage

Embodiment 32. The oligonucleotide compound of embodiment 26, wherein the modified oligonucleotide has an internucleoside linkage motif of soooossssssssssooss; wherein,
s = a phosphorothioate internucleoside linkage and o = a phosphodiester internucleoside linkage.

Embodiment 33. The oligomeric compound of any of embodiments 1-32, wherein the modified oligonucleotide comprises at least one modified nucleobase.

Embodiment 34. The oligomeric compound of embodiment 33, wherein the modified nucleobase is a 5-methyl cytosine.

Embodiment 35. The oligomeric compound of embodiment 34, wherein each cytosine is a 5-methyl cytosine.

Embodiment 36. The oligomeric compound of any of embodiments 1-35, wherein the modified oligonucleotide consists of 12-30, 12-22, 12-20, 14-18, 14-20, 15-17, 15-25, 16-18, 16-20, 17-20, 18-20 or 18-22 linked nucleosides.

Embodiment 37. The oligomeric compound of any of embodiments 1-36, wherein the modified oligonucleotide consists of 16, 17, 18, 19, or 20 linked nucleosides.

Embodiment 38. The oligomeric compound of any of embodiments 1-35, wherein the modified oligonucleotide consists of 20 linked nucleosides.

Embodiment 39. The oligomeric compound of any of embodiments 1-38, consisting of the modified oligonucleotide.

Embodiment 40. The oligomeric compound of any of embodiments 1-38, wherein the oligomeric compound comprises a conjugate group.

Embodiment 41. The oligomeric compound of embodiment 40, wherein the conjugate group comprises a conjugate moiety and a conjugate linker.

Embodiment 42. The oligomeric compound of embodiment 41, wherein the conjugate linker consists of a single bond.

Embodiment 43. The oligomeric compound of embodiment 41 or embodiment 42, wherein the conjugate linker is cleavable.

Embodiment 44. The oligomeric compound of embodiment 41 or embodiment 43, wherein the conjugate linker comprises 1-3 linker-nucleosides.

Embodiment 45. The oligomeric compound of any of embodiments 41-43, wherein the conjugate linker does not comprise any linker nucleosides.

Embodiment 46. The oligomeric compound of any of embodiments 40-45, wherein the conjugate group is attached to the modified oligonucleotide at the 5'-end of the modified oligonucleotide.

Embodiment 47. The oligomeric compound of any of embodiments 40-45, wherein the conjugate group is attached to the modified oligonucleotide at the 3'-end of the modified oligonucleotide.

Embodiment 48. The oligomeric compound of any of embodiments 40-47, wherein the conjugate group comprises a lipid.

Embodiment 49. The oligomeric compound of any of embodiments 40-47, wherein the conjugate group comprises a cell-targeting moiety.

Embodiment 50. The oligomeric compound of any of embodiments 1-49, further comprising a terminal group.

Embodiment 51. The oligomeric compound of any of embodiments 1-49, wherein the oligomeric compound is a singled-stranded oligomeric compound.

Embodiment 52. The oligomeric compound of any of embodiments 1-51, wherein the oligomeric compound is capable of reducing the amount of CHMP7 RNA in a cell.

Embodiment 53. The oligomeric compound of any of embodiments 1-52, wherein the modified oligonucleotide of the oligomeric compound is a pharmaceutically acceptable salt comprising one or more cations selected from sodium, potassium, calcium, and magnesium.

Embodiment 54. An oligomeric duplex, comprising a first oligomeric compound and a second oligomeric compound comprising a second modified oligonucleotide, wherein the first oligomeric compound is an oligomeric compound of any of embodiments 1-53.

Embodiment 55. An antisense agent comprising an antisense compound, wherein the antisense compound is the oligomeric compound of any of embodiments 1-53 or the oligomeric duplex of embodiment 54.

Embodiment 56. The antisense agent of embodiment 55, wherein the antisense agent is the oligomeric duplex of embodiment 54

Embodiment 57. The antisense agent of embodiment 55 or embodiment 56, wherein the antisense agent is:

an RNase H agent capable of reducing the amount of CHMP7 nucleic acid through the activation of RNase H; or

an RNAi agent capable of reducing the amount of CHMP7 nucleic acid through the activation of RISC/Ago2.

Embodiment 58. The antisense agent of any of embodiments 55-57, wherein the antisense agent comprises a conjugate group, wherein the conjugate group comprises a cell-targeting moiety.

Embodiment 59. A pharmaceutical composition comprising the oligomeric compound of any of embodiments 1-53, the oligomeric duplex of embodiment 54, or the antisense agent of any of embodiments 55-58, and a pharmaceutically acceptable diluent.

Embodiment 60. The pharmaceutical composition of embodiment 59, wherein the pharmaceutically acceptable diluent is artificial CSF (aCSF) or phosphate- buffered saline (PBS).

Embodiment 61. The pharmaceutical composition of embodiment 60, wherein the pharmaceutical composition consists essentially of the oligomeric compound, oligomeric duplex, or antisense agent, and artificial CSF (aCSF).

Embodiment 62. The pharmaceutical composition of embodiment 60, wherein the pharmaceutical composition consists essentially of the oligomeric compound, oligomeric duplex, or antisense agent, and phosphate buffered saline (PBS).

Embodiment 63. A chirally enriched population of oligomeric compounds of any of embodiments 1-53, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.

Embodiment 64. The chirally enriched population of embodiment 63, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (Sp) configuration.

Embodiment 65. The chirally enriched population of embodiment 63, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (Rp) configuration.

Embodiment 66. The chirally enriched population of embodiment 63, wherein the population is enriched for oligomeric compounds having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage.

Embodiment 67. The chirally enriched population of embodiment 66, wherein the population is enriched for oligomeric compounds having the (Sp) configuration at each phosphorothioate internucleoside linkage or for modified oligonucleotides having the (Rp) configuration at each phosphorothioate internucleoside linkage.

Embodiment 68. The chirally enriched population of embodiment 66, wherein the population is enriched for oligomeric compounds having the (Rp) configuration at one particular phosphorothioate internucleoside linkage and the (Sp) configuration at each of the remaining phosphorothioate internucleoside linkages.

Embodiment 69. The chirally enriched population of embodiment 66, wherein the population is enriched for oligomeric compounds having at least 3 contiguous phosphorothioate internucleoside linkages in the Sp, Sp, and Rp configurations, in the 5' to 3' direction.

Embodiment 70. A population of oligomeric compounds of any of embodiments 1-53, wherein all of the phosphorothioate internucleoside linkages of the modified oligonucleotide are stereorandom.

Embodiment 71. A pharmaceutical composition comprising the population of oligomeric compounds of any of embodiments 63-70 and a pharmaceutically acceptable diluent.

Embodiment 72. The pharmaceutical composition of embodiment 71, wherein the pharmaceutically acceptable diluent is artificial CSF (aCSF) or phosphate-buffered saline (PBS).

Embodiment 73. The pharmaceutical composition of embodiment 72, wherein the pharmaceutical composition consists essentially of the population of oligomeric compounds and artificial CSF (aCSF).

Embodiment 74. The pharmaceutical composition of embodiment 72, wherein the pharmaceutical composition consists essentially of the population of oligomeric compounds and PBS.

I. Certain Oligonucleotides

In certain embodiments, provided herein are oligomeric compounds comprising oligonucleotides, which consist of linked nucleosides. Oligonucleotides may be unmodified oligonucleotides (RNA or DNA) or may be modified oligonucleotides. Modified oligonucleotides comprise at least one modification relative to unmodified RNA or DNA. That is, modified oligonucleotides comprise at least one modified nucleoside (comprising a modified sugar moiety and/or a modified nucleobase) and/or at least one modified internucleoside linkage.

A. Certain Modified Nucleosides

Modified nucleosides comprise a modified sugar moiety or a modified nucleobase or both a modifed sugar moiety and a modified nucleobase.

1. **Certain Sugar Moieties**

In certain embodiments, modified sugar moieties are non-bicyclic modified sugar moieties. In certain embodiments, modified sugar moieties are bicyclic or tricyclic sugar moieties. In certain embodiments, modified sugar moieties are sugar surrogates. Such sugar surrogates may comprise one or more substitutions corresponding to those of other types of modified sugar moieties.

In certain embodiments, modified sugar moieties are non-bicyclic modified sugar moieties comprising a furanosyl ring with one or more substituent groups none of which bridges two atoms of the furanosyl ring to form a bicyclic structure. Such non bridging substituents may be at any position of the furanosyl, including but not limited to substituents at the 2', 4', and/or 5' positions. In certain embodiments one or more non-bridging substituent of non-bicyclic modified sugar moieties is branched. Examples of 2'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to: 2'-F, 2'-OCH_3 ("OMe" or "O-methyl"), and 2'-$O(CH_2)_2OCH_3$ ("MOE" or "O-methoxyethyl"). In certain embodiments, 2'-substituent groups are selected from among: halo, allyl, amino, azido, SH, CN, OCN, CF_3, OCF_3, O-C_1-C_{10} alkoxy, O-C_1-C_{10} substituted alkoxy, O-C_1-C_{10} alkyl, O-C_1-C_{10} substituted alkyl, S-alkyl, N(R_m)-alkyl, O-alkenyl, S-alkenyl, N(R_m)-alkenyl, O-alkynyl, S-alkynyl, N(R_m)-alkynyl, O-alkylenyl-O-alkyl, alkynyl, alkaryl, aralkyl, O-alkaryl, O-aralkyl, $O(CH_2)_2SCH_3$, $O(CH_2)_2ON(R_m)(R_n)$ or $OCH_2C(=O)$-$N(R_m)(R_n)$, where each R_m and R_n is, independently, H, an amino protecting group, or substituted or unsubstituted C_1-C_{10} alkyl, and the 2'-substituent groups described in Cook et al., U.S. 6,531,584; Cook et al., U.S. 5,859,221; and Cook et al., U.S. 6,005,087. Certain embodiments of these 2'-substituent groups can be further substituted with one or more substituent groups independently selected from among: hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro (NO_2), thiol, thioalkoxy, thioalkyl, halogen, alkyl, aryl, alkenyl and alkynyl. Examples of 4'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to alkoxy (*e.g.*, methoxy), alkyl, and those described in Manoharan et al., WO 2015/106128. Examples of 5'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to: 5'-methyl (R or S), 5'-vinyl, and 5'-methoxy. In certain embodiments, non-bicyclic modified sugar moieties comprise more than one non-bridging sugar substituent, for example, 2'-F-5'-methyl sugar moieties and the modified sugar moieties and modified nucleosides described in Migawa et al., WO 2008/101157 and Rajeev et al., US2013/0203836.

In certain embodiments, a 2'-substituted non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, NH_2, N_3, OCF_3, OCH_3, $O(CH_2)_3NH_2$, $CH_2CH{=}CH_2$, $OCH_2CH{=}CH_2$, $OCH_2CH_2OCH_3$, $O(CH_2)_2SCH_3$, $O(CH_2)_2ON(R_m)(R_n)$, $O(CH_2)_2O(CH_2)_2N(CH_3)_2$, and N-substituted acetamide ($OCH_2C(=O)$-$N(R_m)(R_n)$), where each R_m and R_n is, independently, H, an amino protecting group, or substituted or unsubstituted C_1-C_{10} alkyl.

In certain embodiments, a 2'-substituted non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCF_3, OCH_3, $OCH_2CH_2OCH_3$, $O(CH_2)_2SCH_3$, $O(CH_2)_2ON(CH_3)_2$, $O(CH_2)_2O(CH_2)_2N(CH_3)_2$, and $OCH_2C(=O)$-$N(H)CH_3$ ("NMA").

In certain embodiments, a 2'-substituted non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCH_3, and $OCH_2CH_2OCH_3$.

In certain embodiments, modified furanosyl sugar moieties and nucleosides incorporating such modified furanosyl sugar moieties are further defined by isomeric configuration. For example, a 2'-deoxyfuranosyl sugar moiety may be in seven isomeric configurations other than the naturally occurring β-D-deoxyribosyl configuration. Such modified sugar moieties are described in, e.g., WO 2019/157531, incorporated by reference herein. A 2'-modified sugar moiety has an additional stereocenter at the 2'-position relative to a 2'-deoxyfuranosyl sugar moiety; therefore, such sugar moieties have a total of sixteen possible isomeric configurations. 2'-modified sugar moieties described herein are in the β-D-ribosyl isomeric configuration unless otherwise specified.

Certain modifed sugar moieties comprise a substituent that bridges two atoms of the furanosyl ring to form a second ring, resulting in a bicyclic sugar moiety. Nucleosides comprising such bicyclic sugar moieties have been referred to as bicyclic nucleosides (BNAs), locked nucleosides, or conformationally restricted nucleotides (CRN). Certain such compounds are described in US Patent Publication No. 2013/0190383; and PCT publication WO 2013/036868. In certain such embodiments, the bicyclic sugar moiety comprises a bridge between the 4' and the 2' furanose ring atoms. In certain such embodiments, the furanose ring is a ribose ring. Examples of such 4' to 2' bridging sugar substituents include but are not limited to: 4'-CH_2-2', 4'-$(CH_2)_2$-2', 4'-$(CH_2)_3$-2', 4'-CH_2-O-2' ("LNA"), 4'-CH_2-S-2', 4'-$(CH_2)_2$-O-2' ("ENA"), 4'-CH(CH_3)-O-2' (referred to as "constrained ethyl" or "cEt" when in the *S* configuration), 4'-CH_2-O-CH_2-2', 4'-CH_2-N(R)-2', 4'-CH(CH_2OCH_3)-O-2' ("constrained MOE" or "cMOE") and analogs thereof (*see, e.g.,* Seth et al., U.S. 7,399,845, Bhat et al., U.S. 7,569,686, Swayze et al., U.S. 7,741,457, and Swayze et al., U.S. 8,022,193), 4'-C(CH_3)(CH_3)-O-2' and analogs thereof (*see, e.g.,* Seth et al., U.S. 8,278,283), 4'-CH_2-N(OCH_3)-2' and analogs thereof (*see, e.g.,* Prakash et al., U.S. 8,278,425), 4'-CH_2-O-N(CH_3)-2' (*see, e.g.,* Allerson et al., U.S. 7,696,345 and Allerson et al., U.S. 8,124,745), 4'-CH_2-C(H)(CH_3)-2' (*see, e.g.,* Zhou, *et al., J. Org. Chem.,*2009, *74*, 118-134), 4'-CH_2-C(=CH_2)-2' and analogs thereof (*see e.g.*, Seth et al., U.S. 8,278,426), 4'-C(R_aR_b)-N(R)-O-2', 4'-C(R_aR_b)-O-N(R)-2', 4'-CH_2-O-N(R)-2', and 4'-CH_2-N(R)-O-2', wherein each R, R_a, and R_b is, independently, H, a protecting group, or C_1-C_{12} alkyl (*see, e.g.* Imanishi et al., U.S. 7,427,672).

In certain embodiments, such 4' to 2' bridges independently comprise from 1 to 4 linked groups independently selected from: -[C(R_a)(R_b)]$_n$-, -[C(R_a)(R_b)]$_n$-O-, -C(R_a)=C(R_b)-, -C(R_a)=N-, -C(=NR_a)-, -C(=O)-, -C(=S)-, -O-, -Si(R_a)$_2$-, -S(=O)$_x$-, and -N(R_a)-;

wherein:

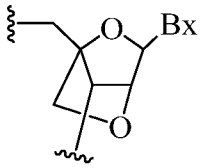
x is 0, 1, or 2;

n is 1, 2, 3, or 4;

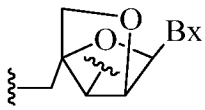
each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1, NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O)-H), substituted acyl, CN, sulfonyl (S(=O)$_2$-J_1), or sulfoxyl (S(=O)-J_1); and

each J_1 and J_2 is, independently, H, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1-C_{12} aminoalkyl, substituted C_1-C_{12} aminoalkyl, or a protecting group.

Additional bicyclic sugar moieties are known in the art, see, for example: Freier et al., Nucleic Acids Research, 1997, 25(22), 4429-4443, Albaek et al., J. Org. Chem., 2006, 71, 7731-7740, Singh et al., Chem. Commun., 1998, 4, 455-456; Koshkin et al., Tetrahedron, 1998, 54, 3607-3630; Wahlestedt et al., Proc. Natl. Acad. Sci. U. S. A., 2000, 97, 5633-5638; Kumar et al., Bioorg. Med. Chem. Lett., 1998, 8, 2219-2222; Singh et al., J. Org. Chem., 1998, 63, 10035-10039; Srivastava et al., J. Am. Chem. Soc., 2007, 129, 8362-8379; Elayadi et al., Curr. Opinion Invens. Drugs, 2001, 2, 558-561; Braasch et al., Chem. Biol., 2001, 8, 1-7; Orum et al., Curr. Opinion Mol. Ther., 2001, 3, 239-243; Wengel et al., U.S. 7,053,207, Imanishi et al., U.S. 6,268,490, Imanishi et al. U.S. 6,770,748, Imanishi et al., U.S. RE44,779; Wengel et al., U.S. 6,794,499, Wengel et al., U.S. 6,670,461; Wengel et al., U.S. 7,034,133, Wengel et al., U.S. 8,080,644; Wengel et al., U.S. 8,034,909; Wengel et al., U.S. 8,153,365; Wengel et al., U.S. 7,572,582; and Ramasamy et al., U.S. 6,525,191, Torsten et al., WO 2004/106356, Wengel et al., WO 1999/014226; Seth et al.,WO 2007/134181; Seth et al., U.S. 7,547,684; Seth et al., U.S. 7,666,854; Seth et al., U.S. 8,088,746; Seth et al., U.S. 7,750,131; Seth et al., U.S. 8,030,467; Seth et al., U.S. 8,268,980; Seth et al., U.S. 8,546,556; Seth et al., U.S. 8,530,640; Migawa et al., U.S. 9,012,421; Seth et al., U.S. 8,501,805; Allerson et al., US2008/0039618; and Migawa et al., US2015/0191727. In certain embodiments, bicyclic sugar moieties and nucleosides incorporating such bicyclic sugar moieties are further defined by isomeric configuration. For example, an LNA nucleoside (described herein) may be in the α-L configuration or in the β-D configuration.



LNA (β-D-configuration)
bridge = 4'-CH_2-O-2'



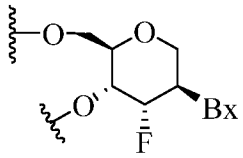
α-*L*-LNA (α-*L*-configuration)
bridge = 4'-CH_2-O-2'

α-L-methyleneoxy (4'-CH_2-O-2') or α-L-LNA bicyclic nucleosides have been incorporated into oligonucleotides that showed antisense activity (Frieden et al., *Nucleic Acids Research,* 2003, *21*, 6365-6372). Herein, general descriptions of bicyclic nucleosides include both isomeric configurations. When the positions of specific bicyclic nucleosides (*e.g.*, LNA or cEt) are identified in exemplified embodiments herein, they are in the β-D configuration, unless otherwise specified.

In certain embodiments, modified sugar moieties comprise one or more non-bridging sugar substituent and one or more bridging sugar substituent (e.g., 5'-substituted and 4'-2' bridged sugars).

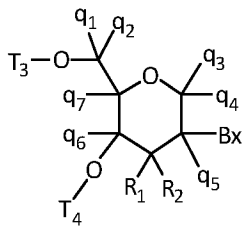
In certain embodiments, modified sugar moieties are sugar surrogates. In certain such embodiments, the oxygen atom of the sugar moiety is replaced, *e.g.,* with a sulfur, carbon or nitrogen atom. In certain such embodiments, such modified sugar moieties also comprise bridging and/or non-bridging substituents as described herein. For example, certain sugar surrogates comprise a 4'-sulfur atom and a substitution at the 2'-position (*see, e.g.,* Bhat et al., U.S. 7,875,733 and Bhat et al., U.S. 7,939,677) and/or the 5' position.

In certain embodiments, sugar surrogates comprise rings having other than 5 atoms. For example, in certain embodiments, a sugar surrogate comprises a six-membered tetrahydropyran ("THP"). Such tetrahydropyrans may be further modified or substituted. Nucleosides comprising such modified tetrahydropyrans include but are not limited to hexitol nucleic acid ("HNA"), anitol nucleic acid ("ANA"), manitol nucleic acid ("MNA") (*see, e.g.,* Leumann, CJ. *Bioorg. & Med. Chem.* 2002, *10*, 841-854), fluoro HNA:



F-HNA

("F-HNA", *see e.g.* Swayze et al., U.S. 8,088,904; Swayze et al., U.S. 8,440,803; Swayze et al., U.S. 8,796,437; and Swayze et al., U.S. 9,005,906; F-HNA can also be referred to as a F-THP or 3'-fluoro tetrahydropyran), and nucleosides comprising additional modified THP compounds having the formula:



wherein, independently, for each of the modified THP nucleosides:

Bx is a nucleobase moiety;

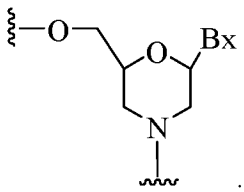
T_3 and T_4 are each, independently, an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide or one of T_3 and T_4 is an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide and the other of T_3 and T_4 is H, a hydroxyl protecting group, a linked conjugate group, or a 5' or 3'-terminal group;

q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each, independently, H, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl, or substituted C_2-C_6 alkynyl; and

each of R_1 and R_2 is independently selected from among: hydrogen, halogen, substituted or unsubstituted alkoxy, NJ_1J_2, SJ_1, N_3, $OC(=X)J_1$, $OC(=X)NJ_1J_2$, $NJ_3C(=X)NJ_1J_2$, and CN, wherein X is O, S or NJ_1, and each J_1, J_2, and J_3 is, independently, H or C_1-C_6 alkyl.

In certain embodiments, modified THP nucleosides are provided wherein q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is other than H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is methyl. In certain embodiments, modified THP nucleosides are provided wherein one of R_1 and R_2 is F. In certain embodiments, R_1 is F and R_2 is H, in certain embodiments, R_1 is methoxy and R_2 is H, and in certain embodiments, R_1 is methoxyethoxy and R_2 is H.

In certain embodiments, sugar surrogates comprise rings having more than 5 atoms and more than one heteroatom. For example, nucleosides comprising morpholino sugar moieties and their use in oligonucleotides have been reported (*see, e.g.,* Braasch et al., Biochemistry, 2002, *41*, 4503-4510 and Summerton et al., U.S. 5,698,685; Summerton et al., U.S. 5,166,315; Summerton et al., U.S. 5,185,444; and Summerton et al., U.S. 5,034,506). As used here, the term "morpholino" means a sugar surrogate having the following structure:



In certain embodiments, morpholinos may be modified, for example by adding or altering various substituent groups from the above morpholino structure. Such sugar surrogates are referred to herein as "modifed morpholinos."

In certain embodiments, sugar surrogates comprise acyclic moieites. Examples of nucleosides and oligonucleotides comprising such acyclic sugar surrogates include but are not limited to: peptide nucleic acid ("PNA"), acyclic butyl nucleic acid (*see, e.g.,* Kumar et al., *Org. Biomol. Chem.*, 2013, *11*, 5853-5865), and nucleosides and oligonucleotides described in Manoharan et al., WO2011/133876.

Many other bicyclic and tricyclic sugar and sugar surrogate ring systems are known in the art that can be used in modified nucleosides.

2. Certain Modified Nucleobases

In certain embodiments, modified oligonucleotides comprise one or more nucleosides comprising an unmodified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleoside comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleoside that does not comprise a nucleobase, referred to as an abasic nucleoside.

In certain embodiments, modified nucleobases are selected from: 5-substituted pyrimidines, 6-azapyrimidines, alkyl or alkynyl substituted pyrimidines, alkyl substituted purines, and N-2, N-6 and O-6 substituted purines. In certain embodiments, modified nucleobases are selected from: 5-methyl cytosine, 2-aminopropyladenine, 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-N-methylguanine, 6-N-methyladenine, 2-propyladenine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-propynyl (-C≡C-CH_3) uracil, 5-propynylcytosine, 6-azouracil, 6-azocytosine, 6-azothymine, 5-ribosyluracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl, 8-aza and other 8-substituted purines, 5-halo, particularly 5-bromo, 5-trifluoromethyl, 5-halouracil, and 5-halocytosine, 7-methylguanine, 7-methyladenine, 2-F-adenine, 2-aminoadenine, 7-deazaguanine, 7-deazaadenine, 3-deazaguanine, 3-deazaadenine, 6-N-benzoyladenine, 2-N-isobutyrylguanine, 4-N-benzoylcytosine, 4-N-benzoyluracil, 5-methyl 4-N-benzoylcytosine, 5-methyl 4-N-benzoyluracil, universal bases, hydrophobic bases, promiscuous bases, size-expanded bases, and fluorinated bases. Further modified nucleobases include tricyclic pyrimidines, such as 1,3-diazaphenoxazine-2-one, 1,3-diazaphenothiazine-2-one and 9-(2-aminoethoxy)-1,3-diazaphenoxazine-2-one (G-clamp). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in Merigan et al., U.S. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, Kroschwitz, J.I., Ed., John Wiley & Sons, 1990, 858-859; Englisch *et al.*, *Angewandte Chemie*, International Edition, 1991, *30*, 613; Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, Crooke, S.T. and Lebleu, B., Eds., CRC Press, 1993, 273-288; and those disclosed in Chapters 6 and 15, *Antisense Drug Technology*, Crooke S.T., Ed., CRC Press, 2008, 163-166 and 442-443.

Publications that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include without limitation, Manoharan et al., US2003/0158403; Manoharan et al., US2003/0175906; Dinh et al., U.S. 4,845,205; Spielvogel et al., U.S. 5,130,302; Rogers et al., U.S. 5,134,066;

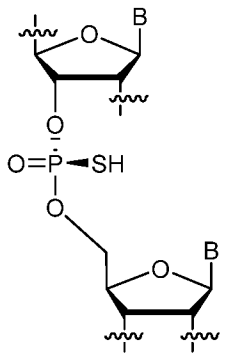
Bischofberger et al., U.S. 5,175,273; Urdea et al., U.S. 5,367,066; Benner et al., U.S. 5,432,272; Matteucci et al., U.S. 5,434,257; Gmeiner et al., U.S. 5,457,187; Cook et al., U.S. 5,459,255; Froehler et al., U.S. 5,484,908; Matteucci et al., U.S. 5,502,177; Hawkins et al., U.S. 5,525,711; Haralambidis et al., U.S. 5,552,540; Cook et al., U.S. 5,587,469; Froehler et al., U.S. 5,594,121; Switzer et al., U.S. 5,596,091; Cook et al., U.S. 5,614,617; Froehler et al., U.S. 5,645,985; Cook et al., U.S. 5,681,941; Cook et al., U.S. 5,811,534; Cook et al., U.S. 5,750,692; Cook et al., U.S. 5,948,903; Cook et al., U.S. 5,587,470; Cook et al., U.S. 5,457,191; Matteucci et al., U.S. 5,763,588; Froehler et al., U.S. 5,830,653; Cook et al., U.S. 5,808,027; Cook et al., 6,166,199; and Matteucci et al., U.S. 6,005,096.

3. Certain Modified Internucleoside Linkages

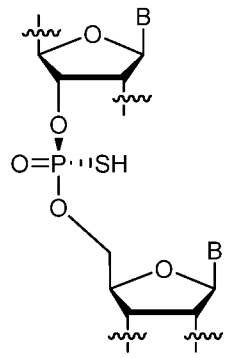
In certain embodiments, nucleosides of modified oligonucleotides may be linked together using any internucleoside linkage. The two main classes of internucleoside linking groups are defined by the presence or absence of a phosphorus atom. Representative phosphorus-containing internucleoside linkages include but are not limited to phosphodiesters, which contain a phosphodiester bond ("$P(O_2)=O$") (also referred to as unmodified or naturally occurring linkages), phosphotriesters, methylphosphonates, phosphoramidates, phosphorothioates ("$P(O_2)=S$"), and phosphorodithioates ("HS-P=S"). Representative non-phosphorus containing internucleoside linking groups include but are not limited to methylenemethylimino ($-CH_2-N(CH_3)-O-CH_2-$), thiodiester, thionocarbamate (-O-C(=O)(NH)-S-); siloxane ($-O-SiH_2-O-$); and N,N'-dimethylhydrazine ($-CH_2-N(CH_3)-N(CH_3)-$). Modified internucleoside linkages, compared to naturally occurring phosphodiester internucleoside linkages, can be used to alter, typically increase, nuclease resistance of the oligonucleotide. In certain embodiments, internucleoside linkages having a chiral atom can be prepared as a racemic mixture, or as separate enantiomers. Methods of preparation of phosphorous-containing and non-phosphorous-containing internucleoside linkages are well known to those skilled in the art.

Representative internucleoside linkages having a chiral center include but are not limited to alkylphosphonates and phosphorothioates. Modified oligonucleotides comprising internucleoside linkages having a chiral center can be prepared as populations of modified oligonucleotides comprising stereorandom internucleoside linkages, or as populations of modified oligonucleotides comprising phosphorothioate internucleoside linkages in particular stereochemical configurations. In certain embodiments, populations of modified oligonucleotides comprise phosphorothioate internucleoside linkages wherein all of the phosphorothioate internucleoside linkages are stereorandom. Such modified oligonucleotides can be generated using synthetic methods that result in random selection of the stereochemical configuration of each phosphorothioate internucleoside linkage. Nonetheless, as is well understood by those of skill in the art, each individual phosphorothioate of each individual oligonucleotide molecule has a defined stereoconfiguration. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising one or more particular phosphorothioate internucleoside linkage in a particular, independently selected stereochemical configuration. In certain embodiments, the particular configuration of the particular phosphorothioate internucleoside linkage is present in at least 65% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate internucleoside linkage is present in at least 70% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate internucleoside linkage is present in at least 80% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate internucleoside linkage is present in at least 90% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate internucleoside linkage is present in at least 99% of the molecules in the population. Such chirally

enriched populations of modified oligonucleotides can be generated using synthetic methods known in the art, *e.g.*, methods described in Oka et al., *JACS*, 2003, *125*, 8307, Wan et al., *Nuc. Acid. Res.*, 2014, 42, 13456, and WO 2017/015555. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one indicated phosphorothioate in the *(Sp)* configuration. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one phosphorothioate in the *(Rp)* configuration. In certain embodiments, modified oligonucleotides comprising *(Rp)* and/or *(Sp)* phosphorothioates comprise one or more of the following formulas, respectively, wherein "B" indicates a nucleobase:



(R_p)



(S_p)

Unless otherwise indicated, chiral internucleoside linkages of modified oligonucleotides described herein can be stereorandom or in a particular stereochemical configuration.

Neutral internucleoside linkages include, without limitation, phosphotriesters, methylphosphonates, MMI (3'-CH_2-N(CH_3)-O-5'), amide-3 (3'-CH_2-C(=O)-N(H)-5'), amide-4 (3'-CH_2-N(H)-C(=O)-5'), formacetal (3'-O-CH_2-O-5'), methoxypropyl (MOP), and thioformacetal (3'-S-CH_2-O-5'). Further neutral internucleoside linkages include nonionic linkages comprising siloxane (dialkylsiloxane), carboxylate ester, carboxamide, sulfide, sulfonate ester and amides (see, for example: *Carbohydrate Modifications in Antisense Research*; Y.S. Sanghvi and P.D. Cook, Eds., ACS Symposium Series 580; Chapters 3 and 4, 40-65). Further neutral internucleoside linkages include nonionic linkages comprising mixed N, O, S and CH_2 component parts.

B. Certain Motifs

In certain embodiments, modified oligonucleotides comprise one or more modified nucleosides comprising a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise one or more modified nucleosides comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more modified internucleoside linkage. In such embodiments, the modified, unmodified, and differently modified sugar moieties, nucleobases, and/or internucleoside linkages of a modified oligonucleotide define a pattern or motif. In certain embodiments, the patterns of sugar moieties, nucleobases, and internucleoside linkages are each independent of one another. Thus, a modified oligonucleotide may be described by its sugar motif, nucleobase motif and/or internucleoside linkage motif (as used herein, nucleobase motif describes the modifications to the nucleobases independent of the sequence of nucleobases).

1. Certain Sugar Motifs

In certain embodiments, oligonucleotides comprise one or more type of modified sugar and/or unmodified sugar moiety arranged along the oligonucleotide or portion thereof in a defined pattern or sugar motif. In certain instances, such sugar motifs include but are not limited to any of the sugar modifications discussed herein.

In certain embodiments, modified oligonucleotides have a gapmer motif, which is defined by two external regions or "wings" and a central or internal region or "gap." The three regions of a gapmer motif (the 5'-wing, the gap, and the 3'-wing) form a contiguous sequence of nucleosides wherein at least some of the sugar moieties of the nucleosides of each of the wings differ from at least some of the sugar moieties of the nucleosides of the gap. Specifically, at least the sugar moieties of the nucleosides of each wing that are closest to the gap (the 3'-most nucleoside of the 5'-wing and the 5'-most nucleoside of the 3'-wing) differ from the sugar moiety of the neighboring gap nucleosides, thus defining the boundary between the wings and the gap (i.e., the wing/gap junction). In certain embodiments, the sugar moieties within the gap are the same as one another. In certain embodiments, the gap includes one or more nucleoside having a sugar moiety that differs from the sugar moiety of one or more other nucleosides of the gap. In certain embodiments, the sugar motifs of the two wings are the same as one another (symmetric gapmer). In certain embodiments, the sugar motif of the 5'-wing differs from the sugar motif of the 3'-wing (asymmetric gapmer).

In certain embodiments, the wings of a gapmer comprise 1-6 nucleosides. In certain embodiments, each nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least one nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least two nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least three nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least four nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least five nucleosides of each wing of a gapmer comprises a modified sugar moiety.

In certain embodiments, the gap of a gapmer comprises 7-12 nucleosides. In certain embodiments, each nucleoside of the gap of a gapmer comprises a 2'-deoxyribosyl sugar moiety. In certain embodiments, at least six nucleosides of the gap of a gapmer comprise a 2'-β-D-deoxyribosyl sugar moiety. In certain embodiments, each nucleoside of the gap of a gapmer comprises a 2'-β-D-deoxyribosyl sugar moiety. In certain embodiments, at least one nucleoside of the gap of a gapmer comprises a modified sugar moiety. In certain embodiments, at least one nucleoside of the gap of a gapmer comprises a 2'-OMe sugar moiety.

In certain embodiments, the gapmer is a deoxy gapmer. In certain embodiments, the nucleosides on the gap side of each wing/gap junction comprise 2'-deoxyribosyl sugar moieties and the nucleosides on the wing sides of each wing/gap junction comprise modified sugar moieties. In certain embodiments, at least six nucleosides of the gap of a gapmer comprise a 2'-β-D-deoxyribosyl sugar moiety. In certain embodiments, each nucleoside of the gap of a gapmer comprises a 2'-deoxyribosyl sugar moiety. In certain embodiments, each nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, one nucleoside of the gap comprises a modified sugar moiety and each remaining nucleoside of the gap comprises a 2'-deoxyribosyl sugar moiety.

In certain embodiments, modified oligonucleotides comprise or consist of a portion having a fully modified sugar motif. In such embodiments, each nucleoside of the fully modified portion of the modified oligonucleotide comprises a modified sugar moiety. In certain embodiments, each nucleoside of the entire modified oligonucleotide comprises a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise or consist of a portion having a fully modified sugar motif, wherein each nucleoside within the fully modified portion comprises the same modified sugar moiety, referred to herein as a uniformly modified sugar motif. In certain embodiments, a fully modified oligonucleotide is a uniformly modified oligonucleotide. In certain embodiments, each nucleoside of a uniformly modified oligonucleotide comprises the same 2'-modification.

Herein, the lengths (number of nucleosides) of the three regions of a gapmer may be provided using the notation [# of nucleosides in the 5'-wing] – [# of nucleosides in the gap] – [# of nucleosides in the 3'-wing]. Thus, a 5-10-5 gapmer consists of 5 linked nucleosides in each wing and 10 linked nucleosides in the gap. Where such nomenclature is followed by a specific modification, that modification is the modification in each sugar moiety of each wing and the gap nucleosides comprises a 2'-β-D-deoxyribosyl sugar moiety. Thus, a 5-10-5 MOE gapmer consists of 5 linked 2'-MOE nucleosides in the 5'-wing, 10 linked a 2'-β-D-deoxynucleosides in the gap, and 5 linked 2'-MOE nucleosides in the 3'-wing. A 3-10-3 cEt gapmer consists of 3 linked cEt nucleosides in the 5'-wing, 10 linked 2'-β-D-deoxynucleosides in the gap, and 3 linked cEt nucleosides in the 3'-wing. A 5-8-5 gapmer consists of 5 linked nucleosides comprising a modified sugar moiety in the 5'-wing, 8 linked a 2'-β-D-deoxynucleosides in the gap, and 5 linked nucleosides comprising a modified sugar moiety in the 3'-wing. A mixed wing gapmer has at least two different modified sugar moieties in the 5' and/or the 3' wing. A 5-8-5 or 5-8-4 mixed wing gapmer has at least two different modified sugar moieties in the 5'- and/or the 3'-wing.

In certain embodiments, modified oligonucleotides are 5-10-5 MOE gapmers. In certain embodiments, modified oligonucleotides are 6-10-4 MOE gapmers. In certain embodiments, modified oligonucleotides are 4-10-6 MOE gapmers. In certain embodiments, modified oligonucleotides are 5-8-4 MOE gapmers. In certain embodiments, modified oligonucleotides are 3-10-7 MOE gapmers. In certain embodiments, modified oligonucleotides are 7-10-3 MOE gapmers. In certain embodiments, modified oligonucleotides are 5-8-5 MOE gapmers. In certain embodiments, modified oligonucleotides are 5-9-5 MOE gapmers. In certain embodiments, modified oligonucleotides are X-Y-Z MOE gapmers, wherein X and Z are independently selected from 1, 2, 3, 4, 5, 6, or 7 linked 2'-MOE nucleosides and Y is selected from 7, 8, 9, 10, or 11 linked deoxynucleosides.

In certain embodiments, modified oligonucleotides have the following sugar motif (5' to 3'): eeeeedyddddddddeeeee, wherein 'd' represents a 2'-deoxyribosyl sugar moiety, 'e' represents a 2'-MOE sugar moiety, and 'y' represents a 2'-OMe sugar moiety.

2. Certain Nucleobase Motifs

In certain embodiments, oligonucleotides comprise modified and/or unmodified nucleobases arranged along the oligonucleotide or portion thereof in a defined pattern or motif. In certain embodiments, each nucleobase is modified. In certain embodiments, none of the nucleobases are modified. In certain embodiments, each purine or each pyrimidine is modified. In certain embodiments, each adenine is modified. In certain embodiments, each guanine is modified. In certain embodiments, each thymine is modified. In certain embodiments, each uracil is modified. In certain embodiments, each cytosine is modified. In certain embodiments, some or all of the cytosine nucleobases in a modified oligonucleotide are 5-methyl cytosines. In certain embodiments, all of the cytosine nucleobases are 5-methyl cytosines and all of the other nucleobases of the modified oligonucleotide are unmodified nucleobases.

In certain embodiments, modified oligonucleotides comprise a block of modified nucleobases. In certain such embodiments, the block is at the 3'-end of the oligonucleotide. In certain embodiments the block is within 3 nucleosides of the 3'-end of the oligonucleotide. In certain embodiments, the block is at the 5'-end of the oligonucleotide. In certain embodiments the block is within 3 nucleosides of the 5'-end of the oligonucleotide.

In certain embodiments, oligonucleotides having a gapmer motif comprise a nucleoside comprising a modified nucleobase. In certain such embodiments, one nucleoside comprising a modified nucleobase is in the central gap of an oligonucleotide having a gapmer motif. In certain such embodiments, the sugar moiety of the nucleoside is a 2'-

deoxyribosyl sugar moiety. In certain embodiments, the modified nucleobase is selected from: a 2-thiopyrimidine and a 5-propynepyrimidine.

3. Certain Internucleoside Linkage Motifs

In certain embodiments, oligonucleotides comprise modified and/or unmodified internucleoside linkages arranged along the oligonucleotide or portion thereof in a defined pattern or motif. In certain embodiments, each internucleoside linking group is a phosphodiester internucleoside linkage (P=O). In certain embodiments, each internucleoside linking group of a modified oligonucleotide is a phosphorothioate internucleoside linkage (P=S). In certain embodiments, each internucleoside linkage of a modified oligonucleotide is independently selected from a phosphorothioate internucleoside linkage and phosphodiester internucleoside linkage. In certain embodiments, each phosphorothioate internucleoside linkage is independently selected from a stereorandom phosphorothioate, a *(Sp)* phosphorothioate, and a *(Rp)* phosphorothioate. In certain embodiments, the sugar motif of a modified oligonucleotide is a gapmer and the internucleoside linkages within the gap are all modified. In certain such embodiments, some or all of the internucleoside linkages in the wings are unmodified phosphodiester internucleoside linkages. In certain embodiments, the terminal internucleoside linkages are modified. In certain embodiments, the sugar motif of a modified oligonucleotide is a gapmer, and the internucleoside linkage motif comprises at least one phosphodiester internucleoside linkage in at least one wing, wherein the at least one phosphodiester internucleoside linkage is not a terminal internucleoside linkage, and the remaining internucleoside linkages are phosphorothioate internucleoside linkages. In certain such embodiments, all of the phosphorothioate internucleoside linkages are stereorandom. In certain embodiments, all of the phosphorothioate internucleoside linkages in the wings are *(S*p*)* phosphorothioates, and the gap comprises at least one *S*p, *S*p, *R*p motif. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising such internucleoside linkage motifs.

In certain embodiments, modified oligonucleotides have an internucleoside linkage motif of soooossssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

C. Certain Lengths

It is possible to increase or decrease the length of an oligonucleotide without eliminating activity. For example, in Woolf et al., *Proc. Natl. Acad. Sci.* USA, 1992, *89*, 7305-7309, 1992), a series of oligonucleotides 13-25 nucleobases in length were tested for their ability to induce cleavage of a target nucleic acid in an oocyte injection model. Oligonucleotides 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the oligonucleotides were able to direct specific cleavage of the target nucleic acid, albeit to a lesser extent than the oligonucleotides that contained no mismatches. Similarly, target specific cleavage was achieved using 13 nucleobase oligonucleotides, including those with 1 or 3 mismatches.

In certain embodiments, oligonucleotides (including modified oligonucleotides) can have any of a variety of ranges of lengths. In certain embodiments, oligonucleotides consist of X to Y linked nucleosides, where X represents the fewest number of nucleosides in the range and Y represents the largest number nucleosides in the range. In certain such embodiments, X and Y are each independently selected from 8, 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, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and 50; provided that X≤Y. For example, in certain embodiments, oligonucleotides consist of 12 to 13, 12 to 14, 12 to 15, 12 to 16, 12 to 17, 12 to 18, 12 to 19, 12 to 20, 12 to 21, 12 to 22, 12 to 23, 12 to 24, 12 to 25, 12 to 26, 12 to 27, 12 to 28, 12 to 29, 12 to

30, 13 to 14, 13 to 15, 13 to 16, 13 to 17, 13 to 18, 13 to 19, 13 to 20, 13 to 21, 13 to 22, 13 to 23, 13 to 24, 13 to 25, 13 to 26, 13 to 27, 13 to 28, 13 to 29, 13 to 30, 14 to 15, 14 to 16, 14 to 17, 14 to 18, 14 to 19, 14 to 20, 14 to 21, 14 to 22, 14 to 23, 14 to 24, 14 to 25, 14 to 26, 14 to 27, 14 to 28, 14 to 29, 14 to 30, 15 to 16, 15 to 17, 15 to 18, 15 to 19, 15 to 20, 15 to 21, 15 to 22, 15 to 23, 15 to 24, 15 to 25, 15 to 26, 15 to 27, 15 to 28, 15 to 29, 15 to 30, 16 to 17, 16 to 18, 16 to 19, 16 to 20, 16 to 21, 16 to 22, 16 to 23, 16 to 24, 16 to 25, 16 to 26, 16 to 27, 16 to 28, 16 to 29, 16 to 30, 17 to 18, 17 to 19, 17 to 20, 17 to 21, 17 to 22, 17 to 23, 17 to 24, 17 to 25, 17 to 26, 17 to 27, 17 to 28, 17 to 29, 17 to 30, 18 to 19, 18 to 20, 18 to 21, 18 to 22, 18 to 23, 18 to 24, 18 to 25, 18 to 26, 18 to 27, 18 to 28, 18 to 29, 18 to 30, 19 to 20, 19 to 21, 19 to 22, 19 to 23, 19 to 24, 19 to 25, 19 to 26, 19 to 29, 19 to 28, 19 to 29, 19 to 30, 20 to 21, 20 to 22, 20 to 23, 20 to 24, 20 to 25, 20 to 26, 20 to 27, 20 to 28, 20 to 29, 20 to 30, 21 to 22, 21 to 23, 21 to 24, 21 to 25, 21 to 26, 21 to 27, 21 to 28, 21 to 29, 21 to 30, 22 to 23, 22 to 24, 22 to 25, 22 to 26, 22 to 27, 22 to 28, 22 to 29, 22 to 30, 23 to 24, 23 to 25, 23 to 26, 23 to 27, 23 to 28, 23 to 29, 23 to 30, 24 to 25, 24 to 26, 24 to 27, 24 to 28, 24 to 29, 24 to 30, 25 to 26, 25 to 27, 25 to 28, 25 to 29, 25 to 30, 26 to 27, 26 to 28, 26 to 29, 26 to 30, 27 to 28, 27 to 29, 27 to 30, 28 to 29, 28 to 30, or 29 to 30 linked nucleosides.

D. Certain Modified Oligonucleotides

In certain embodiments, the above modifications (sugar, nucleobase, internucleoside linkage) are incorporated into a modified oligonucleotide. In certain embodiments, modified oligonucleotides are characterized by their modification motifs and overall lengths. In certain embodiments, such parameters are each independent of one another. Thus, unless otherwise indicated, each internucleoside linkage of an oligonucleotide having a gapmer sugar motif may be modified or unmodified and may or may not follow the gapmer modification pattern of the sugar modifications. For example, the internucleoside linkages within the wing regions of a sugar gapmer may be the same or different from one another and may be the same or different from the internucleoside linkages of the gap region of the sugar motif. Likewise, such sugar gapmer oligonucleotides may comprise one or more modified nucleobase independent of the gapmer pattern of the sugar modifications. Unless otherwise indicated, all modifications are independent of nucleobase sequence.

E. Certain Populations of Modified Oligonucleotides

Populations of modified oligonucleotides in which all of the modified oligonucleotides of the population have the same molecular formula can be stereorandom populations or chirally enriched populations. All of the chiral centers of all of the modified oligonucleotides are stereorandom in a stereorandom population. In a chirally enriched population, at least one particular chiral center is not stereorandom in the modified oligonucleotides of the population. In certain embodiments, the modified oligonucleotides of a chirally enriched population are enriched for β-D ribosyl sugar moieties, and all of the phosphorothioate internucleoside linkages are stereorandom. In certain embodiments, the modified oligonucleotides of a chirally enriched population are enriched for both β-D ribosyl sugar moieties and at least one, particular phosphorothioate internucleoside linkage in a particular stereochemical configuration.

F. Nucleobase Sequence

In certain embodiments, oligonucleotides (unmodified or modified oligonucleotides) are further described by their nucleobase sequence. In certain embodiments oligonucleotides have a nucleobase sequence that is complementary to a second oligonucleotide or an identified reference nucleic acid, such as a target nucleic acid. In certain such embodiments, a portion of an oligonucleotide has a nucleobase sequence that is complementary to a second oligonucleotide or an identified reference nucleic acid, such as a target nucleic acid. In certain embodiments, the

nucleobase sequence of a portion or entire length of an oligonucleotide is at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or 100% complementary to the second oligonucleotide or nucleic acid, such as a target nucleic acid.

II. Certain Oligomeric Compounds

In certain embodiments, provided herein are oligomeric compounds, which consist of an oligonucleotide (modified or unmodified) and optionally one or more conjugate groups and/or terminal groups. Conjugate groups consist of one or more conjugate moiety and a conjugate linker which links the conjugate moiety to the oligonucleotide. Conjugate groups may be attached to either or both ends of an oligonucleotide and/or at any internal position. In certain embodiments, conjugate groups are attached to the 2'-position of a nucleoside of a modified oligonucleotide. In certain embodiments, conjugate groups that are attached to either or both ends of an oligonucleotide are terminal groups. In certain such embodiments, conjugate groups or terminal groups are attached at the 3' and/or 5'-end of oligonucleotides. In certain such embodiments, conjugate groups (or terminal groups) are attached at the 3'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 3'-end of oligonucleotides. In certain embodiments, conjugate groups (or terminal groups) are attached at the 5'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 5'-end of oligonucleotides.

Examples of terminal groups include but are not limited to conjugate groups, capping groups, phosphate moieties, protecting groups, abasic nucleosides, modified or unmodified nucleosides, and two or more nucleosides that are independently modified or unmodified.

A. Certain Conjugate Groups

In certain embodiments, oligonucleotides are covalently attached to one or more conjugate groups. In certain embodiments, conjugate groups modify one or more properties of the attached oligonucleotide, including but not limited to pharmacodynamics, pharmacokinetics, stability, binding, absorption, tissue distribution, cellular distribution, cellular uptake, charge and clearance.

In certain embodiments, conjugation of one or more carbohydrate moieties to a modified oligonucleotide can optimize one or more properties of the modified oligonucleotide. In certain embodiments, the carbohydrate moiety is attached to a modified subunit of the modified oligonucleotide. For example, the ribose sugar of one or more ribonucleotide subunits of a modified oligonucleotide 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), which is a modified sugar moiety. A cyclic carrier may be a carbocyclic ring system, i.e., one or more ring atoms may be a heteroatom, e.g., nitrogen, oxygen, sulphur. 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. In certain embodiments, the modified oligonucleotide is a gapmer.

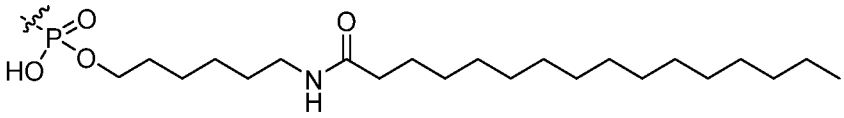
In certain embodiments, conjugate groups impart a new property on the attached oligonucleotide, *e.g.*, fluorophores or reporter groups that enable detection of the oligonucleotide. Certain conjugate groups and conjugate moieties have been described previously, for example: cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1994, *4*, 1053-1060), a thioether, *e.g.,* hexyl-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., do-decan-diol 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-H-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 a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, *1264,* 229-237), an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.,* 1996, *277*, 923-937), a tocopherol group (Nishina et al., *Molecular Therapy Nucleic Acids*, 2015**,** *4*, e220; and Nishina et al., *Molecular Therapy,* 2008, *16*, 734-740), or a GalNAc cluster (*e.g.*, WO2014/179620).

In certain embodiments, the conjugate group may comprise a conjugate moiety selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, C5 alkyl, C22 alkenyl, C20 alkenyl, C16 alkenyl, C10 alkenyl, C21 alkenyl, C19 alkenyl, C18 alkenyl, C15 alkenyl, C14 alkenyl, C13 alkenyl, C12 alkenyl, C11 alkenyl, C9 alkenyl, C8 alkenyl, C7 alkenyl, C6 alkenyl, or C5 alkenyl.

In certain embodiments, the conjugate group may comprise a conjugate moiety selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, or C5 alkyl, where the alkyl chain has one or more unsaturated bonds.

In certain embodiments, a conjugate group is a lipid having the following structure:



1. **Conjugate Moieties**

Conjugate moieties include, without limitation, intercalators, reporter molecules, polyamines, polyamides, peptides, carbohydrates, vitamin moieties, polyethylene glycols, thioethers, polyethers, cholesterols, thiocholesterols, cholic acid moieties, folate, lipids, lipophilic groups, phospholipids, biotin, phenazine, phenanthridine, anthraquinone, adamantane, acridine, fluoresceins, rhodamines, coumarins, fluorophores, and dyes.

In certain embodiments, a conjugate moiety comprises an active drug substance, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fen-bufen, ketoprofen, (*S*)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, fingolimod, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indo-methicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

2. **Conjugate Linkers**

Conjugate moieties are attached to oligonucleotides through conjugate linkers. In certain oligomeric compounds, the conjugate linker is a single chemical bond (i.e., the conjugate moiety is attached directly to an oligonucleotide through a single bond). In certain embodiments, the conjugate linker comprises a chain structure, such as a hydrocarbyl chain, or an oligomer of repeating units such as ethylene glycol, nucleosides, or amino acid units.

In certain embodiments, a conjugate linker comprises one or more groups selected from alkyl, amino, oxo,

amide, disulfide, polyethylene glycol, ether, thioether, and hydroxylamino. In certain such embodiments, the conjugate linker comprises groups selected from alkyl, amino, oxo, amide and ether groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and amide groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and ether groups. In certain embodiments, the conjugate linker comprises at least one phosphorus moiety. In certain embodiments, the conjugate linker comprises at least one phosphate group. In certain embodiments, the conjugate linker includes at least one neutral linking group.

In certain embodiments, conjugate linkers, including the conjugate linkers described above, are bifunctional linking moieties, *e.g.,* those known in the art to be useful for attaching conjugate groups to parent compounds, such as the oligonucleotides provided herein. In general, a bifunctional linking moiety comprises at least two functional groups. One of the functional groups is selected to bind to a particular site on a parent compound and the other is selected to bind to a conjugate group. Examples of functional groups used in a bifunctional linking moiety include but are not limited to electrophiles for reacting with nucleophilic groups and nucleophiles for reacting with electrophilic groups. In certain embodiments, bifunctional linking moieties comprise one or more groups selected from amino, hydroxyl, carboxylic acid, thiol, alkyl, alkenyl, and alkynyl.

Examples of conjugate linkers include but are not limited to pyrrolidine, 8-amino-3,6-dioxaoctanoic acid (ADO), succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC) and 6-aminohexanoic acid (AHEX or AHA). Other conjugate linkers include but are not limited to substituted or unsubstituted C_1-C_{10} alkyl, substituted or unsubstituted C_2-C_{10} alkenyl or substituted or unsubstituted C_2-C_{10} alkynyl, wherein a nonlimiting list of preferred substituent groups includes hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl.

In certain embodiments, conjugate linkers comprise 1-10 linker-nucleosides. In certain embodiments, conjugate linkers comprise 2-5 linker-nucleosides. In certain embodiments, conjugate linkers comprise 1-3 linker nucleosides. In certain embodiments, conjugate linkers comprise exactly 3 linker-nucleosides. In certain embodiments, conjugate linkers comprise the TCA motif. In certain embodiments, such linker-nucleosides are modified nucleosides. In certain embodiments such linker-nucleosides comprise a modified sugar moiety. In certain embodiments, linker-nucleosides are unmodified. In certain embodiments, linker-nucleosides comprise an optionally protected heterocyclic base selected from a purine, substituted purine, pyrimidine or substituted pyrimidine. In certain embodiments, a cleavable moiety is a nucleoside selected from uracil, thymine, cytosine, 4-N-benzoylcytosine, 5-methyl cytosine, 4-N-benzoyl-5-methyl cytosine, adenine, 6-N-benzoyladenine, guanine and 2-N-isobutyrylguanine. It is typically desirable for linker-nucleosides to be cleaved from the oligomeric compound after it reaches a target tissue. Accordingly, linker-nucleosides are typically linked to one another and to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are phosphodiester bonds.

Herein, linker-nucleosides are not considered to be part of the oligonucleotide. Accordingly, in embodiments in which an oligomeric compound comprises an oligonucleotide consisting of a specified number or range of linked nucleosides and/or a specified percent complementarity to a reference nucleic acid and the oligomeric compound also comprises a conjugate group comprising a conjugate linker comprising linker-nucleosides, those linker-nucleosides are not counted toward the length of the oligonucleotide and are not used in determining the percent complementarity of the oligonucleotide for the reference nucleic acid. For example, an oligomeric compound may comprise (1) a modified oligonucleotide consisting of 8-30 nucleosides and (2) a conjugate group comprising 1-10 linker-nucleosides that are

contiguous with the nucleosides of the modified oligonucleotide. The total number of contiguous linked nucleosides in such an oligomeric compound is more than 30. Alternatively, an oligomeric compound may comprise a modified oligonucleotide consisting of 8-30 nucleosides and no conjugate group. The total number of contiguous linked nucleosides in such an oligomeric compound is no more than 30. Unless otherwise indicated conjugate linkers comprise no more than 10 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 5 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 3 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 2 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 1 linker-nucleoside.

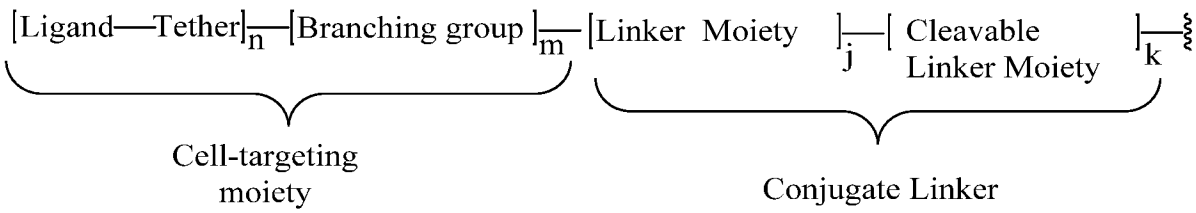
In certain embodiments, it is desirable for a conjugate group to be cleaved from the oligonucleotide. For example, in certain circumstances oligomeric compounds comprising a particular conjugate moiety are better taken up by a particular cell type, but once the oligomeric compound has been taken up, it is desirable that the conjugate group be cleaved to release the unconjugated or parent oligonucleotide. Thus, certain conjugate linkers may comprise one or more cleavable moieties. In certain embodiments, a cleavable moiety is a cleavable bond. In certain embodiments, a cleavable moiety is a group of atoms comprising at least one cleavable bond. In certain embodiments, a cleavable moiety comprises a group of atoms having one, two, three, four, or more than four cleavable bonds. In certain embodiments, a cleavable moiety is selectively cleaved inside a cell or subcellular compartment, such as a lysosome. In certain embodiments, a cleavable moiety is selectively cleaved by endogenous enzymes, such as nucleases.

In certain embodiments, a cleavable bond is selected from among: an amide, an ester, an ether, one or both esters of a phosphodiester, a phosphate ester, a carbamate, or a disulfide. In certain embodiments, a cleavable bond is one or both of the esters of a phosphodiester. In certain embodiments, a cleavable moiety comprises a phosphate or phosphodiester. In certain embodiments, the cleavable moiety is a phosphate or phosphodiester linkage between an oligonucleotide and a conjugate moiety or conjugate group.

In certain embodiments, a cleavable moiety comprises or consists of one or more linker-nucleosides. In certain such embodiments, the one or more linker-nucleosides are linked to one another and/or to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are unmodified phosphodiester bonds. In certain embodiments, a cleavable moiety is 2'-deoxynucleoside that is attached to either the 3' or 5'-terminal nucleoside of an oligonucleotide by a phosphodiester internucleoside linkage and covalently attached to the remainder of the conjugate linker or conjugate moiety by a phosphate or phosphorothioate internucleoside linkage. In certain such embodiments, the cleavable moiety is 2'-deoxyadenosine.

3. **Cell-Targeting Moieties**

In certain embodiments, a conjugate group comprises a cell-targeting moiety. In certain embodiments, a conjugate group has the general formula:



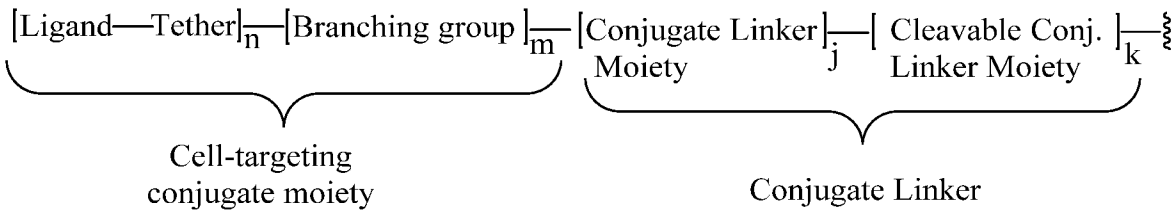
wherein n is from 1 to about 3, m is 0 when n is 1, m is 1 when n is 2 or greater, j is 1 or 0, and k is 1 or 0.

In certain embodiments, n is 1, j is 1 and k is 0. In certain embodiments, n is 1, j is 0 and k is 1. In certain embodiments, n is 1, j is 1 and k is 1. In certain embodiments, n is 2, j is 1 and k is 0. In certain embodiments, n is 2, j is 0 and k is 1. In certain embodiments, n is 2, j is 1 and k is 1. In certain embodiments, n is 3, j is 1 and k is 0. In certain embodiments, n is 3, j is 0 and k is 1. In certain embodiments, n is 3, j is 1 and k is 1.

In certain embodiments, conjugate groups comprise cell-targeting moieties that have at least one tethered ligand. In certain embodiments, cell-targeting moieties comprise two tethered ligands covalently attached to a branching group. In certain embodiments, cell-targeting moieties comprise three tethered ligands covalently attached to a branching group.

In certain embodiments, each ligand of a cell-targeting moiety has an affinity for at least one type of receptor on a target cell. In certain embodiments, each ligand has an affinity for at least one type of receptor on the surface of a mammalian liver cell. In certain embodiments, each ligand has an affinity for the hepatic asialoglycoprotein receptor (ASGP-R). In certain embodiments, each ligand is a carbohydrate.

In certain embodiments, a conjugate group comprises a cell-targeting conjugate moiety. In certain embodiments, a conjugate group has the general formula:



wherein n is from 1 to about 3, m is 0 when n is 1, m is 1 when n is 2 or greater, j is 1 or 0, and k is 1 or 0.

In certain embodiments, n is 1, j is 1 and k is 0. In certain embodiments, n is 1, j is 0 and k is 1. In certain embodiments, n is 1, j is 1 and k is 1. In certain embodiments, n is 2, j is 1 and k is 0. In certain embodiments, n is 2, j is 0 and k is 1. In certain embodiments, n is 2, j is 1 and k is 1. In certain embodiments, n is 3, j is 1 and k is 0. In certain embodiments, n is 3, j is 0 and k is 1. In certain embodiments, n is 3, j is 1 and k is 1.

In certain embodiments, conjugate groups comprise cell-targeting moieties that have at least one tethered ligand. In certain embodiments, cell-targeting moieties comprise two tethered ligands covalently attached to a branching group. In certain embodiments, cell-targeting moieties comprise three tethered ligands covalently attached to a branching group.

B. Certain Terminal Groups

In certain embodiments, oligomeric compounds comprise one or more terminal groups. In certain such embodiments, oligomeric compounds comprise a stabilized 5'-phosphate. Stabilized 5'-phosphates include, but are not limited to 5'-phosphonates, including, but not limited to 5'-vinylphosphonates. In certain embodiments, terminal groups comprise one or more abasic nucleosides and/or inverted nucleosides. In certain embodiments, terminal groups comprise one or more 2'-linked nucleosides. In certain such embodiments, the 2'-linked nucleoside is an abasic nucleoside.

III. Oligomeric Duplexes

In certain embodiments, oligomeric compounds described herein comprise an oligonucleotide, having a nucleobase sequence complementary to that of a target nucleic acid. In certain embodiments, an oligomeric compound is paired with a second oligomeric compound to form an oligomeric duplex. Such oligomeric duplexes comprise a first oligomeric compound having a portion complementary to a target nucleic acid and a second oligomeric compound having a portion complementary to the first oligomeric compound. In certain embodiments, the first oligomeric compound of an oligomeric duplex comprises or consists of (1) a modified or unmodified oligonucleotide and optionally a conjugate group and (2) a second modified or unmodified oligonucleotide and optionally a conjugate group. Either or both oligomeric compounds of an oligomeric duplex may comprise a conjugate group. The oligonucleotides of each oligomeric compound of an oligomeric duplex may include non-complementary overhanging nucleosides.

Certain Oligomeric Duplexes

Certain embodiments are directed to oligomeric duplexes comprising a first oligomeric compound and a second oligomeric compound.

In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases of any of SEQ ID NOs: 10-477; and

a second oligomeric compound comprising a second modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide. In certain embodiments, the nucleobase sequence of the first modified oligonucleotide is at least 85%, at least 90%, at least 95%, or 100% complementary to an equal length portion of the CHMP7 nucleic acid.

In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 contiguous nucleobases complementary to an equal length portion within nucleobases 3950-3983, 4242-4266, 4480-4525, 4534-4566, 5205-5232, 5404-5430, 8323-8344, 16927-16950, 17298-17340, or 18287-18313 of SEQ ID NO: 1; and

a second oligomeric compound comprising a second modified oligonucleotide consisting of 12 to 30 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide. In certain embodiments, the nucleobase sequence of the first modified oligonucleotide is at least 85%, at least 90%, at least 95%, or 100% complementary to an equal length portion of the CHMP7 nucleic acid.

In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases of any of SEQ ID NOs: 10-477; wherein each thymine is replaced by uracil; and

a second oligomeric compound comprising a second modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide. In certain embodiments, the nucleobase sequence of the first modified oligonucleotide is at least 85%, at least 90% In certain embodiments, the first oligomeric compound is an antisense compound. In certain embodiments, the first modified oligonucleotide is an antisense oligonucleotide. In certain embodiments, the second oligomeric compound is a sense compound. In certain embodiments, the second modified oligonucleotide is a sense oligonucleotide.

In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 16 to 50 linked nucleosides wherein the nucleobase sequence of the first modified oligonucleotide comprises the nucleobase sequence of any of SEQ ID NOs 10-477, wherein each thymine is replaced by uracil; and

a second oligomeric compound comprising a second modified oligonucleotide consisting of 16 to 50 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 16 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.

In certain embodiments, the first oligomeric compound is an antisense compound. In certain embodiments, the first modified oligonucleotide is an antisense oligonucleotide. In certain embodiments, the second oligomeric compound is a sense compound. In certain embodiments, the second modified oligonucleotide is a sense oligonucleotide.

In any of the oligomeric duplexes described herein, at least one nucleoside of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a modified sugar moiety. Examples of suitable modified sugar moieties include, but are not limited to, a bicyclic sugar moiety, such as a 2'-4' bridge selected from –O-CH2-; and –O-CH(CH3)-, and a non-bicyclic sugar moiety, such as a 2'-MOE modified sugar moiety, a 2'-F modified sugar moiety, or a 2'-OMe modified sugar moiety. In certain embodiments, at least 80%, at least 90%, or 100% of the nucleosides of the first modified oligonucleotide and/or the second modified oligonucleotide comprises a modified sugar moiety selected from 2'-F and 2'-OMe.

In any of the oligomeric duplexes described herein, at least one nucleoside of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a sugar surrogate. Examples of suitable sugar surrogates include, but are not limited to, morpholino, peptide nucleic acid (PNA), glycol nucleic acid (GNA), and unlocked nucleic acid (UNA). In certain embodiments, at least one nucleoside of the first modified oligonucleotide comprises a sugar surrogate, which can be a GNA.

In any of the oligomeric duplexes described herein, at least one internucleoside linkage of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a modified internucleoside linkage. In certain embodiments, the modified internucleoside linkage is a phosphorothioate internucleoside linkage. In certain embodiments, at least one of the first, second, or third internucleoside linkages from the 5' end and/or the 3' end of the first modified oligonucleotide comprises a phosphorothioate linkage. In certain embodiments, at least one of the first, second, or third internucleoside linkages from the 5' end and/or the 3' end of the second modified oligonucleotide comprises a phosphorothioate linkage.

In any of the oligomeric duplexes described herein, at least one internucleoside linkage of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a phosphodiester internucleoside linkage.

In any of the oligomeric duplexes described herein, each internucleoside linkage of the first modified oligonucleotide and/or the second modified oligonucleotide can be independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.

In any of the oligomeric duplexes described herein, at least one nucleobase of the first modified oligonucleotide and/or the second modified oligonucleotide can be modified nucleobase. In certain embodiments, the modified nucleobase is 5-methylcytosine.

In any of the oligomeric duplexes described herein, the first modified oligonucleotide can comprise a stabilized phosphate group attached to the 5' position of the 5'-most nucleoside. In certain embodiments, the stabilized phosphate group comprises a cyclopropyl phosphonate or an (E)-vinyl phosphonate.

In any of the oligomeric duplexes described herein, the first modified oligonucleotide can comprise a conjugate group. In certain embodiments, the conjugate group comprises a conjugate linker and a conjugate moiety. In certain embodiments, the conjugate group is attached to the first modified oligonucleotide at the 5'-end of the first modified oligonucleotide. In certain embodiments, the conjugate group is attached to the first modified oligonucleotide at the 3'-end of the modified oligonucleotide. In certain embodiments, the conjugate group comprises N-acetyl galactosamine. In certain embodiments, the conjugate group comprises a cell-targeting moiety having an affinity for transferrin receptor (TfR), also known as TfR1 and CD71. In certain embodiments, the conjugate group comprises an anti-TfR1 antibody or fragment thereof. In certain embodiments, the conjugate group comprises a protein or peptide capable of binding TfR1. In certain embodiments, the conjugate group comprises an aptamer capable of binding TfR1. In certain embodiments, the conjugate group may comprise a conjugate moiety selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, C5 alkyl, C22 alkenyl, C20 alkenyl, C16 alkenyl, C10 alkenyl, C21 alkenyl, C19 alkenyl, C18 alkenyl, C15 alkenyl, C14 alkenyl, C13 alkenyl, C12 alkenyl, C11 alkenyl, C9 alkenyl, C8 alkenyl, C7 alkenyl, C6 alkenyl, or C5 alkenyl. In certain embodiments, the conjugate group may comprise a conjugate moiety selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, or C5 alkyl, where the alkyl chain has one or more unsaturated bonds.

In any of the oligomeric duplexes described herein, the second modified oligonucleotide can comprise a conjugate group. In certain embodiments, the conjugate group comprises a conjugate linker and a conjugate moiety. In

certain embodiments, the conjugate group is attached to the second modified oligonucleotide at the 5'-end of the second modified oligonucleotide. In certain embodiments, the conjugate group is attached to the second modified oligonucleotide at the 3'-end of the modified oligonucleotide. In certain embodiments, the conjugate group comprises N-acetyl galactosamine. In certain embodiments, the conjugate group comprises a cell-targeting moiety having an affinity for transferrin receptor (TfR), also known as TfR1 and CD71. In certain embodiments, the conjugate group comprises an anti-TfR1 antibody or fragment thereof. In certain embodiments, the conjugate group comprises a protein or peptide capable of binding TfR1. In certain embodiments, the conjugate group comprises an aptamer capable of binding TfR1. In certain embodiments, the conjugate group may comprise a conjugate moiety selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, C5 alkyl, C22 alkenyl, C20 alkenyl, C16 alkenyl, C10 alkenyl, C21 alkenyl, C19 alkenyl, C18 alkenyl, C15 alkenyl, C14 alkenyl, C13 alkenyl, C12 alkenyl, C11 alkenyl, C9 alkenyl, C8 alkenyl, C7 alkenyl, C6 alkenyl, or C5 alkenyl. In certain embodiments, the conjugate group may comprise a conjugate moiety selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, or C5 alkyl, where the alkyl chain has one or more unsaturated bonds.

In certain embodiments, an antisense agent comprises an antisense compound, which comprises an oligomeric compound or an oligomeric duplex described herein. In certain embodiments, an antisense agent, which can comprise an oligomeric compound or an oligomeric duplex described herein, is an RNAi agent capable of reducing the amount of CHMP7 nucleic acid through the activation of RISC/Ago2.

Certain embodiments provide an oligomeric agent comprising two or more oligomeric duplexes. In certain embodiments, an oligomeric agent comprises two or more of any of the oligomeric duplexes described herein. In certain embodiments, an oligomeric agent comprises two or more of the same oligomeric duplex, which can be any of the oligomeric duplexes described herein. In certain embodiments, the two or more oligomeric duplexes are linked together. In certain embodiments, the two or more oligomeric duplexes are covalently linked together. In certain embodiments, the second modified oligonucleotides of two or more oligomeric duplexes are covalently linked together. In certain embodiments, the second modified oligonucleotides of two or more oligomeric duplexes are covalently linked together at their 3' ends. In certain embodiments, the two or more oligomeric duplexes are covalently linked together by a glycol linker, such as a tetraethylene glycol linker. Certain such compounds are described in, e.g., Alterman, et al., Nature Biotech., 37:844-894, 2019., at least 95%, or 100% complementary to an equal length portion of the CHMP7 nucleic acid.

IV. Antisense Activity

In certain embodiments, oligomeric compounds and oligomeric duplexes are capable of hybridizing to a target nucleic acid, resulting in at least one antisense activity; such oligomeric compounds and oligomeric duplexes are antisense compounds. In certain embodiments, antisense compounds have antisense activity when they reduce the amount or activity of a target nucleic acid by 25% or more in the standard *in vitro* assay. In certain embodiments, antisense compounds selectively affect one or more target nucleic acid. Such antisense compounds comprise a nucleobase sequence that hybridizes to one or more target nucleic acid, resulting in one or more desired antisense

activity and does not hybridize to one or more non-target nucleic acid or does not hybridize to one or more non-target nucleic acid in such a way that results in significant undesired antisense activity.

In certain antisense activities, hybridization of an antisense compound to a target nucleic acid results in recruitment of a protein that cleaves the target nucleic acid. For example, certain antisense compounds result in RNase H mediated cleavage of the target nucleic acid. RNase H is a cellular endonuclease that cleaves the RNA strand of an RNA:DNA duplex. The DNA in such an RNA:DNA duplex need not be unmodified DNA. In certain embodiments, described herein are antisense compounds that are sufficiently "DNA-like" to elicit RNase H activity. In certain embodiments, one or more non-DNA-like nucleoside in the gap of a gapmer is tolerated.

In certain antisense activities, an antisense compound or a portion of an antisense compound is loaded into an RNA-induced silencing complex (RISC), ultimately resulting in cleavage of the target nucleic acid. For example, certain antisense compounds result in cleavage of the target nucleic acid by Argonaute. Antisense compounds that are loaded into RISC are RNAi compounds. RNAi compounds may be double-stranded (siRNA) or single-stranded (ssRNA).

In certain embodiments, hybridization of an antisense compound to a target nucleic acid does not result in recruitment of a protein that cleaves that target nucleic acid. In certain embodiments, hybridization of the antisense compound to the target nucleic acid results in alteration of splicing of the target nucleic acid. In certain embodiments, hybridization of an antisense compound to a target nucleic acid results in inhibition of a binding interaction between the target nucleic acid and a protein or other nucleic acid. In certain embodiments, hybridization of an antisense compound to a target nucleic acid results in alteration of translation of the target nucleic acid.

Antisense activities may be observed directly or indirectly. In certain embodiments, observation or detection of an antisense activity involves observation or detection of a change in an amount of a target nucleic acid or protein encoded by such target nucleic acid, a change in the ratio of splice variants of a nucleic acid or protein and/or a phenotypic change in a cell or subject.

V. Certain Target Nucleic Acids

In certain embodiments, oligomeric compounds comprise or consist of an oligonucleotide comprising a portion that is complementary to a target nucleic acid. In certain embodiments, the target nucleic acid is an endogenous RNA molecule. In certain embodiments, the target nucleic acid encodes a protein. In certain such embodiments, the target nucleic acid is selected from: a mature mRNA and a pre-mRNA, including intronic, exonic and untranslated regions. In certain embodiments, the target nucleic acid is a mature mRNA. In certain embodiments, the target nucleic acid is a pre-mRNA. In certain embodiments, the target region is entirely within an intron. In certain embodiments, the target region spans an intron/exon junction. In certain embodiments, the target region is at least 50% within an intron.

A. Complementarity/Mismatches to the Target Nucleic Acid

It is possible to introduce mismatch bases without eliminating activity. For example, Gautschi et al (J. Natl. Cancer Inst. 93:463-471, March 2001) demonstrated the ability of an oligonucleotide having 100% complementarity to the bcl-2 mRNA and having 3 mismatches to the bcl-xL mRNA to reduce the expression of both bcl-2 and bcl-xL *in vitro* and *in vivo*. Furthermore, this oligonucleotide demonstrated potent anti-tumor activity *in vivo*. Maher and Dolnick (Nuc. Acid. Res. 16:3341-3358, 1988) tested a series of tandem 14 nucleobase oligonucleotides, and a 28 and 42 nucleobase oligonucleotides comprised of the sequence of two or three of the tandem oligonucleotides, respectively, for their ability to arrest translation of human DHFR in a rabbit reticulocyte assay. Each of the three 14 nucleobase

oligonucleotides alone was able to inhibit translation, albeit at a more modest level than the 28 or 42 nucleobase oligonucleotides.

In certain embodiments, oligonucleotides are complementary to the target nucleic acid over the entire length of the oligonucleotide. In certain embodiments, oligonucleotides are 99%, 95%, 90%, 85%, or 80% complementary to the target nucleic acid. In certain embodiments, oligonucleotides are at least 80% complementary to the target nucleic acid over the entire length of the oligonucleotide and comprise a portion that is 100% or fully complementary to a target nucleic acid. In certain embodiments, the portion of full complementarity is 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 nucleobases in length.

In certain embodiments, oligonucleotides comprise one or more mismatched nucleobases relative to the target nucleic acid. In certain embodiments, antisense activity against the target is reduced by such mismatch, but activity against a non-target is reduced by a greater amount. Thus, in certain embodiments selectivity of the oligonucleotide is improved. In certain embodiments, the mismatch is specifically positioned within an oligonucleotide having a gapmer motif. In certain embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 from the 5'-end of the gap region. In certain embodiments, the mismatch is at position 1, 2, 3, 4, 5, or 6 from the 5'-end of the 5' wing region or the 3' wing region.

B. CHMP7

In certain embodiments, oligomeric compounds comprise or consist of an oligonucleotide that is complementary to a target nucleic acid, wherein the target nucleic acid is a CHMP7 nucleic acid. In certain embodiments, the CHMP7 nucleic acid has the nucleobase sequence set forth in SEQ ID NO: 1 (ENSEMBLGene ID ENSG00000147457.14 from ENSEMBL Release 101: August 2020) or SEQ ID NO: 2 (GENBANK Accession No. NM_152272.5).

In certain embodiments, contacting a cell with an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2 reduces the amount of CHMP7 RNA, and in certain embodiments reduces the amount of CHMP7 protein. In certain embodiments, contacting a cell with an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2 reduces the amount of CHMP7 RNA in a cell, and in certain embodiments reduces the amount of CHMP7 protein in a cell. In certain embodiments, the cell is *in vitro*. In certain embodiments, the oligomeric compound consists of a modified oligonucleotide.

In certain embodiments, an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2 is capable of reducing the detectable amount of CHMP7 RNA *in vitro* by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% in the standard *in vitro* assay. In certain embodiments, an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2 is capable of reducing the detectable amount of CHMP7 protein *in vitro* by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% in the standard *in vitro* assay. In certain embodiments, an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2 is capable of reducing the detectable amount of CHMP7 RNA *in vivo* by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2 is capable of reducing the detectable amount of CHMP7 protein *in vivo* by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2, is capable of reducing the

detectable amount of CHMP7 RNA in the CSF of a subject by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. In certain embodiments, an oligomeric compound complementary to SEQ ID NO: 1 or SEQ ID NO: 2, is capable of reducing the detectable amount of CHMP7 protein in the CSF of a subject by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%.

VI. Certain Pharmaceutical Compositions

In certain embodiments, described herein are pharmaceutical compositions comprising one or more oligomeric compounds. In certain embodiments, the one or more oligomeric compounds each consists of a modified oligonucleotide. In certain embodiments, the pharmaceutical composition comprises a pharmaceutically acceptable diluent or carrier. In certain embodiments, a pharmaceutical composition comprises or consists of a sterile saline solution and one or more oligomeric compound. In certain embodiments, the sterile saline is pharmaceutical grade saline. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and sterile water. In certain embodiments, the sterile water is pharmaceutical grade water. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and phosphate-buffered saline (PBS). In certain embodiments, the sterile PBS is pharmaceutical grade PBS. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and artificial cerebrospinal fluid ("artificial CSF" or "aCSF"). In certain embodiments, the artificial cerebrospinal fluid is pharmaceutical grade.

In certain embodiments, a pharmaceutical composition comprises a modified oligonucleotide and artificial cerebrospinal fluid (aCSF). In certain embodiments, a pharmaceutical composition consists of a modified oligonucleotide and artificial cerebrospinal fluid. In certain embodiments, a pharmaceutical composition consists essentially of a modified oligonucleotide and artificial cerebrospinal fluid. In certain embodiments, the artificial cerebrospinal fluid is pharmaceutical grade.

In certain embodiments, aCSF comprises sodium chloride, potassium chloride, sodium dihydrogen phosphate dihydrate, sodium phosphate dibasic anhydrous, calcium chloride dihydrate, and magnesium chloride hexahydrate. In certain embodiments, the pH of an aCSF solution is modulated with a suitable pH-adjusting agent, for example, with acids such as hydrochloric acid and alkalis such as sodium hydroxide, to a range of from about 7.1-7.3, or to about 7.2.

In certain embodiments, pharmaceutical compositions comprise one or more oligomeric compound and one or more excipients. In certain embodiments, excipients are selected from water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylase, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose and polyvinylpyrrolidone.

In certain embodiments, oligomeric compounds may be admixed with pharmaceutically acceptable active and/or inert substances for the preparation of pharmaceutical compositions or formulations. Compositions and methods for the formulation of pharmaceutical compositions depend on a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

In certain embodiments, pharmaceutical compositions comprising an oligomeric compound encompass any pharmaceutically acceptable salts of the oligomeric compound, esters of the oligomeric compound, or salts of such esters. In certain embodiments, pharmaceutical compositions comprising oligomeric compounds comprising one or more oligonucleotide, upon administration to a subject, including a human, are capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to

pharmaceutically acceptable salts of oligomeric compounds, prodrugs, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. In certain embodiments, pharmaceutically acceptable salts comprise inorganic salts, such as monovalent or divalent inorganic salts. Suitable pharmaceutically acceptable salts include, but are not limited to, sodium and, potassium, calcium, and magnesium salts. In certain embodiments, prodrugs comprise one or more conjugate group attached to an oligonucleotide, wherein the conjugate group is cleaved by endogenous nucleases within the body.

In certain embodiments, oligomeric compounds are lyophilized and isolated as sodium salts. In certain embodiments, the sodium salt of an oligomeric compound is mixed with a pharmaceutically acceptable diluent. In certain embodiments, the pharmaceutically acceptable diluent comprises sterile saline, sterile water, PBS, or aCSF. In certain embodiments, the sodium salt of an oligomeric compound is mixed with PBS. In certain embodiments, the sodium salt of an oligomeric compound is mixed with aCSF.

Lipid moieties have been used in nucleic acid therapies in a variety of methods. In certain such methods, the nucleic acid, such as an oligomeric compound, is introduced into preformed liposomes or lipoplexes made of mixtures of cationic lipids and neutral lipids. In certain methods, DNA complexes with mono- or poly-cationic lipids are formed without the presence of a neutral lipid. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to a particular cell or tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to fat tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to muscle tissue.

In certain embodiments, pharmaceutical compositions comprise a delivery system. Examples of delivery systems include, but are not limited to, liposomes and emulsions. Certain delivery systems are useful for preparing certain pharmaceutical compositions including those comprising hydrophobic compounds. In certain embodiments, certain organic solvents such as dimethylsulfoxide are used.

In certain embodiments, pharmaceutical compositions comprise one or more tissue-specific delivery molecules designed to deliver the one or more pharmaceutical agents comprising an oligomeric compound provided herein to specific tissues or cell types. For example, in certain embodiments, pharmaceutical compositions include liposomes coated with a tissue-specific antibody.

In certain embodiments, pharmaceutical compositions comprise a co-solvent system. Certain of such co-solvent systems comprise, for example, benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. In certain embodiments, such co-solvent systems are used for hydrophobic compounds. A non-limiting example of such a co-solvent system is the VPD co-solvent system, which is a solution of absolute ethanol comprising 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant Polysorbate 80™ and 65% w/v polyethylene glycol 300. The proportions of such co-solvent systems may be varied considerably without significantly altering their solubility and toxicity characteristics. Furthermore, the identity of co-solvent components may be varied: for example, other surfactants may be used instead of Polysorbate 80™; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g., polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose.

In certain embodiments, pharmaceutical compositions are prepared for oral administration. In certain embodiments, pharmaceutical compositions are prepared for buccal administration. In certain embodiments, a pharmaceutical composition is prepared for administration by injection (e.g., intravenous, subcutaneous, intramuscular,

intrathecal (IT), intracerebroventricular (ICV), intraneural, perineural, etc.). In certain of such embodiments, a pharmaceutical composition comprises a carrier and is formulated in aqueous solution, such as water or physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. In certain embodiments, other ingredients are included (e.g., ingredients that aid in solubility or serve as preservatives). In certain embodiments, injectable suspensions are prepared using appropriate liquid carriers, suspending agents and the like. Certain pharmaceutical compositions for injection are presented in unit dosage form, e.g., in ampoules or in multi-dose containers. Certain pharmaceutical compositions for injection are suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Certain solvents suitable for use in pharmaceutical compositions for injection include, but are not limited to, lipophilic solvents and fatty oils, such as sesame oil, synthetic fatty acid esters, such as ethyl oleate or triglycerides, and liposomes.

Under certain conditions, certain compounds disclosed herein act as acids. Although such compounds may be drawn or described in protonated (free acid) form, or ionized and in association with a cation (salt) form, aqueous solutions of such compounds exist in equilibrium among such forms. For example, a phosphate linkage of an oligonucleotide in aqueous solution exists in equilibrium among free acid, anion and salt forms. Unless otherwise indicated, compounds described herein are intended to include all such forms. Moreover, certain oligonucleotides have several such linkages, each of which is in equilibrium. Thus, oligonucleotides in solution exist in an ensemble of forms at multiple positions all at equilibrium. The term "oligonucleotide" is intended to include all such forms. Drawn structures necessarily depict a single form. Nevertheless, unless otherwise indicated, such drawings are likewise intended to include corresponding forms. Herein, a structure depicting the free acid of a compound followed by the term "or salt thereof" or "or a pharmaceutically acceptable salt thereof" expressly includes all such forms that may be fully or partially protonated/de-protonated/in association with a cation or a combination of cations. In certain embodiments, one or more specific cation is identified. The cations include, but are not limited to, sodium, potassium, calcium, and magnesium. In certain embodiments, a structure depicting the free acid of a compound followed by the term "or a pharmaceutically acceptable salt thereof" expressly includes all such forms that may be fully or partially protonated/de-protonated/in association with one or more cations selected from sodium, potassium, calcium, and magnesium.

In certain embodiments, modified oligonucleotides or oligomeric compounds are in aqueous solution with sodium. In certain embodiments, modified oligonucleotides or oligomeric compounds are in aqueous solution with potassium. In certain embodiments, modified oligonucleotides or oligomeric compounds are in PBS. In certain embodiments, modified oligonucleotides or oligomeric compounds are in water. In certain such embodiments, the pH of the solution is adjusted with NaOH and/or HCl to achieve a desired pH.

VII. Certain Hotspot Regions

In certain embodiments, nucleobases in the ranges specified below comprise a hotspot region of CHMP7 nucleic acid. In certain embodiments, modified oligonucleotides that are complementary to a hotspot region of CHMP7 nucleic acid achieve an average of more than 60% reduction of CHMP7 RNA in the standard *in vitro* assay

1. Nucleobases 3950-3983 of SEQ ID NO: 1

In certain embodiments, nucleobases 3950-3983 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 3950-3983 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified

oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 220, 302, and 345 are complementary to a portion of nucleobases 3950-3983 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447312, 1447488, and 1447549 are complementary to a portion within nucleobases 3950-3983 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 3950-3983 of SEQ ID NO: 1 achieve at least 84% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 3950-3983 of SEQ ID NO: 1 achieve an average of 88.7% reduction of CHMP7 RNA in the standard *in vitro* assay.

2. Nucleobases 4242-4266 of SEQ ID NO: 1

In certain embodiments, nucleobases 4242-4266 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 4242-4266 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 21, 131, 191, and 465 are complementary to a portion within nucleobases 4242-4266 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447338, 1447449, 1447242, and 1447606 are complementary to a portion within nucleobases 4242-4266 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 4242-4266 of SEQ ID NO: 1 achieve at least 60% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 4242-4266 of SEQ ID NO: 1 achieve an average of 68% reduction of CHMP7 RNA in the standard *in vitro* assay.

3. Nucleobases 4480-4525 of SEQ ID NO: 1

In certain embodiments, nucleobases 4480-4525 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 4480-4525 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of

the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 34, 116, 184, 242, 257, 340, and 474 are complementary to a portion within 4480-4525 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447297, 1447361, 1447311, 1447634, 1447299, 1447279, and 1447636 are complementary to a portion within nucleobases 4480-4525 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 4480-4525 of SEQ ID NO: 1 achieve at least 41% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 4480-4525 of SEQ ID NO: 1 achieve an average of 61% reduction of CHMP7 RNA in the standard *in vitro* assay.

4. Nucleobases 4534-4566 of SEQ ID NO: 1

In certain embodiments, nucleobases 4534-4566 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 4534-4566 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 55, 118, 202, 267, 372, and 422 are complementary to a portion within nucleobases 4534-4566 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447461, 1447313, 1447507, 1447343, 1447400, and 1447387 are complementary to a portion within nucleobases 4534-4566 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 4534-4566 of SEQ ID NO: 1 achieve at least 58% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 4534-4566 of SEQ ID NO: 1 achieve an average of 66% reduction of CHMP7 RNA in the standard *in vitro* assay.

5. Nucleobases 5205-5232 of SEQ ID NO: 1

In certain embodiments, nucleobases 5205-5232 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 5205-5232 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain

embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 73, 136, 197, and 421 are complementary to a portion within nucleobases 5205-5232 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447304, 1447369, 1447481, and 1447520 are complementary to a portion within nucleobases 5205-5232 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 5205-5232 of SEQ ID NO: 1 achieve at least 75% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 5205-5232 of SEQ ID NO: 1 achieve an average of 83% reduction of CHMP7 RNA in the standard *in vitro* assay.

6. Nucleobases 5404-5430 of SEQ ID NO: 1

In certain embodiments, nucleobases 5404-5430 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 5404-5430 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 79, 160, 168, 230, 313, 331, and 464 are complementary to a portion within nucleobases 5404-5430 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447206, 1447236, 1447553, 1447564, 1447595, 1447604, and 1447624 are complementary to a portion within nucleobases 5404-5430 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 5404-5430 of SEQ ID NO: 1 achieve at least 68% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 5404-5430 of SEQ ID NO: 1 achieve an average of 84.3% reduction of CHMP7 RNA in the standard *in vitro* assay.

7. Nucleobases 8323-8344 of SEQ ID NO: 1

In certain embodiments, nucleobases 8323-8344 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 8323-8344 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside

linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 157, 186, and 265 are complementary to a portion within nucleobases 8323-8344 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447315, 1447331, and 1447602 are complementary to a portion within nucleobases 8323-8344 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 8323-8344 of SEQ ID NO: 1 achieve at least 89% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 8323-8344 of SEQ ID NO: 1 achieve an average of 92% reduction of CHMP7 RNA in the standard *in vitro* assay.

8. Nucleobases 16927-16950 of SEQ ID NO: 1

In certain embodiments, nucleobases 16927-16950 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 16927-16950 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 128, 182, and 309 are complementary to a portion within nucleobases 16927-16950 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447285, 1447434, and 1447579 are complementary to a portion within nucleobases 16927-16950 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 16927-16950 of SEQ ID NO: 1 achieve at least 64% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 16927-16950 of SEQ ID NO: 1 achieve an average of 70.7% reduction of CHMP7 RNA in the standard *in vitro* assay.

9. Nucleobases 17298-17340 of SEQ ID NO: 1

In certain embodiments, nucleobases 17298-17340 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 17298-17340 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o")

and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 44, 76, 153, 206, 283, 363, and 416 are complementary to a portion within nucleobases 17298-17340 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447397, 1447283, 1447435, 1447433, 1447416, 1447587, and 1447525 are complementary to a portion within nucleobases 17298-17340 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 17298-17340 of SEQ ID NO: 1 achieve at least 43% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 17298-17340 of SEQ ID NO: 1 achieve an average of 65% reduction of CHMP7 RNA in the standard *in vitro* assay.

10. Nucleobases 18287-18313 of SEQ ID NO: 1

In certain embodiments, nucleobases 18287-18313 of SEQ ID NO: 1 comprise a hotspot region. In certain embodiments, modified oligonucleotides are complementary to a portion within nucleobases 18287-18313 of SEQ ID NO: 1. In certain embodiments, modified oligonucleotides are 20 nucleobases in length. In certain embodiments, modified oligonucleotides are gapmers. In certain embodiments, the gapmers are MOE gapmers. In certain embodiments, all of the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages. In certain embodiments, the internucleoside linkages of the modified oligonucleotides are phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages. In certain embodiments, the phosphodiester ("o") and phosphorothioate ("s") internucleoside linkages are arranged in the order from 5' to 3': soooosssssssssooss, wherein each "s" represents a phosphorothioate internucleoside linkage and each "o" represents a phosphodiester internucleoside linkage.

The nucleobase sequences of SEQ ID NOs: 85, 121, 189, 300, and 354 are complementary to a portion within nucleobases 18287-18313 of SEQ ID NO: 1.

The nucleobase sequence of Compound Nos.: 1447326, 1447379, 1447395, 1447535, and 1447599 are complementary to a portion within nucleobases 18287-18313 of SEQ ID NO: 1.

In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 18287-18313 of SEQ ID NO: 1 achieve at least 63% reduction of CHMP7 RNA in the standard *in vitro* assay. In certain embodiments, modified oligonucleotides complementary to a portion within nucleobases 18287-18313 of SEQ ID NO: 1 achieve an average of 79% reduction of CHMP7 RNA in the standard *in vitro* assay.

Hotspot ID	Start Site SEQ ID NO: 1	Stop Site SEQ ID NO: 1	Min % Red. In vitro	Max % Red. In vitro	Avg % Red. In vitro	Compound Nos. in range	SEQ ID NOs in range
1	3950	3983	84	92	89	1447312, 1447549, 1447488	220, 302, 345
2	4242	4266	60	83	68	1447338, 1447449, 1447242, 1447606	21, 131, 191, 465

3	4480	4525	41	80	61	1447297, 1447361, 1447311, 1447634, 1447299, 1447279, 1447636	34, 116, 184, 242, 257, 340, 474
4	4534	4566	58	76	66	1447461, 1447313, 1447507, 1447343, 1447400, 1447387	55, 118, 202, 267, 372, 422
5	5205	5232	75	90	83	1447369, 1447481, 1447520, 1447304	73, 136, 197, 421
6	5404	5430	68	99	84	1447206, 1447624, 1447553, 1447604, 1447236, 1447595, 1447564	79, 160, 168, 230, 313, 331, 464
7	8323	8344	89	94	92	1447315, 1447331, 1447602	157, 186, 265
8	16927	16950	64	77	70.7	1447285, 1447434, 1447579	128, 182, 309
9	17298	17340	43	82	65	1447397, 1447283, 1447435, 1447433, 1447416, 1447587, 1447525	44, 76, 153, 206, 283, 363, 416
10	18287	18313	63	92	79	1447379, 1447535, 1447326, 1447395, 1447599	85, 121, 189, 300, 354

Nonlimiting disclosure and incorporation by reference

Each of the literature and patent publications listed herein is incorporated by reference in its entirety.

While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references, GenBank accession numbers, and the like recited in the present application is incorporated herein by reference in its entirety.

Although the sequence listing accompanying this filing identifies each sequence as either "RNA" or "DNA" as required, in reality, those sequences may be modified with any combination of chemical modifications. One of skill in the art will readily appreciate that such designation as "RNA" or "DNA" to describe modified oligonucleotides is, in certain instances, arbitrary. For example, an oligonucleotide comprising a nucleoside comprising a 2'-OH sugar moiety and a thymine base could be described as a DNA having a modified sugar moiety (2'-OH in place of one 2'-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) in place of a uracil of RNA). Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic acids containing any combination of natural or modified RNA and/or DNA, including, but not limited to such nucleic acids having modified nucleobases. By way of further example and without limitation, an oligomeric compound having the nucleobase sequence "ATCGATCG" encompasses any oligomeric compounds having such nucleobase sequence, whether modified or unmodified, including, but not limited to, such compounds comprising RNA bases, such as those having sequence "AUCGAUCG" and those having some DNA bases and some RNA bases such as

"AUCGATCG" and oligomeric compounds having other modified nucleobases, such as "AT^{m}CGAUCG," wherein ^{m}C indicates a cytosine base comprising a methyl group at the 5-position.

Certain compounds described herein (e.g., modified oligonucleotides) have one or more asymmetric center and thus give rise to enantiomers, diastereomers, and other stereoisomeric configurations that may be defined, in terms of absolute stereochemistry, as (*R*) or (*S*), as α or β such as for sugar anomers, or as (D) or (L), such as for amino acids, etc. Compounds provided herein that are drawn or described as having certain stereoisomeric configurations include only the indicated compounds. Compounds provided herein that are drawn or described with undefined stereochemistry include all such possible isomers, including their stereorandom and optically pure forms, unless specified otherwise. Likewise, all cis- and trans-isomers and tautomeric forms of the compounds herein are also included unless otherwise indicated. Oligomeric compounds described herein include chirally pure or enriched mixtures as well as racemic mixtures. For example, oligomeric compounds having a plurality of phosphorothioate internucleoside linkages include such compounds in which chirality of the phosphorothioate internucleoside linkages is controlled or is random. Unless otherwise indicated, compounds described herein are intended to include corresponding salt forms.

The compounds described herein include variations in which one or more atoms are replaced with a non-radioactive isotope or radioactive isotope of the indicated element. For example, compounds herein that comprise hydrogen atoms encompass all possible deuterium substitutions for each of the ^{1}H hydrogen atoms. Isotopic substitutions encompassed by the compounds herein include but are not limited to: ^{2}H or ^{3}H in place of ^{1}H, ^{13}C or ^{14}C in place of ^{12}C, ^{15}N in place of ^{14}N, ^{17}O or ^{18}O in place of ^{16}O, and ^{33}S, ^{34}S, ^{35}S, or ^{36}S in place of ^{32}S. In certain embodiments, non-radioactive isotopic substitutions may impart new properties on the oligomeric compound that are beneficial for use as a therapeutic or research tool. In certain embodiments, radioactive isotopic substitutions may make the compound suitable for research or diagnostic purposes such as imaging.

EXAMPLES

The following examples illustrate certain embodiments of the present disclosure and are not limiting. Moreover, where specific embodiments are provided, the inventors have contemplated generic application of those specific embodiments.

Example 1: Effect of 5-10-5 MOE mixed backbone modified oligonucleotides on human CHMP7 RNA *in vitro*, single dose

Modified oligonucleotides complementary to human CHMP7 nucleic acid were designed and tested for their single dose effects on CHMP7 RNA *in vitro*. The modified oligonucleotides were tested in a series of experiments that had the same culture conditions.

The modified oligonucleotides in the tables below are 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages. The gapmers are 20 nucleosides in length, wherein the central gap segment consists of ten 2'-β-D-deoxynucleosides, and wherein the 5' and 3' wing segments each consist of five 2'-MOE modified nucleosides. The sugar motif for the gapmers is (from 5' to 3'): eeeeeddddddddddeeeee; wherein 'd' represents a 2'-β-D-deoxyribosyl sugar, and 'e' represents a 2'-MOE modified sugar moiety. The internucleoside linkage motif for the gapmers is (from

5’ to 3’): soooossssssssssooss; wherein each ‘o’ represents a phosphodiester internucleoside linkage and each ‘s’ represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methyl cytosine.

“Start site” indicates the 5’-most nucleoside to which the modified oligonucleotide is complementary in the target nucleic acid sequence. “Stop site” indicates the 3’-most nucleoside to which the modified oligonucleotide is complementary in the target nucleic acid sequence. Each modified oligonucleotide listed in the tables below is 100% complementary to SEQ ID NO: 1 (ENSEMBLGene ID ENSG00000147457.14 from ENSEMBL Release 101: August 2020), to SEQ ID NO: 2 (GENBANK Accession No. NM_152272.5), or to both. ‘N/A’ indicates that the modified oligonucleotide is not 100% complementary to that particular target nucleic acid sequence.

Cultured A431 cells were treated with modified oligonucleotide at a concentration of 4,000 nM by free uptake at a density of 10,000 cells per well. After a treatment period of approximately 48 hours, total RNA was isolated from the cells and CHMP7 RNA levels were measured by quantitative real-time RTPCR. CHMP7 RNA levels were measured by human primer probe set RTS50844 (forward sequence CAAGTGGACTCTTTCTAACATGC, designated herein as SEQ ID NO: 5; reverse sequence GCGAGTTCTGATACAGACGAT, designated herein as SEQ ID NO: 6; probe sequence CCTCCTCAGCCTTTTCCTTCAACAGC, designated herein as SEQ ID NO: 7). CHMP7 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of CHMP7 RNA is presented in the tables below as percent CHMP7 RNA relative to the amount in untreated control cells (% UTC). Each table represents results from an individual assay plate. The values marked with an “†” indicate that the modified oligonucleotide is complementary to the amplicon region of the primer probe set. Additional assays may be used to measure the potency and efficacy of the modified oligonucleotides complementary to the amplicon region.

Table 1

Reduction of CHMP7 RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages in A431 cells

Compound Number	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	Sequence (5' to 3')	CHMP7 (% UTC)	SEQ ID NO
1447185	1125	1144	N/A	N/A	GGCATTTTATATTCATGGAC	88	10
1447189	16656	16675	1917	1936	AGGACAGTTTCTCAAGTTCA	76	11
1447190	10035	10054	N/A	N/A	ATGTGATGCTATTAATAGGA	24	12
1447191	8219	8238	N/A	N/A	AGTACATAGATCTCTGCACA	49	13
1447202	15172	15191	1685	1704	TTGGATCTGATCCACGAGGC	88	14
1447203	4818	4837	N/A	N/A	AAAGCTGTTAACTATTAGGT	52	15
1447204	56	75	56	75	GACGAGTATACTCAAAGTCA	112	16
1447214	18276	18295	3323	3342	CCCCCAACATTTCCGTTTAC	123	17
1447223	1306	1325	N/A	N/A	GTCAATTCCCATATACCTAT	108	18
1447230	6665	6684	N/A	N/A	AAGGACACTACACTCTGAGC	122	19
1447239	10330	10349	N/A	N/A	ATGATGATCCTTTATTCTGT	38	20
1447242	4246	4265	N/A	N/A	ATCAGAGTTGACTTTCTCCT	40	21
1447244	16319	16338	N/A	N/A	TCTTCCACACTCCAAGCTAA	94	22
1447245	16988	17007	2035	2054	AAGCCTGGTCTCTCTTTTAC	91	23
1447247	17119	17138	2166	2185	GCATCGCTTCCAGAAATTCT	66	24

1447262	12519	12538	N/A	N/A	TGGTCCAGAACTTTTACCTT	126	25
1447264	3703	3722	N/A	N/A	CTCTTAGACCTTCTGCTCCA	46	26
1447266	5854	5873	N/A	N/A	AACTCAGTTATCAACTCAGT	89	27
1447276	5605	5624	979	998	CTGCTGTCTACACTGGCCAT	82	28
1447277	17074	17093	2121	2140	TCCAGATAAAATCAGTGGTT	138	29
1447288	1533	1552	N/A	N/A	TGCTCACACCATTCCTAGTC	110	30
1447289	11791	11810	N/A	N/A	ATGAGCCTCCATACCTTCTC	84	31
1447296	8108	8127	N/A	N/A	TATCGATAGATTATCATGCA	57	32
1447310	18096	18115	3143	3162	TCGCTTCTTCTCGCCATTGC	67	33
1447311	4485	4504	N/A	N/A	ACTGTATGCCATCTCAGAAA	53	34
1447314	5451	5470	N/A	N/A	TCACGACCATTTGTTAAGCA	11	35
1447336	1695	1714	N/A	N/A	TCCAACACCAGCTCATGATA	173	36
1447340	17545	17564	2592	2611	CGACCTCTTTCTCTGAACAC	60	37
1447363	4602	4621	N/A	N/A	GGAAGATGATCCACTTCCAA	137	38
1447368	16311	16330	N/A	N/A	ACTCCAAGCTAAGTCACCAA	78	39
1447371	3900	3919	N/A	N/A	ACAGACCTTTTAAGGGCACT	25	40
1447381	16733	16752	N/A	N/A	GCCCATCAACTCTGTCAGCC	99	41
1447383	10652	10671	N/A	N/A	CCATTTCGCTCATACATGGA	151	42
1447392	16951	16970	1998	2017	GAGGGTCCTACAATGGCTTT	100	43
1447397	17298	17317	2345	2364	CTGCAAATCTTTCCCCTTCA	29	44
1447405	9530	9549	N/A	N/A	AAGTCCTCAGCATATCCACA	47	45
1447411	7531	7550	N/A	N/A	TGTTTGCCAGTACAAACCTC	117	46
1447413	16415	16434	N/A	N/A	ACCAAAACCCGCTTAGCTTT	93	47
1447424	683	702	N/A	N/A	GTACAGATCTTACACCATTC	118	48
1447430	9034	9053	N/A	N/A	CCTGAAATTCAATAGCCATA	70	49
1447436	5732	5751	N/A	N/A	ACCCACCTTCAACAGCTCCA	71†	50
1447439	9291	9310	N/A	N/A	CATCGAGTTTTCATTGATTT	110	51
1447441	13019	13038	N/A	N/A	AAGCCCACATATACTAACAT	130	52
1447450	5814	5833	N/A	N/A	GGTCTTTTTTCAAGAACGCA	52	53
1447458	14167	14186	N/A	N/A	AGGATAAGCTTTTTCAACCC	74	54
1447461	4534	4553	N/A	N/A	CTACTGTTTCTCCTGTTCCC	41	55
1447463	16526	16545	1787	1806	GATGTCCAATTCCTTCTCCA	51	56
1447466	8001	8020	N/A	N/A	GGTGCACACCAATTCCATTT	93	57
1447475	15482	15501	N/A	N/A	TGTCCACTCACCTAAGCCAT	160	58
1447476	5109	5128	N/A	N/A	CTTCTTGCTCTTCCAAGGCA	74	59
1447478	2094	2113	N/A	N/A	CCAGATGGTTTCATTTGATA	140	60
1447485	4052	4071	N/A	N/A	GAGGATAATTCTATCACCTC	95	61
1447490	18205	18224	3252	3271	TGGAGCAAATTCTTCTCCTC	87	62
1447493	14124	14143	N/A	N/A	GGCACATTATACACATCTTC	57	63
1447495	14967	14986	N/A	N/A	GCTCAATTTACCCTATACCC	58	64
1447497	11435	11454	N/A	N/A	GATCTGTGTTTTTAAGCCTT	11	65
1447502	5691	5710	1065	1084	CTGGAACCTTATTATCTCCC	15†	66
1447509	16327	16346	N/A	N/A	GAGATGATTCTTCCACACTC	44	67

1447510	11845	11864	N/A	N/A	GGGCTCACTACTCTATGTAC	163	68
1447512	12548	12567	N/A	N/A	TCAGCAAATGATATTTGGTC	66	69
1447514	11830	11849	N/A	N/A	TGTACTTAATCAATCACTGC	91	70
1447516	2031	2050	N/A	N/A	CCATCTCTTTTATAAGATAG	117	71
1447517	9241	9260	N/A	N/A	GTAACTGCACAGTAACCACA	59	72
1447520	5212	5231	N/A	N/A	GGTGAGATCTCCTTTTACAA	25	73
1447523	14029	14048	N/A	N/A	CTAGACTTTCCCACCTGGAA	58	74
1447524	18068	18087	3115	3134	TCAGACCCTTTCCCGTCTGT	80	75
1447525	17321	17340	2368	2387	GAACTGATTCAGATTTGGCA	35	76
1447540	11248	11267	N/A	N/A	CTGAGGCCTGATTTCCAGCC	105	77
1447544	16269	16288	N/A	N/A	ATGGACCTGACCCTGATTCC	62	78
1447553	5406	5425	N/A	N/A	CATTGTTTATACTCCAGCTC	32	79
1447570	4548	4567	N/A	N/A	ACTGACTTCTTCAACTACTG	65	80
1447571	12898	12917	1380	1399	GAAGCTGTTCACTCTGCATC	77	81
1447572	748	767	N/A	N/A	AGTCTTTTCAACAATGAGCA	81	82
1447581	11152	11171	N/A	N/A	CATCTAATTCCCTTCCAATT	70	83
1447598	11195	11214	N/A	N/A	ACTAGTCCTCAGTATCACTC	59	84
1447599	18294	18313	3341	3360	AGTGATTGTTTCTCTTCACC	37	85
1447623	925	944	N/A	N/A	ACGGATACAACCCAACTTCA	75	86
1447632	12820	12839	N/A	N/A	GGGCAAACTTCACAATCTGA	88	87

Table 2

Reduction of CHMP7 RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages in A431 cells

Compound Number	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	Sequence (5' to 3')	CHMP7 (% UTC)	SEQ ID NO
1447199	11193	11212	N/A	N/A	TAGTCCTCAGTATCACTCTC	53	88
1447201	1299	1318	N/A	N/A	CCCATATACCTATAATGATC	136	89
1447209	52	71	52	71	AGTATACTCAAAGTCAGGCA	82	90
1447211	16250	16269	N/A	N/A	CCACTGCCCTTGAAGGAGGA	121	91
1447229	14166	14185	N/A	N/A	GGATAAGCTTTTTCAACCCA	43	92
1447240	12897	12916	1379	1398	AAGCTGTTCACTCTGCATCA	119	93
1447241	17116	17135	2163	2182	TCGCTTCCAGAAATTCTATC	49	94
1447243	16287	16306	N/A	N/A	GTGTATTCTGTTAACACCAT	63	95
1447252	11338	11357	N/A	N/A	GGGATTTTACACTCCTGCCT	44	96
1447257	5813	5832	N/A	N/A	GTCTTTTTTCAAGAACGCAC	30	97
1447259	4051	4070	N/A	N/A	AGGATAATTCTATCACCTCA	35	98
1447260	5724	5743	1098	1117	TCAACAGCTCCACAGCGACA	25†	99
1447261	670	689	N/A	N/A	ACCATTCACAAAAGCCAGCT	155	100
1447267	10329	10348	N/A	N/A	TGATGATCCTTTATTCTGTA	34	101
1447271	9612	9631	N/A	N/A	TCCAAGATTATGTATACAAC	41	102
1447306	11844	11863	N/A	N/A	GGCTCACTACTCTATGTACT	68	103

1447309	3617	3636	N/A	N/A	ACTGTCACCTCTGTTAGGCT	15	104
1447317	16317	16336	N/A	N/A	TTCCACACTCCAAGCTAAGT	87	105
1447319	16653	16672	1914	1933	ACAGTTTCTCAAGTTCAGCT	46	106
1447322	2093	2112	N/A	N/A	CAGATGGTTTCATTTGATAA	143	107
1447325	7528	7547	N/A	N/A	TTGCCAGTACAAACCTCATC	38	108
1447327	810	829	N/A	N/A	GGCACATGTAAATACAGTCA	157	109
1447329	15470	15489	1748	1767	TAAGCCATTTGTTACCCCAC	41	110
1447334	1993	2012	N/A	N/A	CCAACTGATCCTATGAGGCA	90	111
1447335	16402	16421	N/A	N/A	TAGCTTTACAAAAGATGCCA	89	112
1447349	747	766	N/A	N/A	GTCTTTTCAACAATGAGCAC	61	113
1447351	9521	9540	N/A	N/A	GCATATCCACAGCAAAGATC	47	114
1447360	17930	17949	2977	2996	CCTGCTTCTATTGCACATCC	74	115
1447361	4482	4501	N/A	N/A	GTATGCCATCTCAGAAAGCC	29	116
1447376	12518	12537	N/A	N/A	GGTCCAGAACTTTTACCTTT	87	117
1447387	4547	4566	N/A	N/A	CTGACTTCTTCAACTACTGT	38	118
1447390	17543	17562	2590	2609	ACCTCTTTCTCTGAACACCT	42	119
1447394	11242	11261	N/A	N/A	CCTGATTTCCAGCCTAGCCT	70	120
1447395	18292	18311	3339	3358	TGATTGTTTCTCTTCACCCC	25	121
1447404	4599	4618	N/A	N/A	AGATGATCCACTTCCAATAC	90	122
1447407	18078	18097	3125	3144	GCCAGAGCATTCAGACCCTT	44	123
1447412	8000	8019	N/A	N/A	GTGCACACCAATTCCATTTC	128	124
1447423	12814	12833	N/A	N/A	ACTTCACAATCTGAGGGACA	130	125
1447431	4774	4793	N/A	N/A	TGACACTGCTTTTAATACTA	7	126
1447432	18204	18223	3251	3270	GGAGCAAATTCTTCTCCTCT	70	127
1447434	16931	16950	1978	1997	AGAGTCGGTTCCAATTGCCT	29	128
1447444	11729	11748	1238	1257	CTGCAGCAACACCAAGTAGA	116	129
1447448	4533	4552	N/A	N/A	TACTGTTTCTCCTGTTCCCT	51	130
1447449	4243	4262	N/A	N/A	AGAGTTGACTTTCTCCTTCC	17	131
1447460	17045	17064	2092	2111	CCTCTTCCAAACACATTCTG	96	132
1447462	11113	11132	N/A	N/A	GCCAATTGGCTATACTGCAA	71	133
1447471	8105	8124	N/A	N/A	CGATAGATTATCATGCAGGC	9	134
1447472	1694	1713	N/A	N/A	CCAACACCAGCTCATGATAA	62	135
1447481	5207	5226	N/A	N/A	GATCTCCTTTTACAATTGGT	10	136
1447491	9236	9255	N/A	N/A	TGCACAGTAACCACACACAA	89	137
1447500	16984	17003	2031	2050	CTGGTCTCTCTTTTACATGA	48	138
1447501	5853	5872	N/A	N/A	ACTCAGTTATCAACTCAGTA	112	139
1447503	18274	18293	3321	3340	CCCAACATTTCCGTTTACCA	66	140
1447511	5588	5607	962	981	CATGAAGTCTGACTCCCGCT	132	141
1447518	16524	16543	1785	1804	TGTCCAATTCCTTCTCCAGT	83	142
1447522	5108	5127	N/A	N/A	TTCTTGCTCTTCCAAGGCAA	91	143
1447526	16708	16727	N/A	N/A	GCCATATGCCCTCCAAAGGC	133	144
1447527	11829	11848	N/A	N/A	GTACTTAATCAATCACTGCT	71	145
1447528	14123	14142	N/A	N/A	GCACATTATACACATCTTCC	35	146

1447531	1509	1528	N/A	N/A	CTGTACGGGAAATCCTAGCT	100	147
1447532	12547	12566	N/A	N/A	CAGCAAATGATATTTGGTCT	23	148
1447537	1058	1077	N/A	N/A	GTAGATCCAGTGAAATCCCA	59	149
1447542	5425	5444	N/A	N/A	CTGTGCCAACGACACGCAGC	91	150
1447574	13017	13036	N/A	N/A	GCCCACATATACTAACATTT	102	151
1447575	15136	15155	1649	1668	TGTGACATCCTTCATGGAGA	82	152
1447587	17320	17339	2367	2386	AACTGATTCAGATTTGGCAA	47	153
1447593	9283	9302	N/A	N/A	TTTCATTGATTTGACTGCCC	52	154
1447596	6664	6683	N/A	N/A	AGGACACTACACTCTGAGCA	51	155
1447600	10592	10611	N/A	N/A	ATGCTATGAAAATATAGGGA	56	156
1447602	8325	8344	N/A	N/A	GTGCAACTTATTACAAACTT	11	157
1447603	14008	14027	N/A	N/A	ACAGACTTCAATGTCTGTGT	56	158
1447619	14855	14874	N/A	N/A	TGCAAGTGACCAACACACAC	104	159
1447624	5405	5424	N/A	N/A	ATTGTTTATACTCCAGCTCT	18	160
1447626	17293	17312	2340	2359	AATCTTTCCCCTTCATGGGC	69	161
1447635	8218	8237	N/A	N/A	GTACATAGATCTCTGCACAA	52	162
1447643	16326	16345	N/A	N/A	AGATGATTCTTCCACACTCC	60	163
1447646	3781	3800	N/A	N/A	TGGCAAGATGCCTACAGGCC	81	164
1447647	5690	5709	1064	1083	TGGAACCTTATTATCTCCCA	27†	165

Table 3

Reduction of CHMP7 RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages in A431 cells

Compound Number	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	Sequence (5' to 3')	CHMP7 (% UTC)	SEQ ID NO
1447193	2048	2067	N/A	N/A	GTTGTACCAGTTCTGTGCCA	78	166
1447197	10327	10346	N/A	N/A	ATGATCCTTTATTCTGTAGA	37	167
1447206	5404	5423	N/A	N/A	TTGTTTATACTCCAGCTCTA	29	168
1447208	15115	15134	1628	1647	TTTGAGTGCTCCTACCCCAG	64	169
1447210	11190	11209	N/A	N/A	TCCTCAGTATCACTCTCTGA	62	170
1447212	11205	11224	N/A	N/A	TCACAGCCTCACTAGTCCTC	86	171
1447216	11617	11636	1126	1145	AGACGATACACCTCCTCAGC	59†	172
1447217	16316	16335	N/A	N/A	TCCACACTCCAAGCTAAGTC	51	173
1447222	1822	1841	N/A	N/A	AAGCGGAATTTATTACAGCT	75	174
1447226	16249	16268	N/A	N/A	CACTGCCCTTGAAGGAGGAT	67	175
1447227	13010	13029	N/A	N/A	TATACTAACATTTTGCTGGC	97	176
1447233	9611	9630	N/A	N/A	CCAAGATTATGTATACAACC	20	177
1447234	809	828	N/A	N/A	GCACATGTAAATACAGTCAA	61	178
1447273	13975	13994	N/A	N/A	GGTGTGTCTTTATTAGGGAT	16	179
1447274	9282	9301	N/A	N/A	TTCATTGATTTGACTGCCCT	52	180
1447280	5993	6012	N/A	N/A	GCTGCTTAACATTAATCCCT	41	181
1447285	16930	16949	1977	1996	GAGTCGGTTCCAATTGCCTT	23	182

1447292	17008	17027	2055	2074	TAACTATGTACACACCCAGC	43	183
1447297	4480	4499	N/A	N/A	ATGCCATCTCAGAAAGCCTC	31	184
1447303	15469	15488	1747	1766	AAGCCATTTGTTACCCCACC	43	185
1447315	8324	8343	N/A	N/A	TGCAACTTATTACAAACTTT	7	186
1447316	16624	16643	1885	1904	GCATCTGAGATCCTAGGGTT	54	187
1447324	16692	16711	N/A	N/A	AGGCCTTGGAAAACAGCTCC	83	188
1447326	18291	18310	3338	3357	GATTGTTTCTCTTCACCCCC	8	189
1447337	669	688	N/A	N/A	CCATTCACAAAAGCCAGCTC	93	190
1447338	4242	4261	N/A	N/A	GAGTTGACTTTCTCCTTCCC	37	191
1447341	12792	12811	N/A	N/A	GAGAAATTACTACTGCTGCT	90	192
1447346	16385	16404	N/A	N/A	CCAGGCCTCCTTGCAGATTA	148	193
1447348	11337	11356	N/A	N/A	GGATTTTACACTCCTGCCTC	95	194
1447355	16325	16344	N/A	N/A	GATGATTCTTCCACACTCCA	35	195
1447362	4554	4573	N/A	N/A	TCCCTCACTGACTTCTTCAA	48	196
1447369	5205	5224	N/A	N/A	TCTCCTTTTACAATTGGTGC	19	197
1447372	5516	5535	N/A	N/A	ATGCAATGTCCCATTCCAGT	83	198
1447389	16284	16303	N/A	N/A	TATTCTGTTAACACCATGGA	47	199
1447393	12482	12501	N/A	N/A	CTTGACCGCTTCTCTTTGGT	81	200
1447396	1651	1670	N/A	N/A	GAGGGACACATCCTCCACTT	75	201
1447400	4546	4565	N/A	N/A	TGACTTCTTCAACTACTGTT	42	202
1447403	16980	16999	2027	2046	TCTCTCTTTTACATGAGGGT	66	203
1447408	1054	1073	N/A	N/A	ATCCAGTGAAATCCCAGTGA	76	204
1447415	8075	8094	N/A	N/A	ATCGAGTAAATCCATACTGT	46	205
1447416	17304	17323	2351	2370	GCAAAGCTGCAAATCTTTCC	57	206
1447419	4730	4749	N/A	N/A	GAGAAGTATCATCCTCAGAA	45	207
1447421	18269	18288	3316	3335	CATTTCCGTTTACCAAGGTC	22	208
1447422	688	707	N/A	N/A	TCCAGGTACAGATCTTACAC	87	209
1447442	11795	11814	N/A	N/A	ACAGATGAGCCTCCATACCT	76	210
1447453	7944	7963	N/A	N/A	CGTGTGTATTCACTCACTCA	94	211
1447455	4955	4974	N/A	N/A	ACCTAGGTACAATTATCATC	63	212
1447459	1503	1522	N/A	N/A	GGGAAATCCTAGCTAACACA	70	213
1447464	12535	12554	N/A	N/A	TTTGGTCTTCCTTATTTGGT	53	214
1447465	14084	14103	N/A	N/A	AGGAACTGTTAACACCAACA	47	215
1447469	17494	17513	2541	2560	AAACCTTTTATACTACATGT	65	216
1447470	7527	7546	N/A	N/A	TGCCAGTACAAACCTCATCT	32	217
1447482	11108	11127	N/A	N/A	TTGGCTATACTGCAAACACA	47	218
1447487	18197	18216	3244	3263	ATTCTTCTCCTCTGCTCTAC	64	219
1447488	3964	3983	N/A	N/A	GTATTAGTTATCAATGTTAC	8	220
1447498	2212	2231	N/A	N/A	CACATTTCTTGAAAGCACAC	78	221
1447513	11843	11862	N/A	N/A	GCTCACTACTCTATGTACTT	53	222
1447529	5718	5737	1092	1111	GCTCCACAGCGACAAGGACC	10†	223
1447547	9151	9170	N/A	N/A	ATAGAGCTTTCCCCACCACA	54	224
1447550	14850	14869	N/A	N/A	GTGACCAACACACACGGAGA	57	225

1447554	9383	9402	N/A	N/A	CGTCATGTAAACAAATTCAA	47	226
1447555	5688	5707	1062	1081	GAACCTTATTATCTCCCAGC	4†	227
1447556	16511	16530	1772	1791	CTCCAGTTCTTCACTGTCAA	60	228
1447560	5849	5868	N/A	N/A	AGTTATCAACTCAGTAGCCA	20	229
1447564	5411	5430	N/A	N/A	CGCAGCATTGTTTATACTCC	26	230
1447576	17743	17762	2790	2809	AACAATTTTGCCTCTTTGCA	73	231
1447588	36	55	36	55	GGCAAGCAAGTTTATTGACC	63	232
1447591	5812	5831	N/A	N/A	TCTTTTTTCAAGAACGCACA	70	233
1447592	12889	12908	1371	1390	CACTCTGCATCAGCTGGTAC	104	234
1447601	10343	10362	N/A	N/A	AGTGTAATATCTTATGATGA	59	235
1447607	17292	17311	2339	2358	ATCTTTCCCCTTCATGGGCT	59	236
1447608	14165	14184	N/A	N/A	GATAAGCTTTTTCAACCCAC	50	237
1447612	18077	18096	3124	3143	CCAGAGCATTCAGACCCTTT	48	238
1447614	1218	1237	N/A	N/A	GGTATAAATCTAACACGGTA	83	239
1447616	8152	8171	N/A	N/A	TTGAAATGTCCATCTGCGGA	41	240
1447629	3743	3762	N/A	N/A	GCTTTTTAGCTCTAACCTTC	29	241
1447636	4506	4525	N/A	N/A	GCATGAACGAAAACGGTTTC	48	242
1447638	17111	17130	2158	2177	TCCAGAAATTCTATCTGTCC	59	243

Table 4

Reduction of CHMP7 RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages in A431 cells

Compound Number	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	Sequence (5' to 3')	CHMP7 (% UTC)	SEQ ID NO
1447188	12534	12553	N/A	N/A	TTGGTCTTCCTTATTTGGTC	35	244
1447205	659	678	N/A	N/A	AAGCCAGCTCAAATGGATCA	97	245
1447213	10276	10295	N/A	N/A	GCTAGATTAACAGAAAGCTA	66	246
1447218	5687	5706	1061	1080	AACCTTATTATCTCCCAGCA	8†	247
1447228	4363	4382	N/A	N/A	GCAATATCAATGTCCAGTCC	14	248
1447231	18194	18213	3241	3260	CTTCTCCTCTGCTCTACGCC	50	249
1447238	9610	9629	N/A	N/A	CAAGATTATGTATACAACCT	49	250
1447249	11335	11354	N/A	N/A	ATTTTACACTCCTGCCTCTC	64	251
1447251	18075	18094	3122	3141	AGAGCATTCAGACCCTTTCC	34	252
1447255	11794	11813	N/A	N/A	CAGATGAGCCTCCATACCTT	106	253
1447256	5379	5398	N/A	N/A	CACAACACTTCTGCATGGGA	5	254
1447265	1203	1222	N/A	N/A	CGGTATGTACAAATTCTACA	98	255
1447270	17548	17567	2595	2614	GGGCGACCTCTTTCTCTGAA	59	256
1447279	4498	4517	N/A	N/A	GAAAACGGTTTCCACTGTAT	20	257
1447281	16979	16998	2026	2045	CTCTCTTTTACATGAGGGTC	75	258
1447286	18232	18251	3279	3298	ATTGAACAACGATTTGTGCT	36	259
1447287	9281	9300	N/A	N/A	TCATTGATTTGACTGCCCTA	24	260
1447290	17222	17241	2269	2288	CTGCAGGCTATGAAATGACA	67	261

1447291	5515	5534	N/A	N/A	TGCAATGTCCCATTCCAGTC	46	262
1447294	11839	11858	N/A	N/A	ACTACTCTATGTACTTAATC	79	263
1447323	5777	5796	N/A	N/A	ATGCTGTGATCACACCAGGT	50	264
1447331	8323	8342	N/A	N/A	GCAACTTATTACAAACTTTT	6	265
1447342	14057	14076	N/A	N/A	CGGACATATCCTCTGCCTCC	93	266
1447343	4545	4564	N/A	N/A	GACTTCTTCAACTACTGTTT	24	267
1447344	12481	12500	N/A	N/A	TTGACCGCTTCTCTTTGGTA	111	268
1447345	1494	1513	N/A	N/A	TAGCTAACACAGTTAGCCAA	113	269
1447356	1649	1668	N/A	N/A	GGGACACATCCTCCACTTGA	112	270
1447359	14973	14992	N/A	N/A	ACCCAAGCTCAATTTACCCT	86	271
1447364	10340	10359	N/A	N/A	GTAATATCTTATGATGATCC	17	272
1447366	16568	16587	1829	1848	GTCAGGCAGATCCAAAGGTT	63	273
1447370	4725	4744	N/A	N/A	GTATCATCCTCAGAAATTCT	18	274
1447373	12597	12616	N/A	N/A	CACAATTTTTCCTATAGAAG	84	275
1447382	12880	12899	1362	1381	TCAGCTGGTACACCCCAACA	104	276
1447384	10658	10677	N/A	N/A	ATGTCACCATTTCGCTCATA	29	277
1447388	1821	1840	N/A	N/A	AGCGGAATTTATTACAGCTA	107	278
1447391	16510	16529	1771	1790	TCCAGTTCTTCACTGTCAAA	69	279
1447410	9358	9377	N/A	N/A	TTGGACATTTCAAGAAGTGA	57	280
1447425	5818	5837	N/A	N/A	AGACGGTCTTTTTTCAAGAA	34	281
1447427	16324	16343	N/A	N/A	ATGATTCTTCCACACTCCAA	41	282
1447433	17302	17321	2349	2368	AAAGCTGCAAATCTTTCCCC	18	283
1447438	8129	8148	N/A	N/A	CCTGTTGCATAAATTGTGGC	64	284
1447440	7500	7519	N/A	N/A	TCCATGGGTTTACCTCTCCT	45	285
1447445	797	816	N/A	N/A	ACAGTCAACTGACCTTTCGA	68	286
1447446	13961	13980	N/A	N/A	AGGGATTCCTTGTACAGTCA	45	287
1447447	35	54	35	54	GCAAGCAAGTTTATTGACCT	56	288
1447451	15465	15484	1743	1762	CATTTGTTACCCCACCAGCC	59	289
1447452	1044	1063	N/A	N/A	ATCCCAGTGAAAATCATGGC	61	290
1447473	2036	2055	N/A	N/A	CTGTGCCATCTCTTTTATAA	107	291
1447479	11603	11622	N/A	N/A	CTCAGCCTTTTCCTGTGGGA	83†	292
1447483	5990	6009	N/A	N/A	GCTTAACATTAATCCCTACA	30	293
1447486	687	706	N/A	N/A	CCAGGTACAGATCTTACACC	83	294
1447496	8040	8059	N/A	N/A	AGGCACCTGATACAATGCAA	33	295
1447499	4954	4973	N/A	N/A	CCTAGGTACAATTATCATCA	84	296
1447508	11200	11219	N/A	N/A	GCCTCACTAGTCCTCAGTAT	122	297
1447515	13009	13028	N/A	N/A	ATACTAACATTTTGCTGGCT	76	298
1447533	4553	4572	N/A	N/A	CCCTCACTGACTTCTTCAAC	73	299
1447535	18288	18307	3335	3354	TGTTTCTCTTCACCCCCAAC	19	300
1447548	2198	2217	N/A	N/A	GCACACTCTGCCAAAACACA	133	301
1447549	3961	3980	N/A	N/A	TTAGTTATCAATGTTACCCT	10	302
1447551	3720	3739	N/A	N/A	AGGTTAATGAATCCTATCTC	58	303
1447562	9150	9169	N/A	N/A	TAGAGCTTTCCCCACCACAT	53	304

1447563	4136	4155	N/A	N/A	GTCCCGGTATCACCTTTAAC	53	305
1447565	16315	16334	N/A	N/A	CCACACTCCAAGCTAAGTCA	50	306
1447567	16330	16349	N/A	N/A	GCAGAGATGATTCTTCCACA	11	307
1447578	16068	16087	N/A	N/A	TGTCAAACTCATCACAGCAC	65	308
1447579	16927	16946	1974	1993	TCGGTTCCAATTGCCTTTTT	36	309
1447584	17493	17512	2540	2559	AACCTTTTATACTACATGTT	52	310
1447586	7914	7933	N/A	N/A	ATTGACTGTCTACCAGGTAT	34	311
1447594	17007	17026	2054	2073	AACTATGTACACACCCAGCA	31	312
1447595	5409	5428	N/A	N/A	CAGCATTGTTTATACTCCAG	1	313
1447610	11189	11208	N/A	N/A	CCTCAGTATCACTCTCTGAA	100	314
1447622	14760	14779	1555	1574	AGGATGCCTTGAACAGTGTC	86	315
1447630	14164	14183	N/A	N/A	ATAAGCTTTTTCAACCCACA	51	316
1447639	5694	5713	1068	1087	CAGCTGGAACCTTATTATCT	74†	317
1447642	16686	16705	N/A	N/A	TGGAAAACAGCTCCATACCT	76	318
1447645	17110	17129	2157	2176	CCAGAAATTCTATCTGTCCT	56	319
1447648	5115	5134	N/A	N/A	GAAGGACTTCTTGCTCTTCC	49	320
1447650	16283	16302	N/A	N/A	ATTCTGTTAACACCATGGAC	109	321

Table 5

Reduction of CHMP7 RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages in A431 cells

Compound Number	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	Sequence (5' to 3')	CHMP7 (% UTC)	SEQ ID NO
1447186	12533	12552	N/A	N/A	TGGTCTTCCTTATTTGGTCC	38	322
1447194	16529	16548	1790	1809	GAGGATGTCCAATTCCTTCT	80	323
1447195	11334	11353	N/A	N/A	TTTTACACTCCTGCCTCTCA	65	324
1447198	5514	5533	N/A	N/A	GCAATGTCCCATTCCAGTCT	46	325
1447207	4362	4381	N/A	N/A	CAATATCAATGTCCAGTCCA	57	326
1447215	5735	5754	N/A	N/A	AGTACCCACCTTCAACAGCT	81†	327
1447220	12879	12898	1361	1380	CAGCTGGTACACCCCAACAT	100	328
1447224	5297	5316	N/A	N/A	GCCAAATTTACACCATGATA	9	329
1447235	13008	13027	N/A	N/A	TACTAACATTTTGCTGGCTC	57	330
1447236	5408	5427	N/A	N/A	AGCATTGTTTATACTCCAGC	2	331
1447246	16329	16348	N/A	N/A	CAGAGATGATTCTTCCACAC	44	332
1447248	10656	10675	N/A	N/A	GTCACCATTTCGCTCATACA	19	333
1447253	16963	16982	2010	2029	GGTCCTTCACTTGAGGGTCC	98	334
1447258	18231	18250	3278	3297	TTGAACAACGATTTGTGCTC	40	335
1447263	17547	17566	2594	2613	GGCGACCTCTTTCTCTGAAC	44	336
1447268	5686	5705	1060	1079	ACCTTATTATCTCCCAGCAT	12†	337
1447284	2034	2053	N/A	N/A	GTGCCATCTCTTTTATAAGA	111	338
1447295	1414	1433	N/A	N/A	GAAGACATAATTATCCATGC	74	339
1447299	4496	4515	N/A	N/A	AAACGGTTTCCACTGTATGC	59	340

1447300	12480	12499	N/A	N/A	TGACCGCTTCTCTTTGGTAA	71	341
1447305	18074	18093	3121	3140	GAGCATTCAGACCCTTTCCC	44	342
1447307	16282	16301	N/A	N/A	TTCTGTTAACACCATGGACC	71	343
1447308	17003	17022	2050	2069	ATGTACACACCCAGCAAGCC	59	344
1447312	3950	3969	N/A	N/A	TGTTACCCTCAGATACCGCC	16	345
1447330	16314	16333	N/A	N/A	CACACTCCAAGCTAAGTCAC	73	346
1447339	8005	8024	N/A	N/A	GCAGGGTGCACACCAATTCC	109	347
1447347	4129	4148	N/A	N/A	TATCACCTTTAACTAGCTGT	24	348
1447353	16503	16522	N/A	N/A	CTTCACTGTCAAAATCTGGA	92	349
1447354	10213	10232	N/A	N/A	GCAAGGAGACCATTTACACA	47	350
1447358	16322	16341	N/A	N/A	GATTCTTCCACACTCCAAGC	59	351
1447365	12589	12608	N/A	N/A	TTCCTATAGAAGATTCATTC	77	352
1447375	9299	9318	N/A	N/A	GACACAGACATCGAGTTTTC	52	353
1447379	18287	18306	3334	3353	GTTTCTCTTCACCCCCAACA	16	354
1447386	17080	17099	2127	2146	GTAGCATCCAGATAAAATCA	38	355
1447398	11793	11812	N/A	N/A	AGATGAGCCTCCATACCTTC	106	356
1447399	15489	15508	N/A	N/A	ACCACCTTGTCCACTCACCT	62	357
1447417	4552	4571	N/A	N/A	CCTCACTGACTTCTTCAACT	64	358
1447420	11836	11855	N/A	N/A	ACTCTATGTACTTAATCAAT	108	359
1447426	10335	10354	N/A	N/A	ATCTTATGATGATCCTTTAT	58	360
1447428	11199	11218	N/A	N/A	CCTCACTAGTCCTCAGTATC	62	361
1447429	14432	14451	N/A	N/A	ACTCACCAGCTGCTTCTTTC	154	362
1447435	17300	17319	2347	2366	AGCTGCAAATCTTTCCCCTT	33	363
1447454	14160	14179	N/A	N/A	GCTTTTTCAACCCACAGGGA	110	364
1447467	7864	7883	N/A	N/A	TGGCACTGTTCCCTTCTAGT	24	365
1447468	1043	1062	N/A	N/A	TCCCAGTGAAAATCATGGCT	72	366
1447477	17206	17225	2253	2272	GACAGGTCAGACACAGGACT	19	367
1447484	14969	14988	N/A	N/A	AAGCTCAATTTACCCTATAC	80	368
1447489	5817	5836	N/A	N/A	GACGGTCTTTTTTCAAGAAC	77	369
1447504	294	313	N/A	N/A	ACCAAAGAAGATCTACCAAC	91	370
1447505	11516	11535	N/A	N/A	AAACCATGATCACACAAGGC	54	371
1447507	4541	4560	N/A	N/A	TCTTCAACTACTGTTTCTCC	27	372
1447519	1539	1558	N/A	N/A	AATGTCTGCTCACACCATTC	107	373
1447521	2168	2187	N/A	N/A	CAGACCACTTGAATATGTTT	85	374
1447530	1820	1839	N/A	N/A	GCGGAATTTATTACAGCTAG	122	375
1447534	14035	14054	N/A	N/A	ACAAGGCTAGACTTTCCCAC	61	376
1447536	7499	7518	N/A	N/A	CCATGGGTTTACCTCTCCTC	62	377
1447541	11164	11183	N/A	N/A	TGGATGAAATGACATCTAAT	80	378
1447558	4914	4933	N/A	N/A	CTGATTGCTAAAGACAGCAT	40	379
1447559	17463	17482	2510	2529	ATGGCAGCTAAGTCCCCTCA	53	380
1447561	1202	1221	N/A	N/A	GGTATGTACAAATTCTACAT	71	381
1447566	4651	4670	N/A	N/A	AGAGACTTTAATACCACCAT	63	382
1447568	8111	8130	N/A	N/A	GCATATCGATAGATTATCAT	43	383

1447580	18100	18119	3147	3166	GCGATCGCTTCTTCTCGCCA	85	384
1447583	13790	13809	N/A	N/A	TAACATTCACAGTCATGGTC	57	385
1447585	8253	8272	N/A	N/A	TCCGAAAAATCAATTCCATA	36	386
1447589	5114	5133	N/A	N/A	AAGGACTTCTTGCTCTTCCA	20	387
1447590	5693	5712	1067	1086	AGCTGGAACCTTATTATCTC	52†	388
1447597	9265	9284	N/A	N/A	CCTACCAGATATGCAACCAC	64	389
1447605	9148	9167	N/A	N/A	GAGCTTTCCCCACCACATAC	80	390
1447615	15186	15205	N/A	N/A	CCTTTCTGTACCTCTTGGAT	77	391
1447617	16684	16703	N/A	N/A	GAAAACAGCTCCATACCTCC	83	392
1447627	9601	9620	N/A	N/A	GTATACAACCTATCAGTGGA	52	393
1447628	3719	3738	N/A	N/A	GGTTAATGAATCCTATCTCT	34	394
1447633	685	704	N/A	N/A	AGGTACAGATCTTACACCAT	102	395
1447637	5901	5920	N/A	N/A	TCCCACTAATGAATATTACA	53	396
1447640	796	815	N/A	N/A	CAGTCAACTGACCTTTCGAA	71	397
1447644	32	51	32	51	AGCAAGTTTATTGACCTGCC	98	398
1447652	16922	16941	1969	1988	TCCAATTGCCTTTTTGGAGA	60	399

Table 6

Reduction of CHMP7 RNA by 5-10-5 MOE gapmers with mixed PO/PS internucleoside linkages in A431 cells

Compound Number	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	Sequence (5' to 3')	CHMP7 (% UTC)	SEQ ID NO
1447187	7543	7562	N/A	N/A	GCAGGCTTTCTTTGTTTGCC	59	400
1447192	1307	1326	N/A	N/A	AGTCAATTCCCATATACCTA	81	401
1447196	8002	8021	N/A	N/A	GGGTGCACACCAATTCCATT	84	402
1447200	14968	14987	N/A	N/A	AGCTCAATTTACCCTATACC	71	403
1447219	266	285	N/A	N/A	AGTATATGATAATATGCCCA	79	404
1447221	18072	18091	3119	3138	GCATTCAGACCCTTTCCCGT	57	405
1447225	5684	5703	1058	1077	CTTATTATCTCCCAGCATGT	13†	406
1447232	12875	12894	1357	1376	TGGTACACCCCAACATCTAC	86	407
1447237	11982	12001	N/A	N/A	AGGTCCCATCACACTACTCA	65	408
1447250	17200	17219	2247	2266	TCAGACACAGGACTGTATAA	51	409
1447254	9051	9070	N/A	N/A	TGCCTTCCTAAACAAGACCT	86	410
1447269	15185	15204	N/A	N/A	CTTTCTGTACCTCTTGGATC	80	411
1447272	11515	11534	N/A	N/A	AACCATGATCACACAAGGCA	60	412
1447275	9532	9551	N/A	N/A	GAAAGTCCTCAGCATATCCA	60	413
1447278	16313	16332	N/A	N/A	ACACTCCAAGCTAAGTCACC	72	414
1447282	11792	11811	N/A	N/A	GATGAGCCTCCATACCTTCT	90	415
1447283	17299	17318	2346	2365	GCTGCAAATCTTTCCCCTTC	23	416
1447293	4650	4669	N/A	N/A	GAGACTTTAATACCACCATA	82	417
1447298	5454	5473	N/A	N/A	TCATCACGACCATTTGTTAA	78	418
1447301	17002	17021	2049	2068	TGTACACACCCAGCAAGCCT	92	419

1447302	9298	9317	N/A	N/A	ACACAGACATCGAGTTTTCA	78	420
1447304	5213	5232	N/A	N/A	CGGTGAGATCTCCTTTTACA	14	421
1447313	4536	4555	N/A	N/A	AACTACTGTTTCTCCTGTTC	34	422
1447318	17546	17565	2593	2612	GCGACCTCTTTCTCTGAACA	62	423
1447320	16528	16547	1789	1808	AGGATGTCCAATTCCTTCTC	111	424
1447321	17075	17094	2122	2141	ATCCAGATAAAATCAGTGGT	53	425
1447328	5815	5834	N/A	N/A	CGGTCTTTTTTCAAGAACGC	51	426
1447332	16657	16676	1918	1937	AAGGACAGTTTCTCAAGTTC	99	427
1447333	10655	10674	N/A	N/A	TCACCATTTCGCTCATACAT	42	428
1447350	18099	18118	3146	3165	CGATCGCTTCTTCTCGCCAT	71	429
1447352	4549	4568	N/A	N/A	CACTGACTTCTTCAACTACT	58	430
1447357	4903	4922	N/A	N/A	AGACAGCATAAAATTTGTGC	40	431
1447367	16277	16296	N/A	N/A	TTAACACCATGGACCTGACC	70	432
1447374	11249	11268	N/A	N/A	GCTGAGGCCTGATTTCCAGC	91	433
1447377	13097	13116	N/A	N/A	GCTTTCCATGATTTCTGCAT	73	434
1447378	5862	5881	N/A	N/A	AGCAGATAAACTCAGTTATC	45	435
1447380	17420	17439	2467	2486	TCTCATTCTTACCAGTGAAA	31	436
1447385	16425	16444	N/A	N/A	GACTGAGGTTACCAAAACCC	49	437
1447401	10332	10351	N/A	N/A	TTATGATGATCCTTTATTCT	65	438
1447402	1197	1216	N/A	N/A	GTACAAATTCTACATAAGGA	106	439
1447406	5734	5753	N/A	N/A	GTACCCACCTTCAACAGCTC	81†	440
1447409	1817	1836	N/A	N/A	GAATTTATTACAGCTAGGCA	113	441
1447414	16321	16340	N/A	N/A	ATTCTTCCACACTCCAAGCT	70	442
1447418	14422	14441	1465	1484	TGCTTCTTTCCTGCTCGGCA	65	443
1447437	2165	2184	N/A	N/A	ACCACTTGAATATGTTTATA	101	444
1447443	27	46	27	46	GTTTATTGACCTGCCGGCCT	111	445
1447456	16805	16824	N/A	N/A	AGTCTTAATATAAACAACCC	110	446
1447457	927	946	N/A	N/A	GGACGGATACAACCCAACTT	75	447
1447474	8109	8128	N/A	N/A	ATATCGATAGATTATCATGC	43	448
1447480	18279	18298	3326	3345	TCACCCCCAACATTTCCGTT	61	449
1447492	14030	14049	N/A	N/A	GCTAGACTTTCCCACCTGGA	58	450
1447494	18207	18226	3254	3273	CCTGGAGCAAATTCTTCTCC	81	451
1447506	12549	12568	N/A	N/A	CTCAGCAAATGATATTTGGT	55	452
1447538	684	703	N/A	N/A	GGTACAGATCTTACACCATT	108	453
1447539	5692	5711	1066	1085	GCTGGAACCTTATTATCTCC	11†	454
1447543	2033	2052	N/A	N/A	TGCCATCTCTTTTATAAGAT	120	455
1447545	8220	8239	N/A	N/A	AAGTACATAGATCTCTGCAC	60	456
1447546	5110	5129	N/A	N/A	ACTTCTTGCTCTTCCAAGGC	23	457
1447552	14125	14144	N/A	N/A	GGGCACATTATACACATCTT	60	458
1447557	3712	3731	N/A	N/A	GAATCCTATCTCTTAGACCT	59	459
1447569	10068	10087	N/A	N/A	GTGGAAAGTCACTATGGATT	46	460
1447573	11156	11175	N/A	N/A	ATGACATCTAATTCCCTTCC	46	461
1447577	7021	7040	N/A	N/A	GTGCTCAGTCAACACACACA	75	462

1447582	15488	15507	N/A	N/A	CCACCTTGTCCACTCACCTA	73	463
1447604	5407	5426	N/A	N/A	GCATTGTTTATACTCCAGCT	2	464
1447606	4247	4266	N/A	N/A	CATCAGAGTTGACTTTCTCC	35	465
1447609	3909	3928	N/A	N/A	GTATCTCCTACAGACCTTTT	28	466
1447611	1534	1553	N/A	N/A	CTGCTCACACCATTCCTAGT	84	467
1447613	12520	12539	N/A	N/A	TTGGTCCAGAACTTTTACCT	69	468
1447618	16953	16972	2000	2019	TTGAGGGTCCTACAATGGCT	43	469
1447620	11197	11216	N/A	N/A	TCACTAGTCCTCAGTATCAC	69	470
1447621	16328	16347	N/A	N/A	AGAGATGATTCTTCCACACT	67	471
1447625	9247	9266	N/A	N/A	ACTGCAGTAACTGCACAGTA	111	472
1447631	11831	11850	N/A	N/A	ATGTACTTAATCAATCACTG	73	473
1447634	4494	4513	N/A	N/A	ACGGTTTCCACTGTATGCCA	33	474
1447641	749	768	N/A	N/A	GAGTCTTTTCAACAATGAGC	82	475
1447649	14395	14414	1438	1457	CGGGCTTCTTCTTTACACCT	76	476
1447651	4053	4072	N/A	N/A	TGAGGATAATTCTATCACCT	12	477

Example 2: Dose-dependent inhibition of human CHMP7 in A431 cells by modified oligonucleotides

Modified oligonucleotides selected from Example 1 above were tested at various doses in A431 cells. Cultured A431 cells at a density of 10,000 cells per well were treated by free uptake with various concentrations of modified oligonucleotide as specified in the tables below. After a treatment period of approximately 48 hours, total RNA was isolated from the cells and CHMP7 RNA levels were measured by quantitative real-time RTPCR. Human CHMP7 primer-probe set RTS50844 (described herein in Example 1) was used to measure RNA levels as described above. CHMP7 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of CHMP7 RNA is presented in the tables below as percent CHMP7 RNA, relative to untreated control cells (% UTC). Modified oligonucleotides marked with an "†" indicate that the modified oligonucleotide is complementary to the amplicon region of the primer probe set. Additional assays may be used to measure the potency and efficacy of the modified oligonucleotides complementary to the amplicon region.

The half maximal inhibitory concentration (IC_{50}) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in Excel and is also presented in the tables below.

Table 7

Dose-dependent reduction of human CHMP7 RNA in A431 cells by modified oligonucleotides

Compound No.	CHMP7 RNA (% UTC)				IC_{50} (μM)
	62.5 nM	250.0 nM	1,000.0 nM	4,000.0 nM	
1447190	75	48	22	9	0.25
1447260†	86	79	56	26	1.13
1447309	55	26	9	5	0.06
1447314	56	25	11	7	0.06
1447315	60	28	10	3	0.08
1447326	75	29	16	8	0.16

1447431	37	13	4	1	<0.0625
1447449	78	51	25	11	0.29
1447471	60	26	9	6	0.07
1447481	56	24	14	6	0.06
1447488	70	28	12	4	0.13
1447497	54	28	15	8	0.06
1447502†	96	76	58	38	1.72
1447520	61	30	15	9	0.09
1447532	86	48	33	16	0.39
1447555†	70	45	19	4	0.19
1447602	64	30	10	4	0.10
1447624	75	45	22	9	0.24

Table 8

Dose-dependent reduction of human CHMP7 RNA in A431 cells by modified oligonucleotides

Compound No.	CHMP7 RNA (% UTC)				IC_{50} (μM)
	62.5 nM	250.0 nM	1,000.0 nM	4,000.0 nM	
1447218†	87	55	29	12	0.40
1447228	80	40	23	9	0.24
1447233	80	70	44	22	0.65
1447256	64	37	16	6	0.13
1447273	85	51	34	19	0.42
1447279	110	62	30	18	0.63
1447285	83	61	40	29	0.65
1447331	55	26	8	2	0.06
1447364	81	56	28	11	0.36
1447369	63	42	21	14	0.15
1447370	78	57	29	12	0.34
1447421	104	76	49	33	1.22
1447433	105	86	62	45	2.60
1447535	94	42	18	7	0.31
1447549	62	42	21	5	0.14
1447560	74	43	14	8	0.20
1447567	79	47	28	13	0.30
1447595	26	5	1	1	<0.0625

Table 9

Dose-dependent reduction of human CHMP7 RNA in A431 cells by modified oligonucleotides

Compound No.	CHMP7 RNA (% UTC)				IC_{50} (μM)
	62.5 nM	250.0 nM	1,000.0 nM	4,000.0 nM	
1447224	70	39	14	3	0.16
1447225†	84	64	33	17	0.49

1447236	33	7	1	0	<0.0625
1447248	64	41	24	13	0.15
1447268†	90	60	26	10	0.42
1447283	79	42	22	13	0.25
1447304	58	26	14	7	0.07
1447312	99	55	28	14	0.48
1447343	74	57	34	16	0.36
1447347	64	43	23	10	0.16
1447379	79	41	18	5	0.23
1447467	82	44	26	19	0.31
1447477	76	54	27	9	0.30
1447539†	92	67	71	31	1.64
1447546	68	34	16	6	0.14
1447589	61	33	18	8	0.10
1447604	26	7	2	1	<0.0625
1447651	84	56	18	8	0.32

Example 3: Design of 5-10-5 MOE gapmer modified oligonucleotides with PS internucleoside linkages complementary to a human CHMP7 nucleic acid

Modified oligonucleotides complementary to human CHMP7 nucleic acid were designed and synthesized. "Start site" in all the tables below indicates the 5'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. "Stop site" in all the tables below indicates the 3'-most nucleoside of the target sequence to which the modified oligonucleotide is complementary. As shown in the tables below, the modified oligonucleotides are complementary to either SEQ ID NO: 1 (described herein above), and/or to SEQ ID NO: 2 (described herein above). 'N/A' indicates that the modified oligonucleotide is not complementary to that particular target sequence with 100% complementarity.

The modified oligonucleotides in the table below are 5-10-5 MOE gapmers. The sugar motif of the gapmers is (from 5' to 3'): eeeeeddddddddddeeeee; wherein 'd' represents a 2'-β-D-deoxyribosyl sugar moiety, and 'e' represents a 2'- MOE modified sugar moiety. The internucleoside motif of the gapmers is (from 5' to 3'): sssssssssssssssssss, wherein each "s" represents a phosphorothioate internucleoside linkage. Each cytosine nucleoside is a 5-methyl cytosine.

Table 10

5-10-5 MOE gapmers PS internucleoside linkages complementary to human CHMP7

Compound No.	Sequence (5' to 3')	SEQ ID No: 1 Start Site	SEQ ID No: 1 Stop Site	SEQ ID No: 2 Start Site	SEQ ID No: 2 Stop Site	SEQ ID No.
1508916	GAAAACGGTTTCCACTGTAT	4498	4517	N/A	N/A	257
1508917	TGTTACCCTCAGATACCGCC	3950	3969	N/A	N/A	345
1508918	ATGTGATGCTATTAATAGGA	10035	10054	N/A	N/A	12

Example 4: Dose-dependent inhibition of human CHMP7 in A431 cells by modified oligonucleotides

Modified oligonucleotides described in Example 3 above were tested at various doses in A431 cells. Cultured A431 cells at a density of 10,000 cells per well were treated by free uptake with various concentrations of modified oligonucleotide as specified in the tables below. After a treatment period of approximately 48 hours, total RNA was isolated from the cells and CHMP7 RNA levels were measured by quantitative real-time RTPCR. Human CHMP7 primer-probe set RTS50844 (described herein in Example 1) was used to measure RNA levels as described above. CHMP7 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of CHMP7 RNA is presented in the tables below as percent CHMP7 RNA, relative to untreated control cells (% UTC).

The half maximal inhibitory concentration (IC_{50}) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in Excel and is also presented in the tables below.

Table 11

Dose-dependent reduction of human CHMP7 RNA in A431 cells by modified oligonucleotides

Compound No.	CHMP7 RNA (% UTC)										IC_{50} (μM)
	0.02 nM	0.06 nM	0.24 nM	0.98 nM	3.91 nM	15.63 nM	62.5 nM	250.0 nM	1000.0 nM	4000.0 nM	
1508916	121	107	106	107	104	99	73	51	28	18	0.37
1508917	96	97	93	91	91	77	40	18	6	3	0.03
1508918	110	98	103	101	112	105	89	70	39	27	2.96

CLAIMS:

1. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to an equal length portion of a CHMP7 nucleic acid, and wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.
2. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides and having a nucleobase sequence comprising at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or 20 contiguous nucleobases of any of the nucleobases of SEQ ID NOs: 10-477, wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.
3. The oligomeric compound of claim 2, wherein the modified oligonucleotide has a nucleobase sequence consisting of the nucleobase sequence of any of SEQ ID NOs: 10-477.
4. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 contiguous nucleobases complementary to:

    an equal length portion within nucleobases 3950-3983 of SEQ ID NO: 1;
    an equal length portion within nucleobases 4242-4266 of SEQ ID NO: 1;
    an equal length portion within nucleobases 4480-4525 of SEQ ID NO: 1;
    an equal length portion within nucleobases 4534-4566 of SEQ ID NO: 1;
    an equal length portion within nucleobases 5205-5232 of SEQ ID NO: 1;
    an equal length portion within nucleobases 5404-5430 of SEQ ID NO: 1;
    an equal length portion within nucleobases 8323-8344 of SEQ ID NO: 1;
    an equal length portion within nucleobases 16927-16950 of SEQ ID NO: 1;
    an equal length portion within nucleobases 17298-17340 of SEQ ID NO: 1; or
    an equal length portion within nucleobases 18287-18313 of SEQ ID NO: 1;

    wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.
5. An oligomeric compound comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, or at least 18 contiguous nucleobases of a sequence selected from:

    SEQ ID NOs: 220, 302, and 345;
    SEQ ID NOs: 21, 131, 191, and 465;
    SEQ ID NOs: 34, 116, 184, 242, 257, 340, and 474;
    SEQ ID NOs: 55, 118, 202, 267, 372, and 422;
    SEQ ID NOs: 73, 136, 197, and 421;
    SEQ ID NOs: 79, 160, 168, 230, 313, 331, and 464;

SEQ ID NOs: 157, 186, and 265;

SEQ ID NOs: 128, 182, and 309;

SEQ ID NOs: 44, 76, 153, 206, 283, 363, and 416; or

SEQ ID NOs: 85, 121, 189, 300, and 354;

wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

6. The oligomeric compound of any of claims 1-5, wherein the modified oligonucleotide has a nucleobase sequence that is at least 80%, 85%, 90%, 95%, or 100% complementary to the nucleobase sequence of SEQ ID NO: 1 or SEQ ID NO: 2 when measured across the entire nucleobase sequence of the modified oligonucleotide.

7. The oligomeric compound of any of claims 1-6, wherein the modified oligonucleotide comprises at least one modified nucleoside.

8. The oligomeric compound of claim 7, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a modified sugar moiety.

9. The oligomeric compound of claim 8, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety.

10. The oligomeric compound of claim 9, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a bicyclic sugar moiety having a 2'-4' bridge, wherein the 2'-4' bridge is selected from -O-CH_2-; and -O-CH(CH_3)-.

11. The oligomeric compound of any of claims 7-10, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a non-bicyclic modified sugar moiety.

12. The oligomeric compound of claim 11, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a non-bicyclic modified sugar moiety comprising a 2'-MOE modified sugar moiety or a 2'-OMe modified sugar moiety.

13. The oligomeric compound of any of claims 7-12, wherein the modified oligonucleotide comprises at least one modified nucleoside comprising a sugar surrogate.

14. The oligomeric compound of claim 13, wherein the sugar surrogate is selected from any of morpholino, modified morpholino, PNA, THP, and F-HNA.

15. The oligomeric compound of any of claims 1-8 or 11-14, wherein the modified oligonucleotide does not comprise a bicyclic modified sugar moiety.

16. The oligomeric compound of any of claims 1-15, wherein the modified oligonucleotide is a gapmer.

17. The oligomeric compound of any of claims 1-16 wherein the modified oligonucleotide comprises a deoxy region consisting of 5-12 linked 2'-deoxynucleosides.

18. The oligomeric compound of any of claims 1-16, wherein the modified oligonucleotide comprises a deoxy region consisting of 5-12 linked 2'-β-D-deoxynucleosides.

19. The oligomeric compound of claim 17 or claim 18, wherein the deoxy region consists of 6, 7, 8, 9, 10, or 6-10 linked nucleosides.

20. The oligomeric compound of any of claims 17-19, wherein each nucleoside immediately adjacent to the deoxy region comprises a modified sugar moiety.

21. The oligomeric compound of any of claims 17-20, wherein the deoxy region is flanked on the 5'-side by a 5'-external region consisting of 1-6 linked 5'-external region nucleosides and on the 3'-side by a 3'-external region consisting of 1-6 linked 3'-external region nucleosides; wherein

the 3'-most nucleoside of the 5' external region comprises a modified sugar moiety; and

the 5'-most nucleoside of the 3' external region comprises a modified sugar moiety.

22. The oligomeric compound of claim 21, wherein each nucleoside of the 3' external region comprises a modified sugar moiety.

23. The oligomeric compound of claim 21 or claim 22, wherein each nucleoside of the 5' external region comprises a modified sugar moiety.

24. The oligomeric compound of any of claims 1-23, wherein the modified oligonucleotide comprises:

a 5'-region consisting of 1-7 linked 5'-region nucleosides;

a central region consisting of 6-10 linked central region nucleosides; and

a 3'-region consisting of 1-7 linked 3'-region nucleosides; wherein

each of the 5'-region nucleosides and each of the 3'-region nucleosides comprises a modified sugar moiety and each of the central region nucleosides comprises a 2'-β-D-deoxyfuranosyl sugar moiety.

25. The oligomeric compound of claim 24, wherein the modified oligonucleotide comprises:

a 5'-region consisting of 5 linked 5'-region nucleosides;

a central region consisting of 10 linked central region nucleosides; and

a 3'-region consisting of 5 linked 3'-region nucleosides; wherein

each of the 5'-region nucleosides and each of the 3'-region nucleosides is a 2'-MOE nucleoside and each of the central region nucleosides is a 2'-β-D-deoxynucleoside.

26. The oligomeric compound of any of claims 1-25, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.

27. The oligomeric compound of claim 26, wherein each internucleoside linkage of the modified oligonucleotide is a modified internucleoside linkage.

28. The oligomeric compound of claim 26 or claim 27 wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

29. The oligomeric compound of claim 26 or claim 28 wherein the modified oligonucleotide comprises at least one phosphodiester internucleoside linkage.

30. The oligomeric compound of any of claims 26, 28, or 29, wherein each internucleoside linkage is either a phosphodiester internucleoside linkage or a phosphorothioate internucleoside linkage.

31. The oligomeric compound of claim 27, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage

32. The oligonucleotide compound of claim 26, wherein the modified oligonucleotide has an internucleoside linkage motif of soooossssssssssooss; wherein,

s = a phosphorothioate internucleoside linkage and o = a phosphodiester internucleoside linkage.

33. The oligomeric compound of any of claims 1-32, wherein the modified oligonucleotide comprises at least one modified nucleobase.

34. The oligomeric compound of claim 33, wherein the modified nucleobase is a 5-methyl cytosine.

35. The oligomeric compound of claim 34, wherein each cytosine is a 5-methyl cytosine.
36. The oligomeric compound of any of claims 1-35, wherein the modified oligonucleotide consists of 12-30, 12-22, 12-20, 14-18, 14-20, 15-17, 15-25, 16-18, 16-20, 17-20, 18-20 or 18-22 linked nucleosides.
37. The oligomeric compound of any of claims 1-36, wherein the modified oligonucleotide consists of 16, 17, 18, 19, or 20 linked nucleosides.
38. The oligomeric compound of any of claims 1-35, wherein the modified oligonucleotide consists of 20 linked nucleosides.
39. The oligomeric compound of any of claims 1-38, consisting of the modified oligonucleotide.
40. The oligomeric compound of any of claims 1-38, wherein the oligomeric compound comprises a conjugate group.
41. The oligomeric compound of claim 40, wherein the conjugate group comprises a conjugate moiety and a conjugate linker.
42. The oligomeric compound of claim 41, wherein the conjugate linker consists of a single bond.
43. The oligomeric compound of claim 41 or claim 42, wherein the conjugate linker is cleavable.
44. The oligomeric compound of claim 41 or claim 43, wherein the conjugate linker comprises 1-3 linker-nucleosides.
45. The oligomeric compound of any of claims 41-43, wherein the conjugate linker does not comprise any linker nucleosides.
46. The oligomeric compound of any of claims 40-45, wherein the conjugate group is attached to the modified oligonucleotide at the 5'-end of the modified oligonucleotide.
47. The oligomeric compound of any of claims 40-45, wherein the conjugate group is attached to the modified oligonucleotide at the 3'-end of the modified oligonucleotide.
48. The oligomeric compound of any of claims 40-47, wherein the conjugate group comprises a lipid.
49. The oligomeric compound of any of claims 40-47, wherein the conjugate group comprises a cell-targeting moiety.
50. The oligomeric compound of any of claims 1-49, further comprising a terminal group.
51. The oligomeric compound of any of claims 1-49, wherein the oligomeric compound is a singled-stranded oligomeric compound.
52. The oligomeric compound of any of claims 1-51, wherein the oligomeric compound is capable of reducing the amount of CHMP7 RNA in a cell.
53. The oligomeric compound of any of claims 1-52, wherein the modified oligonucleotide of the oligomeric compound is a pharmaceutically acceptable salt comprising one or more cations selected from sodium, potassium, calcium, and magnesium.
54. An oligomeric duplex, comprising a first oligomeric compound and a second oligomeric compound comprising a second modified oligonucleotide, wherein the first oligomeric compound is an oligomeric compound of any of claims 1-53.
55. An antisense agent comprising an antisense compound, wherein the antisense compound is the oligomeric compound of any of claims 1-53 or the oligomeric duplex of claim 54.
56. The antisense agent of claim 55, wherein the antisense agent is the oligomeric duplex of claim 54

57. The antisense agent of claim 55 or claim 56, wherein the antisense agent is:

an RNase H agent capable of reducing the amount of CHMP7 nucleic acid through the activation of RNase H; or

an RNAi agent capable of reducing the amount of CHMP7 nucleic acid through the activation of RISC/Ago2.

58. The antisense agent of any of claims 55-57, wherein the antisense agent comprises a conjugate group, wherein the conjugate group comprises a cell-targeting moiety.

59. A pharmaceutical composition comprising the oligomeric compound of any of claims 1-53, the oligomeric duplex of claim 54, or the antisense agent of any of claims 55-58, and a pharmaceutically acceptable diluent.

60. The pharmaceutical composition of claim 59, wherein the pharmaceutically acceptable diluent is artificial CSF (aCSF) or phosphate- buffered saline (PBS).

61. The pharmaceutical composition of claim 60, wherein the pharmaceutical composition consists essentially of the oligomeric compound, oligomeric duplex, or antisense agent, and artificial CSF (aCSF).

62. The pharmaceutical composition of claim 60, wherein the pharmaceutical composition consists essentially of the oligomeric compound, oligomeric duplex, or antisense agent, and phosphate buffered saline (PBS).

63. A chirally enriched population of oligomeric compounds of any of claims 1-53, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.

64. The chirally enriched population of claim 63, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (Sp) configuration.

65. The chirally enriched population of claim 63, wherein the population is enriched for oligomeric compounds comprising at least one particular phosphorothioate internucleoside linkage having the (Rp) configuration.

66. The chirally enriched population of claim 63, wherein the population is enriched for oligomeric compounds having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage.

67. The chirally enriched population of claim 66, wherein the population is enriched for oligomeric compounds having the (Sp) configuration at each phosphorothioate internucleoside linkage or for modified oligonucleotides having the (Rp) configuration at each phosphorothioate internucleoside linkage.

68. The chirally enriched population of claim 66, wherein the population is enriched for oligomeric compounds having the (Rp) configuration at one particular phosphorothioate internucleoside linkage and the (Sp) configuration at each of the remaining phosphorothioate internucleoside linkages.

69. The chirally enriched population of claim 66, wherein the population is enriched for oligomeric compounds having at least 3 contiguous phosphorothioate internucleoside linkages in the Sp, Sp, and Rp configurations, in the 5’ to 3’ direction.

70. A population of oligomeric compounds of any of claims 1-53, wherein all of the phosphorothioate internucleoside linkages of the modified oligonucleotide are stereorandom.

71. A pharmaceutical composition comprising the population of oligomeric compounds of any of claims 63-70 and a pharmaceutically acceptable diluent.

72. The pharmaceutical composition of claim 71, wherein the pharmaceutically acceptable diluent is artificial CSF (aCSF) or phosphate-buffered saline (PBS).

73. The pharmaceutical composition of claim 72, wherein the pharmaceutical composition consists essentially of the population of oligomeric compounds and artificial CSF (aCSF).

74. The pharmaceutical composition of claim 72, wherein the pharmaceutical composition consists essentially of the population of oligomeric compounds and PBS.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 21/53107

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C12N 15/11, C12N 15/113, A61P 25/00, A61P 25/28 (2021.01)

CPC - C12N 2310/14, C12N 2320/12, C12N 15/111, C12N 15/113, C12N 15/1137

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2013/0190385 A1 (DUCHATEAU et al.) 25 July 2013 (25.07.2013) Abstract; Claim 49; Claim 51; para [0044]; para [0057]; para [0158]; para [0167]; para [0187]	1
A	US 9,689,040 B2 (LIEBERMAN et al.) 27 June 2017 (27.06.2017) Abstract	1

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
30 December 2021 (30.12.2021)	FEB 23 2022
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer Kari Rodriquez Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 21/53107

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:

      ☒ in the form of an Annex C/ST.25 text file.

      ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

      ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 21/53107

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 7-74
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
----Please see continuation in first extra sheet ----------

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 21/53107

Continuation of Box No. III. Observations where unity of invention is lacking.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I+, Claims 1-6, directed to an oligomeric compound comprising a modified oligonucleotide. The oligomeric compound will be searched to the extent that the oligomeric compound encompasses a modified oligonucleotide consisting of 12 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 100% complementary to an equal length portion of a CHMP7 nucleic acid, and wherein the modified oligonucleotide comprises a single modification selected from a modified sugar moiety (note, this is the first claimed modified oligonucleotide for the oligomeric compound embodiment). It is believed that claim 1 encompasses this first named invention, and thus these claims will be searched without fee to the extent that the oligomeric compound encompasses a modified oligonucleotide consisting of 12 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 100% complementary to an equal length portion of a CHMP7 nucleic acid, and wherein the modified oligonucleotide comprises a single modification selected from a modified sugar moiety. Additional oligomeric compound(s) comprising additional oligonucleotide(s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected oligomeric compound(s) comprising additional oligonucleotide(s). Applicants must further indicate, if applicable, the claims which encompass the first named invention, if different than what was indicated above for this group. Failure to clearly identify how any paid additional invention fees are to be applied to the "+" group(s) will result in only the first claimed invention to be searched. An exemplary election would be an oligomeric compound comprising a modified oligonucleotide consisting of 12 linked nucleosides and having a nucleobase sequence comprising at least 12 contiguous nucleobases of the nucleobases of SEQ ID NO: 10, wherein the modified oligonucleotide comprises a single modification selected from a modified sugar moiety (claims 2-3).

The inventions listed as Group I+ do not relate to a single special technical feature under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special technical features

The inventions of Group I+ each include the special technical feature of a unique nucleic acid sequence. Each nucleic acid sequence has a unique target sequence, and is considered a distinct technical feature.

Common technical features

No technical features are shared between the oligonucleotide nucleic acid sequences of Group I+ and, accordingly, these groups lack unity a priori.

Additionally, even if Group I+ inventions were considered to share the technical features of including:
an oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to an equal length portion of a CHMP7 nucleic acid, and wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage;
these shared technical features are previously disclosed by US 2013/0190385 A1 to Duchateau et al., (hereinafter 'Duchateau').

Duchateau teaches an oligomeric compound comprising a modified oligonucleotide consisting of 12 to 50 linked nucleosides wherein the nucleobase sequence of the modified oligonucleotide is at least 90% complementary to an equal length portion of a CHMP7 nucleic acid, and wherein the modified oligonucleotide comprises at least one modification selected from a modified sugar moiety and a modified internucleoside linkage (Claim 49 - 'A method of increasing endonuclease-induced homologous recombination in a eukaryotic cell, tissue or organ with an interfering RNA.'; Claim 51 - 'The method of claim 49, wherein said interfering RNA is a siRNA, a miRNA or a shRNA.'; para [0158] . 'Table I ... CHMP7'; para [0167] - 'The iRNAs according to the invention may optionally be chemically modified.'; para [0044] - 'A "short interfering RNA" or "siRNA" comprises a RNA duplex (double-stranded region) and can further comprises one or two single-stranded overhangs, 3' or 5' overhangs. Each molecule of the duplex can comprise between 17 and 29 nucleotides, including 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, and 29 nucleotides. siRNAs can additionally be chemically modified.').

As the technical features were known in the art at the time of the invention, they cannot be considered special technical features that would otherwise unify the groups.

Therefore, Group I+ inventions lack unity under PCT Rule 13 because they do not share the same or corresponding special technical feature.

*Continuation of Item 4 above: claims 7-74 are held unsearchable because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).