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(54) Title: iRNA COMPOSITIONS AND METHODS FOR TARGETING ANGPTL7

(57) Abstract: The disclosure relates to double-stranded ribonucleic acid (dsRNA) compositions targeting ANGPTL7. The invention also relates to methods of using such dsRNA compositions to inhibit expression of ANGPTL7 and to methods of treating ANGPTL7-associated disorders, *e.g.*, glaucoma, using such dsRNA compositions.

iRNA COMPOSITIONS AND METHODS FOR TARGETING ANGPTL7

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of priority to U.S. Provisional Application No. 63/251,203, filed on October 1, 2021, and U.S. Provisional Application No. 63/287,414, filed on December 8, 2021. Each of the foregoing applications is incorporated herein by reference in its entirety.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. The XML copy, created on September 30, 2022, is named A108868_1510WO_SL.xml and is 1,323,084 bytes in size.

FIELD OF THE DISCLOSURE

The disclosure relates to the specific inhibition of the expression of ANGPTL7.

BACKGROUND OF THE INVENTION

Glaucoma is a leading cause of vision loss. Glaucoma results from damage to the optic nerve and loss of nerve fibers, often related to increased intraocular pressure. Lowering intraocular pressure can reduce development and progression of glaucoma and associated vision loss.

Human angiopoietin-like 7 (ANGPTL7), encoding the angiopoietin-like 7 protein (ANGPTL7), is located in the chromosomal region 1p36.22 on chromosome 1 and consists of 6 exons. ANGPTL7 belongs to the ANGPTL protein family, and is expressed in, among other sites, the stromal layer of the cornea. Elevated levels of the ANGPTL7 protein were reported in aqueous humor of glaucoma patients. A human genomic analysis has shown that missense and nonsense variants in ANGPTL7 are associated with lower intraocular pressure and a lower risk of glaucoma. These findings indicate interference with ANGPTL7 as a therapeutic strategy for glaucoma.

Accordingly, there is a need for agents that can selectively and efficiently inhibit expression of the ANGPTL7 gene such that subjects having an ANGPTL7-associated disorder, such as glaucoma, can be effectively treated.

BRIEF SUMMARY OF THE INVENTION

The present disclosure describes methods and iRNA compositions for modulating the expression of ANGPTL7. In certain embodiments, expression of ANGPTL7 is reduced or inhibited using an ANGPTL7-specific iRNA. Such inhibition can be useful in treating disorders related to ANGPTL7 expression, such as ocular disorders (*e.g.,* glaucoma or conditions associated with glaucoma).

Accordingly, described herein are compositions and methods that effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of ANGPTL7, such as in a cell or in a subject (*e.g.,* in a mammal, such as a human subject). Also described are compositions and methods for treating a disorder related to expression of ANGPTL7, such as glaucoma or conditions associated with glaucoma.

The iRNAs (*e.g.,* dsRNAs) included in the compositions featured herein include an RNA strand (the antisense strand) having a region, *e.g.,* a region that is 30 nucleotides or less, generally 19-24 nucleotides in length, that is substantially complementary to at least part of an mRNA transcript of ANGPTL7 (*e.g.,* a human ANGPTL7) (also referred to herein as a "ANGPTL7-specific iRNA"). In some embodiments, the ANGPTL7 mRNA transcript is a human ANGPTL7 mRNA transcript, *e.g.,* SEQ ID NO: 3 herein. In some embodiments, the ANGPTL7 mRNA transcript is a mouse ANGPTL7 mRNA transcript, *e.g.,* SEQ ID NO: 1 herein.

In some embodiments, the iRNA (*e.g.,* dsRNA) described herein comprises an antisense strand having a region that is substantially complementary to a region of a human ANGPTL7 mRNA. In some embodiments, the human ANGPTL7 mRNA has the sequence NM_021146.4 (SEQ ID NO: 3). The sequence of NM_021146.4 is herein incorporated by reference in its entirety. The reverse complement of SEQ ID NO: 3 is provided as SEQ ID NO: 4 herein.

In some embodiments, the ANGPTL7 mRNA transcript is a mouse ANGPTL7 mRNA transcript, *e.g.,* SEQ ID NO: 1 herein.

In some embodiments, the iRNA (*e.g.,* dsRNA) described herein comprises an antisense strand having a region that is substantially complementary to a region of a mouse ANGPTL7 mRNA. In some embodiments, the mouse ANGPTL7 mRNA has the sequence NM_001039554.3 (SEQ ID NO: 1). The sequence of NM_001039554.3 is herein incorporated by reference in its entirety. The reverse complement of SEQ ID NO: 1 is provided as SEQ ID NO: 2 herein.

In some embodiments, the iRNA that is substantially complementary to a region of a mouse ANGPTL7 mRNA cross-reacts with human ANGPTL7 mRNA. In some embodiments, the iRNA that is substantially complementary to a region of a mouse ANGPTL7 mRNA cross-reacts with monkey and rat ANGPTL7 mRNA.

In some aspects, the present disclosure provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ANGPTL7, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 or 4 such that the sense strand is complementary to the at least 15 contiguous nucleotides in the antisense strand.

In some aspects, the present disclosure provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ANGPTL7, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a

nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 or 4 such that the sense strand is complementary to the at least 15 contiguous nucleotides in the antisense strand.

In some aspects, the present disclosure provides a human cell or tissue comprising a reduced level of ANGPTL7 mRNA or a level of ANGPTL7 protein as compared to an otherwise similar untreated cell or tissue, wherein optionally the cell or tissue is not genetically engineered (*e.g.,* wherein the cell or tissue comprises one or more naturally arising mutations, *e.g.,* ANGPTL7), wherein optionally the level is reduced by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%. In some embodiments, the human cell or tissue is an optic nerve cell, a trabecular meshwork cell, a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel.

The present disclosure also provides, in some aspects, a cell containing the dsRNA agent described herein.

In another aspect, provided herein is a human ocular cell (*e.g.,* an optic nerve cell, a trabecular meshwork cell), a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel) comprising a reduced level of ANGPTL7 mRNA or a level of ANGPTL7 protein as compared to an otherwise similar untreated cell. In some embodiments, the level is reduced by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%.

In some aspects, the present disclosure also provides a pharmaceutical composition for inhibiting expression of a gene encoding ANGPTL7, comprising the dsRNA agent described herein.

The present disclosure also provides, in some aspects, a method of inhibiting expression of ANGPTL7 in a cell, the method comprising:

(a) contacting the cell with the dsRNA agent described herein, or the pharmaceutical composition described herein; and

(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of ANGPTL7, thereby inhibiting expression of the ANGPTL7 in the cell.

The present disclosure also provides, in some aspects, a method of inhibiting expression of ANGPTL7 in a cell, the method comprising:

(a) contacting the cell with the dsRNA agent described herein, or the pharmaceutical composition described herein; and

(b) maintaining the cell produced in step (a) for a time sufficient to reduce levels of ANGPTL7 mRNA, ANGPTL7 protein, or both of ANGPTL7 mRNA and protein, thereby inhibiting expression of ANGPTL7 in the cell.

The present disclosure also provides, in some aspects, a method of inhibiting expression of ANGPTL7 in an ocular cell or tissue, the method comprising:

(a) contacting the cell or tissue with a dsRNA agent that binds ANGPTL7; and

(b) maintaining the cell or tissue produced in step (a) for a time sufficient to reduce levels of ANGPTL7 mRNA, ANGPTL7 protein, or both of ANGPTL7 mRNA and protein, thereby inhibiting expression of ANGPTL7 in the cell or tissue.

The present disclosure also provides, in some aspects, a method of treating a subject diagnosed with ANGPTL7-associated disorder, *e.g.*, glaucoma, comprising administering to the subject a therapeutically effective amount of the dsRNA agent described herein or a pharmaceutical composition described herein, thereby treating the disorder.

In any of the aspects herein, *e.g.,* the compositions and methods above, any of the embodiments herein (*e.g.,* below) may apply.

In some embodiments, the coding strand of mouse ANGPTL7 has the sequence of SEQ ID NO: 1. In some embodiments, the non-coding strand of mouse ANGPTL7 has the sequence of SEQ ID NO: 2. In some embodiments, the coding strand of human ANGPTL7 has the sequence of SEQ ID NO: 3. In some embodiments, the non-coding strand of human ANGPTL7 has the sequence of SEQ ID NO: 4.

In some embodiments, the dsRNA agent comprises a sense strand and an antisense strand, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of any one of SEQ ID NOs: 1 or 3 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of any one of SEQ ID NOs: 2 or 4.

In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3. In some embodiments, the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 2 or SEQ ID NO: 4.

In some embodiments, the dsRNA agent comprises a sense strand and an antisense strand, wherein the antisense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 or SEQ ID NO: 4 such that the sense strand is complementary to the at least 17 contiguous nucleotides in the antisense strand. In some embodiments, the sense strand comprises a nucleotide sequence

comprising at least 17 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3.

In some embodiments, the dsRNA agent comprises a sense strand and an antisense strand, wherein the antisense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 or SEQ ID NO: 4 such that the sense strand is complementary to the at least 19 contiguous nucleotides in the antisense strand. In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3.

In some embodiments, the dsRNA agent comprises a sense strand and an antisense strand, wherein the antisense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 or SEQ ID NO: 4 such that the sense strand is complementary to the at least 21 contiguous nucleotides in the antisense strand. In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3.

In some embodiments, the portion of the sense strand is a portion within a sense strand in any one of Tables 2-7.

In some embodiments, the portion of the antisense strand is a portion within an antisense strand in any one of Tables 2-7.

In some embodiments, the dsRNA agent for inhibiting expression of ANGPTL7 comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In some embodiments, the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7. In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In some embodiments, the antisense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7. In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In some embodiments, the antisense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7. In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In some embodiments, the antisense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7. In some embodiments, the sense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In some embodiments, the sense strand of the dsRNA agent is at least 23 nucleotides in length, *e.g.,* 23-30 nucleotides in length.

In some embodiments, at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties. In some embodiments, the lipophilic moiety is conjugated to one or more internal positions on at least one strand of the dsRNA agent. In some embodiments, the lipophilic moiety is conjugated via a linker or carrier. In some embodiments, lipophilicity of the lipophilic moiety, measured by logKow, exceeds 0. In some embodiments,

In some embodiments, the hydrophobicity of the double-stranded RNAi agent, measured by the unbound fraction in a plasma protein binding assay of the double-stranded RNAi agent, exceeds 0.2. In some embodiments, the plasma protein binding assay is an electrophoretic mobility shift assay using human serum albumin protein.

In various embodiments of the aforementioned dsRNA agents, the dsRNA agent targets a hotspot region of an mRNA encoding ANGPTL7, such as a mouse mRNA encoding ANGPTL7 or a human mRNA encoding ANGPTL7. In one embodiment, the hotspot region comprises nucleotides 1562-1584, 546-568, 709-731, 862-884, and/or 232-256 of SEQ ID NO: 1. In another embodiment, the hotspot region comprises nucleotides 1993-2146, 1910-1932, 1726-1823, 1628-1685, 1591-1613, 1551-1573, 1420-1442, 1380-1402, 1243-1265, 1195-1217, 1096-1118, 940-962, and/or 299-321 of SEQ ID NO: 3. The dsRNA agent may be selected from the group consisting of AD-1094991, AD-1093984, AD-1094129, AD-1094262, AD-1093670, AD-1093672, AD-1565389, AD-1565368, AD-1565357, AD-1565345, AD-1565324, AD-1565303, AD-1565288, AD-1565212, AD-1565141, AD-1565126, AD-1565113, AD-1565091, AD-1565034, AD-1565015, AD-1565004, AD-1564969, AD-1094381, AD-1564428, AD-1564936, AD-1564823, AD-1564802, AD-1564666, AD-1564618, and AD-1563396.

In another aspect, the present invention provides a dsRNA agent that targets a hotspot region of an angiopoietin-like 7 (ANGPTL7) mRNA.

In some embodiments, the dsRNA agent comprises at least one modified nucleotide. In some embodiments, no more than five of the sense strand nucleotides and not more than five of the

nucleotides of the antisense strand are unmodified nucleotides. In some embodiments, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand are modified nucleotides.

In some embodiments, at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-O-allyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a phosphorothioate group, a nucleotide comprising a methylphosphonate group, a nucleotide comprising a 5'-phosphate, a nucleotide comprising a 5'-phosphate mimic, a glycol modified nucleotide, and a 2-O-(N-methylacetamide) modified nucleotide; and combinations thereof. In some embodiments, no more than five of the sense strand nucleotides and not more than five of the nucleotides of the antisense strand include modifications other than 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, unlocked nucleic acids (UNA) or glycerol nucleic acid (GNA).

In some embodiments, the dsRNA comprises a non-nucleotide spacer (wherein optionally the non-nucleotide spacer comprises a C3-C6 alkyl) between two of the contiguous nucleotides of the sense strand or between two of the contiguous nucleotides of the antisense strand.

In some embodiments, each strand is no more than 30 nucleotides in length. In some embodiments, the sense strand, the antisense strand, or each of the sense strand and antisense strand comprises a 3' overhang of at least 1 nucleotide. In some embodiments, the sense strand, the antisense strand, or each of the sense strand and antisense strand comprises a 3' overhang of at least 2 nucleotides. In some embodiments, the sense strand, the antisense strand, or each of the sense strand and antisense strand comprises a 3' overhang of 2 nucleotides.

In some embodiments, the double stranded region is 15-30 nucleotide pairs in length. In some embodiments, the double stranded region is 17-23 nucleotide pairs in length. In some embodiments, the double stranded region is 17-25 nucleotide pairs in length. In some embodiments, the double stranded region is 23-27 nucleotide pairs in length. In some embodiments, the double stranded region is 19-21 nucleotide pairs in length. In some embodiments, the double stranded region is 21-23 nucleotide pairs in length. In some embodiments, each strand has 19-30 nucleotides. In some embodiments, each strand has 19-23 nucleotides. In some embodiments, each strand has 21-23 nucleotides.

In some embodiments, the agent comprises at least one phosphorothioate or methylphosphonate internucleotide linkage. In some embodiments, the phosphorothioate or

methylphosphonate internucleotide linkage is at the 3'-terminus of one strand. In some embodiments, the strand is the antisense strand. In some embodiments, the strand is the sense strand.

In some embodiments, the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand. In some embodiments, the strand is the antisense strand. In some embodiments, the strand is the sense strand.

In some embodiments, each of the 5'- and 3'-terminus of one strand comprises a phosphorothioate or methylphosphonate internucleotide linkage. In some embodiments, the strand is the antisense strand.

In some embodiments, the base pair at the 1 position of the 5′-end of the antisense strand of the duplex is an AU base pair.

In some embodiments, the sense strand has a total of 21 nucleotides and the antisense strand has a total of 23 nucleotides.

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

In some embodiments, the internal positions include all positions except the terminal two positions from each end of the at least one strand. In some embodiments, the internal positions include all positions except the terminal three positions from each end of the at least one strand. In some embodiments, the internal positions exclude a cleavage site region of the sense strand. In some embodiments, the internal positions include all positions except positions 9-12, counting from the 5'-end of the sense strand. In some embodiments, the internal positions include all positions except positions 11-13, counting from the 3'-end of the sense strand. In some embodiments, the internal positions exclude a cleavage site region of the antisense strand. In some embodiments, the internal positions include all positions except positions 12-14, counting from the 5'-end of the antisense strand. In some embodiments, the internal positions include all positions except positions 11-13 on the sense strand, counting from the 3'-end, and positions 12-14 on the antisense strand, counting from the 5'-end.

In some embodiments, the one or more lipophilic moieties are conjugated to one or more of the internal positions selected from the group consisting of positions 4-8 and 13-18 on the sense strand, and positions 6-10 and 15-18 on the antisense strand, counting from the 5'end of each strand. In some embodiments, the one or more lipophilic moieties are conjugated to one or more of the internal positions selected from the group consisting of positions 5, 6, 7, 15, and 17 on the sense strand, and positions 15 and 17 on the antisense strand, counting from the 5'-end of each strand.

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

In some embodiments, the sense strand is 21 nucleotides in length, the antisense strand is 23 nucleotides in length, and the lipophilic moiety is conjugated to position 21, position 20, position 15,

position 1, position 7, position 6, or position 2 of the sense strand or position 16 of the antisense strand. In some embodiments, the lipophilic moiety is conjugated to position 21, position 20, position 15, position 1, or position 7 of the sense strand. In some embodiments, the lipophilic moiety is conjugated to position 21, position 20, or position 15 of the sense strand. In some embodiments, the lipophilic moiety is conjugated to position 20 or position 15 of the sense strand. In some embodiments, the lipophilic moiety is conjugated to position 16 of the antisense strand. In some embodiments, the lipophilic moiety is conjugated to position 6, counting from the 5'-end of the sense strand.

In some embodiments, the lipophilic moiety is an aliphatic, alicyclic, or polyalicyclic compound. In some embodiments, the lipophilic moiety is selected from the group consisting of lipid, cholesterol, retinoic acid, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-bis-O(hexadecyl)glycerol, geranyloxyhexyanol, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine. In some embodiments, the lipophilic moiety contains a saturated or unsaturated C4-C30 hydrocarbon chain, and an optional functional group selected from the group consisting of hydroxyl, amine, carboxylic acid, sulfonate, phosphate, thiol, azide, and alkyne. In some embodiments, the lipophilic moiety contains a saturated or unsaturated C6-C18 hydrocarbon chain. In some embodiments, the lipophilic moiety contains a saturated or unsaturated C16 hydrocarbon chain.

In some embodiments, the lipophilic moiety is conjugated via a carrier that replaces the one or more nucleotide(s) in the internal position(s) or the double stranded region. In some embodiments, the carrier is a cyclic group selected from the group consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuranyl, and decalinyl; or is an acyclic moiety based on a serinol backbone or a diethanolamine backbone.

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

In some embodiments, the lipophilic moiety is conjugated to a nucleobase, sugar moiety, or internucleosidic linkage.

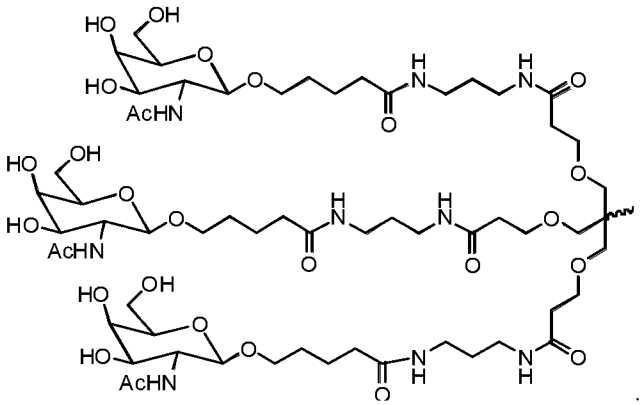
In some embodiments, the lipophilic moiety or targeting ligand is conjugated via a bio-cleavable linker selected from the group consisting of DNA, RNA, disulfide, amide, functionalized monosaccharides or oligosaccharides of galactosamine, glucosamine, glucose, galactose, mannose, and combinations thereof.

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

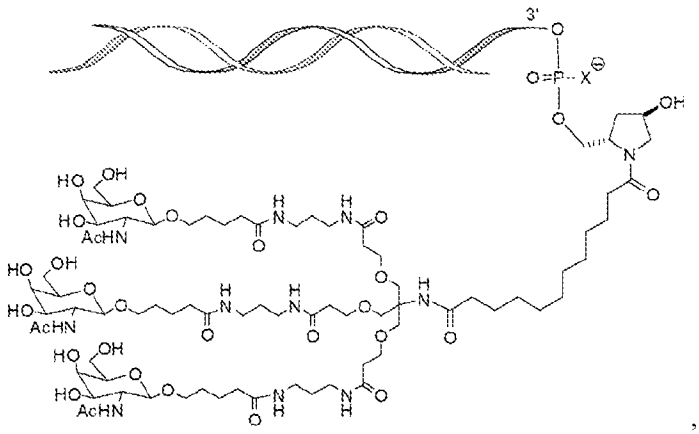
In some embodiments, the dsRNA agent further comprises a targeting ligand. In some embodiments, the targeting ligand targets an ocular tissue. In some embodiments, the ocular tissue is an optic nerve, a trabecular meshwork, a juxtacanalicular tissue, a ganglion (*e.g.*, including a retinal ganglion), episcleral veins or a Schlemm's canal (*e.g.*, including an endothelial cell).

In some embodiments, the ligand is conjugated to the sense strand. In some embodiments, the ligand is conjugated to the 3' end or the 5' end of the sense strand. In some embodiments, the ligand is conjugated to the 3' end of the sense strand.

In some embodiments, the ligand comprises N-acetylgalactosamine (GalNAc). In some embodiments, the targeting ligand comprises one or more GalNAc conjugates or one or more GalNAc derivatives. In some embodiments, the ligand is one or more GalNAc conjugates or one or more GalNAc derivatives are attached through a monovalent linker, or a bivalent, trivalent, or tetravalent branched linker. In some embodiments, the ligand is



In some embodiments, the dsRNA agent is conjugated to the ligand as shown in the following schematic



wherein X is O or S. In some embodiments, the X is O.

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

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

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

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

chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

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

In some embodiments, the dsRNA agent further comprises a phosphate or phosphate mimic at the 5'-end of the antisense strand. In some embodiments, the phosphate mimic is a 5'-vinyl phosphonate (VP).

In some embodiments, a cell described herein, *e.g.,* a human cell, was produced by a process comprising contacting a human cell with the dsRNA agent described herein.

In some embodiments, a pharmaceutical composition described herein comprises the dsRNA agent and a lipid formulation.

In some embodiments (*e.g.,* embodiments of the methods described herein), the cell is within a subject. In some embodiments, the subject is a human. In some embodiments, the level of ANGPTL7 mRNA is inhibited by at least 50%. In some embodiments, the level of ANGPTL7 protein is inhibited by at least 50%. In some embodiments, the expression of ANGPTL7 is inhibited by at least 50%. In some embodiments, inhibiting expression of ANGPTL7 decreases the ANGPTL7 protein level in a biological sample (*e.g.,* an optic nerve sample) from the subject by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95%. In some embodiments, inhibiting expression of ANGPTL7 gene decreases the ANGPTL7 mRNA level in a biological sample (*e.g.,* an optic nerve sample) from the subject by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95%.

In some embodiments, the subject has been diagnosed with an ANGPTL7-associated disorder. In some embodiments, the subject meets at least one diagnostic criterion for an ANGPTL7-associated disorder. In some embodiments, the ANGPTL7 associated disorder is glaucoma or conditions associated with glaucoma. In some embodiments, glaucoma is primary open-angle glaucoma.

In some embodiments, the ocular cell or tissue is an optic nerve cell, a trabecular meshwork cell, a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel.

In some embodiments, the treating comprises amelioration of at least one sign or symptom of the disorder. In some embodiments, the at least one sign or symptom includes a measure of one or more of intraocular pressure, vision loss, optic nerve damage, ocular inflammation, visual acuity, or presence, level, or activity of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein).

In some embodiments, a level of ANGPTL7 that is higher than a reference level is indicative that the subject has glaucoma or a glaucoma associated condition.

In some embodiments, treating comprises prevention of progression of the disorder. In some embodiments, the treating comprises one or more of (a) inhibiting or reducing intraocular pressure; (b) inhibiting or reducing the expression or activity of ANGPTL7; (c) increasing drainage of aqueous humor; (d) inhibiting or reducing optic nerve damage; or (e) inhibiting or reducing retinal ganglion cell death.

In some embodiments, the treating results in at least a 30% mean reduction from baseline of ANGPTL7 mRNA in the cell or tissue. In some embodiments, the treating results in at least a 60% mean reduction from baseline of ANGPTL7 mRNA in the cell or tissue. In some embodiments, the treating results in at least a 90% mean reduction from baseline of ANGPTL7 mRNA in the cell or tissue.

In some embodiments, after treatment the subject experiences at least an 8-week duration of knockdown following a single dose of dsRNA as assessed by ANGPTL7 protein in, for example, the optic nerve. In some embodiments, treating results in at least a 12-week duration of knockdown following a single dose of dsRNA as assessed by ANGPTL7 protein in, for example, the optic nerve. In some embodiments, treating results in at least a 16-week duration of knockdown following a single dose of dsRNA as assessed by ANGPTL7 protein in, for example, the optic nerve.

In some embodiments, the subject is human.

In some embodiments, the dsRNA agent is administered at a dose of about 0.01 mg/kg to about 50 mg/kg.

In some embodiments, the dsRNA agent is administered to the subject intraocularly. In some embodiments, the intraocular administration comprises intravitreal administration, *e.g.*, intravitreal injection; transscleral administration, *e.g.*, transscleral injection; subconjunctival administration, *e.g.*, subconjunctival injection; retrobulbar administration, *e.g.*, retrobulbar injection; intracameral administration, *e.g.*, intracameral injection, or subretinal administration, *e.g.*, subretinal injection.

In some embodiments, the dsRNA agent is administered to the subject intravenously. In some embodiments, the dsRNA agent is administered to the subject topically.

In some embodiments, a method described herein further comprises measuring a level of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein) in the subject. In some embodiments, measuring the level of ANGPTL7 in the subject comprises measuring the level of ANGPTL7 protein in a biological sample from the subject (*e.g.,* an optic nerve sample). In some

embodiments, a method described herein further comprises performing a blood test, an imaging test, a tonometry test or an optic nerve biopsy.

In some embodiments, a method described herein further measuring level of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein) in the subject is performed prior to treatment with the dsRNA agent or the pharmaceutical composition. In some embodiments, upon determination that a subject has a level of ANGPTL7 that is greater than a reference level, the dsRNA agent or the pharmaceutical composition is administered to the subject. In some embodiments, measuring level of ANGPTL7 in the subject is performed after treatment with the dsRNA agent or the pharmaceutical composition.

In some embodiments, a method described herein further comprises treating the subject with a therapy suitable for treatment or prevention of an ANGPTL7-associated disorder, *e.g.,* glaucoma, wherein the therapy comprises medication to reduce intraocular pressure, laser treatment, surgery or trabeculectomy. In some embodiments, a method described herein further comprises administering to the subject an additional agent suitable for treatment or prevention of an ANGPTL7-associated disorder. In some embodiments, the additional agent comprises a prostaglandin analog, a beta blocker, an alpha-adrenergic agonist, a carbonic anhydrase inhibitor, a ROCK inhibitor, a ROCK iRNA agent, an inhibitor of a Rho GTPase, an anti-Rho GTPase agent, or an anti-ANGPTL7 agent.

In some embodiments, the anti-Rho GTPase agent comprises an anti-Rho GTPase antibody or antigen-binding fragment thereof.

All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

The details of various embodiments of the disclosure are set forth in the description below. Other features, objects, and advantages of the disclosure will be apparent from the description and the drawings, and from the claims.

BRIEF SUMMARY OF THE DRAWINGS

The accompanying figures, which are incorporated in and constitute a part of this specification, illustrate several features of the present disclosure.

FIG.1 shows inhibition of dexamethasone-21-acetate (DEX-Ac)-induced ocular hypertension in ANGPTL7 knockout (KO) mice relative to wild-type (WT) mice.

FIG. 2 depicts effect of ANGPTL7 siRNA on intraocular pressure (IOP) of wild-type mice. Intravitreal injection with 15μg of ANGPTL7-siRNA significantly lowered IOP in two of six siRNAs tested (n=6-8/group) compared to the PBS-treated (n=6) and naïve (no injection, n=5) groups starting at week 2 and through the end of the study. siRNAs #3 and #5 represent AD-1094129 and AD-1094991, respectively. Error bars represent standard error of the mean (SEM).

FIG. 3 depicts effect of ANGPTL7 siRNA on ANGPTL7 expression in the limbal ring of wild-type mice *in vivo*. qPCR results from micro-dissected limbal ring showed the highest level of

knockdown (>50%) of ANGPTL7 mRNA with siRNAs #3 and #5 compared to PBS-treated or naïve (no injection) mice, which is consistent with the IOP lowering observed in mice injected with one of these two siRNAs (shown in FIG. 2). Error bars represent SEM.

FIG. 4 depicts effect of ANGPTL7 siRNA on reducing dexamethasone-21-acetate (DEX-Ac)-induced ocular hypertension in wild-type mice. Error bars represent SEM.

DETAILED DESCRIPTION

iRNA directs the sequence-specific degradation of mRNA through a process known as RNA interference (RNAi). Described herein are iRNAs and methods of using them for modulating (*e.g.*, inhibiting) the expression of ANGPTL7. Also provided are compositions and methods for treatment of disorders related to ANGPTL7 expression, such as glaucoma or conditions associated with glaucoma.

Human ANGPTL7, also known as angiopoietin like 7, Angptl7, angiopoietin-related protein 7, angiopoietin-like protein 7, AngX, CDT6, cornea-derived transcript 6 protein, angiopoietin-like factor (CDT6), or dJ647M16.1, is a protein encoded by the ANGPTL7 gene. ANGPTL7 is typically expressed in a variety of tissues including the optic nerve, trabecular meshwork, Schlemm's canal (*e.g.*, including endothelial cells), juxtacanalicular tissue, ciliary muscle, retina, astrocytes, pericytes, Müller cells, ganglion cells (*e.g.*, including retinal ganglion cells), endothelial cells, photoreceptor cells, retinal blood vessels (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel.

Without wishing to be bound by theory, ANGPTL7 may exacerbate the pathogenesis of glaucoma, *e.g.*, by increasing intraocular pressure. Elevated levels of the ANGPTL7 protein were reported in aqueous humor from patients with glaucoma compared to control patients. Glaucoma stimuli induced secretion of the ANGPTL7 protein in primary human trabecular meshwork cells and corneoscleral explants. Overexpression of ANGPTL7 in immortalized human travecular meshwork cells increased expression of collagen type I, a potential mechanism for development of glaucoma (Kuchtey *et al.*, 2008 *Invest. Ophthalmol. Vis Sci.* 49:3438). Overexpression of ANGPTL7 in primary human travecular meshwork cells altered expression of extracellular matrix proteins, including collagens type I, IV, and V, fibronectin, myocilin, versican, and MMP1. Silencing ANGPTL7 during the glucocorticoid insult affected the expression of other steroid-responsive proteins (Comes *et al.*, 2011 *Genes to Cells* 16:243-259). A human genomic analysis showed that missense and nonsense variants in ANGPTL7, including p.Gln175His and p.Arg220Cys, are associated with lower intraocular pressure and a lower risk of glaucoma (Tanigawa *et al.*, 2020 *PLOS Genet.* 16(5):e1008682). These findings indicate interference with ANGPTL7 as a therapeutic strategy for glaucoma.

The following description discloses how to make and use compositions containing iRNAs to inhibit the expression of ANGPTL7, as well as compositions and methods for treating disorders related to elevated expression of ANGPTL7.

In some aspects, pharmaceutical compositions containing ANGPTL7 iRNA and a pharmaceutically acceptable carrier, methods of using the compositions to inhibit expression of ANGPTL7, and methods of using the pharmaceutical compositions to treat disorders related to expression of ANGPTL7 (*e.g.,* glaucoma or conditions associated with glaucoma) are featured herein.

I. Definitions

For convenience, the meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below. If there is an apparent discrepancy between the usage of a term in other parts of this specification and its definition provided in this section, the definition in this section shall prevail.

The term "about" when referring to a number or a numerical range means that the number or numerical range referred to is an approximation within experimental variability (or within statistical experimental error), and thus the number or numerical range may vary from, for example, between 1% and 15% of the stated number or numerical range.

The term "at least" prior to a number or series of numbers is understood to include the number adjacent to the term "at least", and all subsequent numbers or integers that could logically be included, as clear from context. For example, the number of nucleotides in a nucleic acid molecule must be an integer. For example, "at least 17 nucleotides of a 20-nucleotide nucleic acid molecule" means that 17, 18, 19, or 20 nucleotides have the indicated property. When at least is present before a series of numbers or a range, it is understood that "at least" can modify each of the numbers in the series or range.

As used herein, "no more than" or "less than" is understood as the value adjacent to the phrase and logical lower values or integers, as logical from context, to zero. For example, a duplex with mismatches to a target site of "no more than 2 nucleotides" has a 2, 1, or 0 mismatches. When "no more than" is present before a series of numbers or a range, it is understood that "no more than" can modify each of the numbers in the series or range.

As used herein, "up to" as in "up to 10" is understood as up to and including 10, *i.e.*, 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

Ranges provided herein are understood to include all individual integer values and all subranges within the ranges.

The terms "activate," "enhance," "up-regulate the expression of," "increase the expression of," and the like, in so far as they refer to an ANGPTL7 gene, herein refer to the at least partial activation of the expression of an ANGPTL7 gene, as manifested by an increase in the amount of ANGPTL7 mRNA, which may be isolated from or detected in a first cell or group of cells in which an ANGPTL7 gene is transcribed and which has or have been treated such that the expression of an ANGPTL7 gene is increased, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has or have not been so treated (control cells).

In some embodiments, expression of an ANGPTL7 gene is activated by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% by administration of an iRNA as described herein. In some embodiments, an ANGPTL7 gene is activated by at least about 60%, 70%, or 80% by administration of an iRNA featured in the disclosure. In some embodiments, expression of an ANGPTL7 gene is activated by at least about 85%, 90%, or 95% or more by administration of an iRNA as described herein. In some embodiments, the ANGPTL7 gene expression is increased by at least 1-fold, at least 2-fold, at least 5-fold, at least 10-fold, at least 50-fold, at least 100-fold, at least 500-fold, at least 1000-fold or more in cells treated with an iRNA as described herein compared to the expression in an untreated cell. Activation of expression by small dsRNAs is described, for example, in Li *et al.*, 2006 *Proc. Natl. Acad. Sci. U.S.A.* 103:17337-42, and in US2007/0111963 and US2005/226848, each of which is incorporated herein by reference.

The terms "silence," "inhibit expression of," "down-regulate expression of," "suppress expression of," and the like, in so far as they refer to ANGPTL7, herein refer to the at least partial suppression of the expression of ANGPTL7, as assessed, *e.g.,* based on ANGPTL7 mRNA expression, ANGPTL7 protein expression, or another parameter functionally linked to ANGPTL7 expression. For example, inhibition of ANGPTL7 expression may be manifested by a reduction of the amount of ANGPTL7 mRNA which may be isolated from or detected in a first cell or group of cells in which ANGPTL7 is transcribed and which has or have been treated such that the expression of ANGPTL7 is inhibited, as compared to a control. The control may be a second cell or group of cells substantially identical to the first cell or group of cells, except that the second cell or group of cells have not been so treated (control cells). The degree of inhibition is usually expressed as a percentage of a control level, *e.g.,*

$$\frac{(\text{mRNA in control cells}) - (\text{mRNA in treated cells})}{(\text{mRNA in control cells})} \bullet 100\%$$

Alternatively, the degree of inhibition may be given in terms of a reduction of a parameter that is functionally linked to ANGPTL7 expression, *e.g.,* the amount of protein encoded by an ANGPTL7 gene. The reduction of a parameter functionally linked to ANGPTL7 expression may similarly be expressed as a percentage of a control level. In principle, ANGPTL7 silencing may be determined in any cell expressing ANGPTL7, either constitutively or by genomic engineering, and by any appropriate assay.

For example, in certain instances, expression of ANGPTL7 is suppressed by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% by administration of an iRNA disclosed herein. In some embodiments, ANGPTL7 is suppressed by at least about 60%, 65%, 70%, 75%, or 80% by administration of an iRNA disclosed herein. In some embodiments, ANGPTL7 is suppressed by at least about 85%, 90%, 95%, 98%, 99%, or more by administration of an iRNA as described herein.

The term "antisense strand" or "guide strand" refers to the strand of an iRNA, *e.g.,* a dsRNA, which includes a region that is substantially complementary to a target sequence.

As used herein, the term "region of complementarity" refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches may be in the internal or terminal regions of the molecule. In some embodiments, the region of complementarity comprises 0, 1, or 2 mismatches.

The term "sense strand" or "passenger strand" as used herein, refers to the strand of an iRNA that includes a region that is substantially complementary to a region of the antisense strand as that term is defined herein.

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

As used herein, and unless otherwise indicated, the term "complementary," when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Such conditions can, for example, be stringent conditions, where stringent conditions may include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50°C or 70°C for 12-16 hours followed by washing. Other conditions, such as physiologically relevant conditions as may be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

Complementary sequences within an iRNA, *e.g.,* within a dsRNA as described herein, include base-pairing of the oligonucleotide or polynucleotide comprising a first nucleotide sequence to an oligonucleotide or polynucleotide comprising a second nucleotide sequence over the entire length of one or both nucleotide sequences. Such sequences can be referred to as "fully complementary" with respect to each other herein. However, where a first sequence is referred to as "substantially complementary" with respect to a second sequence herein, the two sequences can be fully complementary, or they may form one or more, but generally not more than 5, 4, 3 or 2 mismatched base pairs upon hybridization for a duplex up to 30 base pairs, while retaining the ability to hybridize under the conditions most relevant to their ultimate application, *e.g.,* inhibition of gene expression via a RISC pathway. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide

21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, may yet be referred to as "fully complementary" for the purposes described herein.

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

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

As used herein, a polynucleotide that is "substantially complementary to at least part of" a messenger RNA (mRNA) refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest (*e.g.,* an mRNA encoding an ANGPTL7 protein). For example, a polynucleotide is complementary to at least a part of an ANGPTL7 mRNA if the sequence is substantially complementary to a non-interrupted portion of an mRNA encoding ANGPTL7. The term "complementarity" refers to the capacity for pairing between nucleobases of a first nucleic acid and a second nucleic acid.

As used herein, the term "region of complementarity" refers to the region of one nucleotide sequence agent that is substantially complementary to another sequence, *e.g.,* the region of a sense sequence and corresponding antisense sequence of a dsRNA, or the antisense strand of an iRNA and a target sequence, *e.g.,* an ANGPTL7 nucleotide sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches can be in the internal or terminal regions of the antisense strand of the iRNA. Generally, the most tolerated mismatches are in the terminal regions, *e.g.,* within 5, 4, 3, or 2 nucleotides of the 5'- or 3'-terminus of the iRNA agent.

"Contacting," as used herein, includes directly contacting a cell, as well as indirectly contacting a cell. For example, a cell within a subject may be contacted when a composition comprising an iRNA is administered (*e.g.,* intraocularly, topically, or intravenously) to the subject.

"Introducing into a cell," when referring to an iRNA, means facilitating or effecting uptake or absorption into the cell. Absorption or uptake of an iRNA can occur through unaided diffusive or active cellular processes, or by auxiliary agents or devices. The meaning of this term is not limited to cells *in vitro*; an iRNA may also be "introduced into a cell," wherein the cell is part of a living organism. In such an instance, introduction into the cell will include the delivery to the organism. For example, for *in vivo* delivery, iRNA can be injected into a tissue site or administered systemically. *In vivo* delivery can also be by a β-glucan delivery system, such as those described in U.S. Patent Nos. 5,032,401 and 5,607,677, and U.S. Publication No. 2005/0281781, which are hereby

incorporated by reference in their entirety. *In vitro* introduction into a cell includes methods known in the art such as electroporation and lipofection. Further approaches are described herein below or known in the art. As used herein, a "disorder related to ANGPTL7 expression," a "disease related to ANGPTL7 expression," a "pathological process related to ANGPTL7 expression," "an ANGPTL7-associated disorder," "an ANGPTL7-associated disease," or the like includes any condition, disorder, or disease in which ANGPTL7 expression is altered (*e.g.,* decreased or increased relative to a reference level, *e.g.*, a level characteristic of a non-diseased subject). In some embodiments, ANGPTL7 expression is decreased. In some embodiments, ANGPTL7 expression is increased. In some embodiments, the decrease or increase in ANGPTL7 expression is detectable in a tissue sample from the subject (*e.g.,* in an optic nerve sample). The decrease or increase may be assessed relative the level observed in the same individual prior to the development of the disorder or relative to other individual(s) who do not have the disorder. The decrease or increase may be limited to a particular organ, tissue, or region of the body (*e.g.,* the eye). ANGPTL7-associated disorders include, but are not limited to, glaucoma or conditions associated with glaucoma.

The term "condition(s) associated with glaucoma," as used herein, means any disease or condition that is associated with an increase in intraocular pressure. Non-limiting examples of conditions associated with glaucoma that are treatable using methods provided herein include ocular inflammation, systemic inflammation, anterior uveitis, acute retinal necrosis, Sturge-Weber syndrome, Axenfeld-Rieger syndrome, Marfan syndrome, homocystinuria, Weill-Marchesani syndrome, and autoimmune diseases, such as juvenile rheumatoid arthritis and Marie-Strumpell ankylosing spondylitis.

The term "double-stranded RNA," "dsRNA," or "siRNA" as used herein, refers to an iRNA that includes an RNA molecule or complex of molecules having a hybridized duplex region that comprises two anti-parallel and substantially complementary nucleic acid strands, which will be referred to as having "sense" and "antisense" orientations with respect to a target RNA. The duplex region can be of any length that permits specific degradation of a desired target RNA, *e.g.,* through a RISC pathway, but will typically range from 9 to 36 base pairs in length, *e.g.,* 15-30 base pairs in length. Considering a duplex between 9 and 36 base pairs, the duplex can be any length in this range, for example, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 and any sub-range therein between, including, but not limited to 15-30 base pairs, 15-26 base pairs, 15-23 base pairs, 15-22 base pairs, 15-21 base pairs, 15-20 base pairs, 15-19 base pairs, 15-18 base pairs, 15-17 base pairs, 18-30 base pairs, 18-26 base pairs, 18-23 base pairs, 18-22 base pairs, 18-21 base pairs, 18-20 base pairs, 19-30 base pairs, 19-26 base pairs, 19-23 base pairs, 19-22 base pairs, 19-21 base pairs, 19-20 base pairs, 20-30 base pairs, 20-26 base pairs, 20-25 base pairs, 20-24 base pairs, 20-23 base pairs, 20-22 base pairs, 20-21 base pairs, 21-30 base pairs, 21-26 base pairs, 21-25 base pairs, 21-24 base pairs, 21-23 base pairs, or 21-22 base pairs. dsRNAs generated in the cell by processing with Dicer and similar enzymes are generally in the range of 19-22

base pairs in length. One strand of the duplex region of a dsDNA comprises a sequence that is substantially complementary to a region of a target RNA. The two strands forming the duplex structure can be from a single RNA molecule having at least one self-complementary region, or can be formed from two or more separate RNA molecules. Where the duplex region is formed from two strands of a single molecule, the molecule can have a duplex region separated by a single stranded chain of nucleotides (herein referred to as a "hairpin loop") between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure. The hairpin loop can comprise at least one unpaired nucleotide; in some embodiments the hairpin loop can comprise at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 20, at least 23 or more unpaired nucleotides. Where the two substantially complementary strands of a dsRNA are comprised by separate RNA molecules, those molecules need not, but can be covalently connected. In some embodiments, the two strands are connected covalently by means other than a hairpin loop, and the connecting structure is a linker.

In some embodiments, the iRNA agent may be a "single-stranded siRNA" that is introduced into a cell or organism to inhibit a target mRNA. In some embodiments, single-stranded RNAi agents can bind to the RISC endonuclease Argonaute 2, which then cleaves the target mRNA. The single-stranded siRNAs are generally 15-30 nucleotides and are optionally chemically modified. The design and testing of single-stranded siRNAs are described in U.S. Patent No. 8,101,348 and in Lima *et al.*, 2012 *Cell* 150:883-894, the entire contents of each of which are hereby incorporated herein by reference. Any of the antisense nucleotide sequences described herein (*e.g.,* sequences provided in Tables 2-7) may be used as a single-stranded siRNA as described herein and optionally as chemically modified, *e.g.,* as described herein, *e.g.,* by the methods described in Lima *et al.*, 2012 *Cell* 150:883-894.

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

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

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

As used herein, the term “iRNA,” “RNAi”, “iRNA agent,” or “RNAi agent” or “RNAi molecule” refers to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript, *e.g.,* via an RNA-induced silencing complex (RISC) pathway. In some embodiments, an iRNA as described herein effects inhibition of ANGPTL7 expression, *e.g.,* in a cell or mammal. Inhibition of ANGPTL7 expression may be assessed based on a reduction in the level of ANGPTL7 mRNA or a reduction in the level of the ANGPTL7 protein.

The term "linker" or “linking group” means an organic moiety that connects two parts of a compound, *e.g.,* covalently attaches two parts of a compound.

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

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

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

In some embodiments, the plasma protein binding assay determined is an electrophoretic mobility shift assay (EMSA) using human serum albumin protein. An exemplary protocol of this binding assay is illustrated in detail in, *e.g.,* PCT/US2019/031170. The hydrophobicity of the double-stranded RNAi agent, measured by fraction of unbound siRNA in the binding assay, exceeds 0.15, exceeds 0.2, exceeds 0.25, exceeds 0.3, exceeds 0.35, exceeds 0.4, exceeds 0.45, or exceeds 0.5 for an enhanced *in vivo* delivery of siRNA.

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

The term "lipid nanoparticle" or "LNP" is a vesicle comprising a lipid layer encapsulating a pharmaceutically active molecule, such as a nucleic acid molecule, *e.g.,* a RNAi agent or a plasmid from which a RNAi agent is transcribed. LNPs are described in, for example, U.S. Patent Nos. 6,858,225, 6,815,432, 8,158,601, and 8,058,069, the entire contents of which are hereby incorporated herein by reference.

As used herein, the term "modulate the expression of," refers to an at least partial "inhibition" of a gene (*e.g.,* ANGPTL7 gene) expression in a cell treated with an iRNA composition as described herein compared to the expression of the corresponding gene in a control cell. A control cell includes an untreated cell, or a cell treated with a non-targeting control iRNA.

The skilled artisan will recognize that the term "RNA molecule" or "ribonucleic acid molecule" encompasses not only RNA molecules as expressed or found in nature, but also analogs and derivatives of RNA comprising one or more ribonucleotide/ribonucleoside analogs or derivatives as described herein or as known in the art. Strictly speaking, a "ribonucleoside" includes a nucleoside base and a ribose sugar, and a "ribonucleotide" is a ribonucleoside with one, two or three phosphate moieties or analogs thereof (*e.g.,* phosphorothioate). However, the terms "ribonucleoside" and "ribonucleotide" can be considered to be equivalent as used herein. The RNA can be modified in the nucleobase structure, in the ribose structure, or in the ribose-phosphate backbone structure, *e.g.,* as described herein below. However, the molecules comprising ribonucleoside analogs or derivatives must retain the ability to form a duplex. As non-limiting examples, an RNA molecule can also include at least one modified ribonucleoside including but not limited to a 2'-O-methyl modified nucleoside, a nucleoside comprising a 5' phosphorothioate group, a terminal nucleoside linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group, a locked nucleoside, an abasic nucleoside, an acyclic nucleoside, a glycol nucleotide, a 2'-deoxy-2'-fluoro modified nucleoside, a 2'-amino-

modified nucleoside, 2'-alkyl-modified nucleoside, morpholino nucleoside, a phosphoramidate or a non-natural base comprising nucleoside, or any combination thereof. Alternatively, or in combination, an RNA molecule can comprise at least two modified ribonucleosides, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20 or more, up to the entire length of the dsRNA molecule. The modifications need not be the same for each of such a plurality of modified ribonucleosides in an RNA molecule. In some embodiments, modified RNAs contemplated for use in methods and compositions described herein are peptide nucleic acids (PNAs) that have the ability to form the required duplex structure and that permit or mediate the specific degradation of a target RNA, *e.g.,* via a RISC pathway. For clarity, it is understood that the term "iRNA" does not encompass a naturally occurring double stranded DNA molecule or a 100% deoxynucleoside-containing DNA molecule.

In some aspects, a modified ribonucleoside includes a deoxyribonucleoside. In such an instance, an iRNA agent can comprise one or more deoxynucleosides, including, for example, a deoxynucleoside overhang(s), or one or more deoxynucleosides within the double stranded portion of a dsRNA. In certain embodiments, the RNA molecule comprises a percentage of deoxyribonucleosides of at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95% or higher (but not 100%) deoxyribonucleosides, *e.g.,* in one or both strands.

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

In some embodiments, the antisense strand of a dsRNA has a 1-10 nucleotide overhang at the 3' end and/or the 5' end. In some embodiments, the sense strand of a dsRNA has a 1-10 nucleotide overhang at the 3' end and/or the 5' end. In some embodiments, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

In certain embodiments, the antisense strand of a dsRNA has a 1-15 nucleotide overhang at the 3'-end. In other embodiments, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

As used herein, a "pharmaceutical composition" comprises a pharmacologically effective amount of a therapeutic agent (*e.g.,* an iRNA) and a pharmaceutically acceptable carrier. As used herein, "pharmacologically effective amount," "therapeutically effective amount" or simply "effective amount" refers to that amount of an agent (*e.g.,* iRNA) effective to produce the intended

pharmacological, therapeutic or preventive result. For example, in a method of treating a disorder related to ANGPTL7 expression (*e.g.,* glaucoma or conditions associated with glaucoma), an effective amount includes an amount effective to reduce one or more symptoms associated with the disorder, *e.g.,* an amount effective to (a) inhibit or reduce intraocular pressure; (b) inhibit or reduce the expression or activity of ANGPTL7; (c) increase drainage of aqueous humor; (d) inhibit or reduce optic nerve damage; or (e) inhibit or reduce retinal ganglion cell death or an amount effective to reduce the risk of developing conditions associated with the disorder. For example, if a given clinical treatment is considered effective when there is at least a 10% reduction in a measurable parameter associated with a disease or disorder, a therapeutically effective amount of a drug for the treatment of that disease or disorder is the amount necessary to obtain at least a 10% reduction in that parameter. For example, a therapeutically effective amount of an iRNA targeting ANGPTL7 can reduce a level of ANGPTL7 mRNA or a level of ANGPTL7 protein by any measurable amount, *e.g.,* by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%.

The term “pharmaceutically acceptable carrier” refers to a carrier for administration of a therapeutic agent. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The term specifically excludes cell culture medium. For drugs administered orally, pharmaceutically acceptable carriers include, but are not limited to pharmaceutically acceptable excipients such as inert diluents, disintegrating agents, binding agents, lubricating agents, sweetening agents, flavoring agents, coloring agents and preservatives. Suitable inert diluents include sodium and calcium carbonate, sodium and calcium phosphate, and lactose, while corn starch and alginic acid are suitable disintegrating agents. Binding agents may include starch and gelatin, while the lubricating agent, if present, will generally be magnesium stearate, stearic acid or talc. If desired, the tablets may be coated with a material such as glyceryl monostearate or glyceryl distearate, to delay absorption in the gastrointestinal tract. Agents included in drug formulations are described further herein below.

As used herein, the term "SNALP" refers to a stable nucleic acid-lipid particle. A SNALP represents a vesicle of lipids coating a reduced aqueous interior comprising a nucleic acid such as an iRNA or a plasmid from which an iRNA is transcribed. SNALPs are described, *e.g.,* in U.S. Patent Application Publication Nos. 2006/0240093, 2007/0135372, and in International Application No. WO 2009/082817. These applications are incorporated herein by reference in their entirety. In some embodiments, the SNALP is a SPLP. As used herein, the term “SPLP” refers to a nucleic acid-lipid particle comprising plasmid DNA encapsulated within a lipid vesicle.

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

As used herein, a "subject" to be treated according to the methods described herein, includes a human or non-human animal, *e.g.,* a mammal. The mammal may be, for example, a rodent (*e.g.,* a rat or mouse) or a primate (*e.g.,* a monkey). In some embodiments, the subject is a human.

A "subject in need thereof" includes a subject having, suspected of having, or at risk of developing a disorder related to ANGPTL7 expression, *e.g.*, overexpression (*e.g.,* glaucoma or conditions associated with glaucoma). In some embodiments, the subject has, or is suspected of having, a disorder related to ANGPTL7 expression or overexpression. In some embodiments, the subject is at risk of developing a disorder related to ANGPTL7 expression or overexpression.

As used herein, "target sequence" refers to a contiguous portion of the nucleotide sequence of an mRNA molecule formed during the transcription of a gene, *e.g.,* ANGPTL7, including mRNA that is a product of RNA processing of a primary transcription product. The target portion of the sequence will be at least long enough to serve as a substrate for iRNA-directed cleavage at or near that portion. For example, the target sequence will generally be from 9-36 nucleotides in length, *e.g.,* 15-30 nucleotides in length, including all sub-ranges therebetween. As non-limiting examples, the target sequence can be from 15-30 nucleotides, 15-26 nucleotides, 15-23 nucleotides, 15-22 nucleotides, 15-21 nucleotides, 15-20 nucleotides, 15-19 nucleotides, 15-18 nucleotides, 15-17 nucleotides, 18-30 nucleotides, 18-26 nucleotides, 18-23 nucleotides, 18-22 nucleotides, 18-21 nucleotides, 18-20 nucleotides, 19-30 nucleotides, 19-26 nucleotides, 19-23 nucleotides, 19-22 nucleotides, 19-21 nucleotides, 19-20 nucleotides, 20-30 nucleotides, 20-26 nucleotides, 20-25 nucleotides, 20-24 nucleotides, 20-23 nucleotides, 20-22 nucleotides, 20-21 nucleotides, 21-30 nucleotides, 21-26 nucleotides, 21-25 nucleotides, 21-24 nucleotides, 21-23 nucleotides, or 21-22 nucleotides.

As used herein, the phrases "therapeutically effective amount" and "prophylactically effective amount" and the like refer to an amount that provides a therapeutic benefit in the treatment, prevention, or management of any disorder or pathological process related to ANGPTL7 expression (*e.g.,* glaucoma or conditions associated with glaucoma). The specific amount that is therapeutically effective may vary depending on factors known in the art, such as, for example, the type of disorder or pathological process, the patient's history and age, the stage of the disorder or pathological process, and the administration of other therapies.

In the context of the present disclosure, the terms "treat," "treatment," and the like mean to prevent, delay, relieve or alleviate at least one symptom associated with a disorder related to ANGPTL7 expression, or to slow or reverse the progression or anticipated progression of such a disorder. For example, the methods featured herein, when employed to treat glaucoma or conditions associated with glaucoma, may serve to reduce or prevent one or more symptoms of glaucoma or conditions associated with glaucoma, as described herein, or to reduce the risk or severity of associated conditions. Thus, unless the context clearly indicates otherwise, the terms "treat," "treatment," and the like are intended to encompass prophylaxis, *e.g.,* prevention of disorders and/or

symptoms of disorders related to ANGPTL7 expression. Treatment can also mean prolonging survival as compared to expected survival in the absence of treatment.

By "lower" in the context of a disease marker or symptom is meant any decrease, *e.g.,* a statistically or clinically significant decrease in such level. The decrease can be, for example, at least 10%, at least 20%, at least 30%, at least 40%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%. The decrease can be down to a level accepted as within the range of normal for an individual without such disorder.

As used herein, "ANGPTL7" refers to "angiopoietin like 7," the corresponding mRNA ("ANGPTL7 mRNA"), or the corresponding protein ("ANGPTL7 protein"). The sequence of a human ANGPTL7 mRNA transcript can be found at SEQ ID NO: 3. The sequence of a mouse ANGPTL7 mRNA transcript can be found at SEQ ID NO: 1.

II. iRNA Agents

Described herein are iRNA agents that inhibit the expression of ANGPTL7.

In some embodiments, the iRNA agent activates the expression of ANGPTL7 in a cell or mammal.

In some embodiments, the iRNA agent includes double-stranded ribonucleic acid (dsRNA) molecules for inhibiting the expression of ANGPTL7 in a cell or in a subject (*e.g.,* in a mammal, *e.g.,* in a human), where the dsRNA includes an antisense strand having a region of complementarity which is complementary to at least a part of an mRNA formed in the expression of ANGPTL7, and where the region of complementarity is 30 nucleotides or less in length, generally 19-24 nucleotides in length, and where the dsRNA, upon contact with a cell expressing ANGPTL7, inhibits the expression of ANGPTL7, *e.g.,* by at least 10%, 20%, 30%, 40%, or 50%.

The modulation (*e.g.,* inhibition) of expression of ANGPTL7 can be assayed by, for example, a PCR or branched DNA (bDNA)-based method, or by a protein-based method, such as by Western blot. Expression of ANGPTL7 in cell culture, such as in COS cells, ARPE-19 cells, hTERT RPE-1 cells, RPE-J cells, HeLa cells, primary hepatocytes, HepG2 cells, primary cultured cells or in a biological sample from a subject can be assayed by measuring ANGPTL7 mRNA levels, such as by bDNA or TaqMan assay, or by measuring protein levels, such as by immunofluorescence analysis, using, for example, Western Blotting or flow cytometric techniques.

A dsRNA typically includes two RNA strands that are sufficiently complementary to hybridize to form a duplex structure under conditions in which the dsRNA will be used. One strand of a dsRNA (the antisense strand) typically includes a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence, derived from the sequence of an mRNA formed during the expression of ANGPTL7. The other strand (the sense strand) typically includes a region that is complementary to the antisense strand, such that the two strands hybridize and form a duplex structure when combined under suitable conditions. Generally, the duplex structure is between 15 and 30 inclusive, more generally between 18 and 25 inclusive, yet more generally

between 19 and 24 inclusive, and most generally between 19 and 21 base pairs in length, inclusive. Similarly, the region of complementarity to the target sequence is between 15 and 30 inclusive, more generally between 18 and 25 inclusive, yet more generally between 19 and 24 inclusive, and most generally between 19 and 21 nucleotides in length, inclusive.

In some embodiments, the dsRNA is between 15 and 20 nucleotides in length, inclusive, and in other embodiments, the dsRNA is between 25 and 30 nucleotides in length, inclusive. As the ordinarily skilled person will recognize, the targeted region of an RNA targeted for cleavage will most often be part of a larger RNA molecule, often an mRNA molecule. Where relevant, a "part" of an mRNA target is a contiguous sequence of an mRNA target of sufficient length to be a substrate for RNAi-directed cleavage (*i.e.*, cleavage through a RISC pathway). dsRNAs having duplexes as short as 9 base pairs can, under some circumstances, mediate RNAi-directed RNA cleavage. Most often a target will be at least 15 nucleotides in length, *e.g.,* 15-30 nucleotides in length.

One of skill in the art will also recognize that the duplex region is a primary functional portion of a dsRNA, *e.g.,* a duplex region of 9 to 36, *e.g.,* 15-30 base pairs. Thus, in some embodiments, to the extent that it becomes processed to a functional duplex of *e.g.,* 15-30 base pairs that targets a desired RNA for cleavage, an RNA molecule or complex of RNA molecules having a duplex region greater than 30 base pairs is a dsRNA. Thus, an ordinarily skilled artisan will recognize that in some embodiments, then, a miRNA is a dsRNA. In some embodiments, a dsRNA is not a naturally occurring miRNA. In some embodiments, an iRNA agent useful to target ANGPTL7 expression is not generated in the target cell by cleavage of a larger dsRNA.

A dsRNA as described herein may further include one or more single-stranded nucleotide overhangs. The dsRNA can be synthesized by standard methods known in the art as further discussed below, *e.g.,* by use of an automated DNA synthesizer, such as are commercially available from, for example, Biosearch, Applied Biosystems, Inc.

In some embodiments, ANGPTL7 is a human ANGPTL7.

In specific embodiments, the dsRNA comprises a sense strand that comprises or consists of a sense sequence selected from the sense sequences provided in Tables 2-7 and an antisense strand that comprises or consists of an antisense sequence selected from the antisense sequences provided in Tables 2-7.

In some aspects, a dsRNA will include at least sense and antisense nucleotide sequences, whereby the sense strand is selected from the sequences provided in Tables 2-7 and the corresponding antisense strand is selected from the sequences provided in Tables 2-7.

In these aspects, one of the two sequences is complementary to the other of the two sequences, with one of the sequences being substantially complementary to a sequence of an mRNA generated by the expression of ANGPTL7. As such, a dsRNA will include two oligonucleotides, where one oligonucleotide is described as the sense strand, and the second oligonucleotide is described as the corresponding antisense strand. As described elsewhere herein and as known in the

art, the complementary sequences of a dsRNA can also be contained as self-complementary regions of a single nucleic acid molecule, as opposed to being on separate oligonucleotides.

The skilled person is well aware that dsRNAs having a duplex structure of between 20 and 23, but specifically 21, base pairs have been hailed as particularly effective in inducing RNA interference (Elbashir *et al.*, 2001 *EMBO* 20:6877-6888). However, others have found that shorter or longer RNA duplex structures can be effective as well.

In the embodiments described above, by virtue of the nature of the oligonucleotide sequences provided in Tables 2-7, dsRNAs described herein can include at least one strand of a length of minimally 19 nucleotides. It can be reasonably expected that shorter duplexes having one of the sequences of Tables 2-7 minus only a few nucleotides on one or both ends will be similarly effective as compared to the dsRNAs described above.

In some embodiments, the dsRNA has a partial sequence of at least 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from one of the sequences of Tables 2-7.

In some embodiments, the dsRNA has an antisense sequence that comprises at least 15, 16, 17, 18, or 19 contiguous nucleotides of an antisense sequence provided in Tables 2-7 and a sense sequence that comprises at least 15, 16, 17, 18, or 19 contiguous nucleotides of a corresponding sense sequence provided in Tables 2-7.

In some embodiments, the dsRNA comprises an antisense sequence that comprises at least 15, 16, 17, 18, 19, 20, 21, 22, or 23 contiguous nucleotides of an antisense sequence provided in Tables 2-7 and a sense sequence that comprises at least 15, 16, 17, 18, 19, 20, or 21 contiguous nucleotides of a corresponding sense sequence provided in Tables 2-7.

In some such embodiments, the dsRNA, although it comprises only a portion of the sequences provided in Tables 2-7 is equally effective in inhibiting a level of ANGPTL7 expression as is a dsRNA that comprises the full-length sequences provided in Tables 2-7. In some embodiments, the dsRNA differs in its inhibition of a level of expression of ANGPTL7 by not more than 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 % inhibition compared with a dsRNA comprising the full sequence disclosed herein.

The iRNAs of Tables 2, 3, 4, and 5 were designed based on mouse ANGPTL7 sequence. The iRNAs of Tables 6-7 were designed based on human ANGPTL7 sequence. Without wishing to be bound by theory, ANGPTL7 sequence is conserved sufficiently between species such that certain iRNAs designed based on a mouse sequence have activity against ANGPTL7 from primates and other species, including, for example, human, monkey, and rat, and certain iRNAs designed based on a human sequence have activity against ANGPTL7 from primates and other species. In some embodiments, the iRNAs of Tables 2-5 have cross-reactivity with human ANGPTL7. In some embodiments, the iRNAs of Tables 6 and 7 have cross-reactivity with ANGPTL7 of monkey, mouse, rat, and other species.

Consequently, in some embodiments, an iRNA of Tables 2-7 decreases ANGPTL7 protein or ANGPTL7 mRNA levels in a cell. In some embodiments, the cell is a rodent cell (*e.g.*, a rat cell), or a primate cell (*e.g.*, a monkey cell or a human cell). In some embodiments, ANGPTL7 protein or ANGPTL7 mRNA levels are reduced by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95%. In some embodiments, the iRNA of Tables 2-7 that inhibits ANGPTL7 in a human cell has less than 5, 4, 3, 2, or 1 mismatches to the corresponding portion of human ANGPTL7. In some embodiments, the iRNA of Tables 2-7 that inhibits ANGPTL7 in a human cell has no mismatches to the corresponding portion of human ANGPTL7.

iRNAs designed based on rodent sequences can have utility, *e.g.*, for inhibiting ANGPTL7 in human cells, *e.g.*, for therapeutic purposes, or for inhibiting ANGPTL7 in rodent cells, *e.g.*, for research characterizing ANGPTL7 in a rodent model.

In some embodiments, an iRNA described herein comprises an antisense strand comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 4. In some embodiments, an iRNA described herein comprises a sense strand comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 3. A human ANGPTL7 mRNA may have the sequence of SEQ ID NO: 3 provided herein.

In some embodiments, an iRNA described herein comprises an antisense strand comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2. In some embodiments, an iRNA described herein comprises a sense strand comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1. A mouse ANGPTL7 mRNA may have the sequence of SEQ ID NO: 1 provided herein.

In some embodiments, an iRNA described herein comprises an antisense strand comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 6. In some embodiments, an iRNA described herein comprises a sense strand comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 5. A cynomolgus monkey ANGPTL7 mRNA may have the sequence of SEQ ID NO: 5 provided herein.

In some embodiments, an iRNA described herein comprises an antisense strand comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 8. In some embodiments, an iRNA described herein comprises a sense strand comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 7. A rat ANGPTL7 mRNA may have the sequence of SEQ ID NO: 7 provided herein.

In some embodiments, an iRNA described herein includes at least 15 contiguous nucleotides from one of the sequences provided in Tables 2-7, and may optionally be coupled to additional nucleotide sequences taken from the region contiguous to the selected sequence in ANGPTL7.

While a target sequence is generally 15-30 nucleotides in length, there is wide variation in the suitability of particular sequences in this range for directing cleavage of any given target RNA. Various software packages and the guidelines set out herein provide guidance for the identification of optimal target sequences for any given gene target, but an empirical approach can also be taken in which a "window" or "mask" of a given size (as a non-limiting example, 21 nucleotides) is literally or figuratively (including, *e.g.,* in silico) placed on the target RNA sequence to identify sequences in the size range that may serve as target sequences. By moving the sequence "window" progressively one nucleotide upstream or downstream of an initial target sequence location, the next potential target sequence can be identified, until the complete set of possible sequences is identified for any given target size selected. This process, coupled with systematic synthesis and testing of the identified sequences (using assays described herein or known in the art) to identify those sequences that perform optimally can identify those RNA sequences that, when targeted with an iRNA agent, mediate the best inhibition of target gene expression. Thus, it is contemplated that further optimization of inhibition efficiency can be achieved by progressively "walking the window" one nucleotide upstream or downstream of the given sequences to identify sequences with equal or better inhibition characteristics.

Further, it is contemplated that for any sequence identified, *e.g.,* in Tables 2-7, further optimization can be achieved by systematically either adding or removing nucleotides to generate longer or shorter sequences and testing those and sequences generated by walking a window of the longer or shorter size up or down the target RNA from that point. Again, coupling this approach to generating new candidate targets with testing for effectiveness of iRNAs based on those target sequences in an inhibition assay as known in the art or as described herein can lead to further improvements in the efficiency of inhibition. Further still, such optimized sequences can be adjusted by, *e.g.,* the introduction of modified nucleotides as described herein or as known in the art, addition or changes in overhang, or other modifications as known in the art and/or discussed herein to further optimize the molecule (*e.g.,* increasing serum stability or circulating half-life, increasing thermal stability, enhancing transmembrane delivery, targeting to a particular location or cell type, increasing interaction with silencing pathway enzymes, increasing release from endosomes, *etc.*) as an expression inhibitor.

In some embodiments, the disclosure provides an iRNA of any of Tables 2-7 that un-modified or un-conjugated. In some embodiments, an RNAi agent of the disclosure has a nucleotide sequence as provided in any of Tables 2-7, but lacks one or more ligand or moiety shown in the table. A ligand or moiety (*e.g.,* a lipophilic ligand or moiety) can be included in any of the positions provided in the instant application.

An iRNA as described herein can contain one or more mismatches to the target sequence. In some embodiments, an iRNA as described herein contains no more than 3 mismatches. In some embodiments, when the antisense strand of the iRNA contains mismatches to a target sequence, the area of mismatch is not located in the center of the region of complementarity. In some embodiments, when the antisense strand of the iRNA contains mismatches to the target sequence, the mismatch is restricted to be within the last 5 nucleotides from either the 5' or 3' end of the region of complementarity. For example, for a 23 nucleotide iRNA agent RNA strand which is complementary to a region of ANGPTL7, the RNA strand generally does not contain any mismatch within the central 13 nucleotides. The methods described herein, or methods known in the art can be used to determine whether an iRNA containing a mismatch to a target sequence is effective in inhibiting the expression of ANGPTL7. Consideration of the efficacy of iRNAs with mismatches in inhibiting expression of ANGPTL7 is important, especially if the particular region of complementarity in an ANGPTL7 gene is known to have polymorphic sequence variation within the population.

An RNA target may have regions, or spans of the target RNA's nucleotide sequence, which are relatively more susceptible or amenable than other regions of the RNA target to mediating cleavage of the RNA target via RNA interference induced by the binding of an RNAi agent to that region. The increased susceptibility to RNA interference within such "hotspot regions" (or simply "hotspots") means that iRNA agents targeting the region will likely have higher efficacy in inducing iRNA interference than iRNA agents which target other regions of the target RNA. For example, without being bound by theory, the accessibility of a target region of a target RNA may influence the efficacy of iRNA agents which target that region, with some hotspot regions having increased accessibility. Secondary structures, for instance, that form in the RNA target (e.g., within or proximate to hotspot regions) may affect the ability of the iRNA agent to bind the target region and induce RNA interference.

According to certain aspects of the invention, an iRNA agent may be designed to target a hotspot region of any of the target RNAs described herein, including any identified portions of a target RNA (e.g., a particular exon). As used herein, a hotspot region may refer to an approximately 19-200, 19-150, 19-100, 19-75, 19-50, 21-200, 21-150, 21-100, 21-75, 21-50, 50-200, 50-150, 50-100, 50-75, 75-200, 75-150, 75-100, 100-200, or 100-150 nucleotide region of a target RNA sequence for which targeting using RNAi agents provides an observably higher probability of efficacious silencing relative to targeting other regions of the same target RNA. According to certain aspects of the invention, a hotspot region may comprise a limited region of the target RNA, and in some cases, a substantially limited region of the target, including for example, less than half of the length of the target RNA, such as about 5%, 10%, 15%, 20%, 25%, or 30% of the length of the target RNA. Conversely, the other regions against which a hotspot is compared may cumulatively comprise at least a majority of the length of the target RNA. For example, the other regions may cumulatively comprise

at least about 60%, or at least about 70%, or at least about 80%, or at least about 90%, or at least about 95% of the length of the target RNA.

Compared regions of the target RNA may be empirically evaluated for identification of hotspots using efficacy data obtained from in vitro or in vivo screening assays. For example, RNAi agents targeting various regions that span a target RNA may be compared for frequency of efficacious iRNA agents (e.g., the amount by which target gene expression is inhibited, such as measured by mRNA expression or protein expression) that bind each region. In general, a hotspot can be recognized by observing clustering of multiple efficacious RNAi agents that bind to a limited region of the RNA target. A hotspot may be sufficiently characterized as such by observing efficacy of iRNA agents which cumulatively span at least about 60% of the target region identified as a hotspot, such as about 70%, about 80%, about 90%, or about 95% or more of the length of the region, including both ends of the region (i.e. at least about 60%, 70%, 80%, 90%, or 95% or more of the nucleotides within the region, including the nucleotides at each end of the region, were targeted by an iRNA agent). According to some aspects of the invention, an iRNA agent which demonstrates at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% inhibition over the region (e.g., no more than about 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% mRNA remaining) may be identified as efficacious.

Amenability to targeting of RNA regions may also be assessed using quantitative comparison of inhibition measurements across different regions of a defined size (e.g., 25, 30, 40, 50, 60, 70, 80, 90, or 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 nts). For example, an average level of inhibition may be determined for each region and the averages of each region may be compared. The average level of inhibition within a hotspot region may be substantially higher than the average of averages for all evaluated regions. According to some aspects, the average level of inhibition in a hotspot region may be at least about 10%, 20%, 30%, 40%, or 50% higher than the average of averages. According to some aspects, the average level of inhibition in a hotspot region may be at least about 1.0, 1.1, 1.2, 1.3, 1.4, 1.5 1.6, 1.7, 1.8. 1.9, or 2.0 standard deviations above the average of averages. The average level of inhibition may be higher by a statistically significant (e.g., $p < 0.05$) amount. According to some aspects, each inhibition measurement within a hotspot region may be above a threshold amount (e.g., at or below a threshold amount of mRNA remaining). According to some aspects, each inhibition measurement within the region may be substantially higher than an average of all inhibition measurements across all the measured regions. For example, each inhibition measurement in a hotspot region may be at least about 10%, 20%, 30%, 40%, or 50% higher than the average of all inhibition measurements. According to some aspects, each inhibition measurement may be at least about 1.0, 1.1, 1.2, 1.3, 1.4, 1.5 1.6, 1.7, 1.8. 1.9, or 2.0 standard deviations above the average of all inhibition measurements. Each inhibition measurement may be higher by a statistically significant (e.g., $p < 0.05$) amount than the average of all inhibition measurements. A standard for evaluating a hotspot may comprise various combinations of the above standards where compatible

(e.g., an average level of inhibition of at least about a first amount and having no inhibition measurements below a threshold level of a second amount, lesser than the first amount).

It is therefore expressly contemplated that any iRNA agent, including the specific exemplary iRNA agents described herein, which targets a hotspot region of a target RNA, may be preferably selected for inducing RNA interference of the target mRNA as targeting such a hotspot region is likely to exhibit a robust inhibitory response relative to targeting a region which is not a hotspot region. RNAi agents targeting target sequences that substantially overlap (e.g., by at least about 70%, 75%, 80%, 85%, 90%, 95% of the target sequence length) or, preferably, that reside fully within the hotspot region may be considered to target the hotspot region. Hotspot regions of the RNA target(s) of the instant invention may include any region for which the data disclosed herein demonstrates higher frequency of targeting by efficacious RNAi agents, including by any of the standards described elsewhere herein, whether or not the range(s) of such hotspot region(s) are explicitly specified.

In various embodiments, a dsRNA agent of the present invention targets a hotspot region of an mRNA encoding ANGPTL7. In some embodiments, a dsRNA agent of the present invention targets a hotspot region of a mouse mRNA encoding ANGPTL7. In one embodiment, the hotspot region comprises nucleotides 1562-1584, 546-568, 709-731, 862-884, and/or 232-256 of SEQ ID NO: 1. In other embodiments, a dsRNA agent of the present invention targets a hotspot region of a human mRNA encoding ANGPTL7 mRNA. In one embodiment, the hotspot region comprises nucleotides 1993-2146, 1910-1932, 1726-1823, 1628-1685, 1591-1613, 1551-1573, 1420-1442, 1380-1402, 1243-1265, 1195-1217, 1096-1118, 940-962, and/or 299-321 of SEQ ID NO: 3. The dsRNA agent may be selected from the group consisting of AD-1094991, AD-1093984, AD-1094129, AD-1094262, AD-1093670, AD-1093672, AD-1565389, AD-1565368, AD-1565357, AD-1565345, AD-1565324, AD-1565303, AD-1565288, AD-1565212, AD-1565141, AD-1565126, AD-1565113, AD-1565091, AD-1565034, AD-1565015, AD-1565004, AD-1564969, AD-1094381, AD-1564428, AD-1564936, AD-1564823, AD-1564802, AD-1564666, AD-1564618, and AD-1563396.

In some embodiments, at least one end of a dsRNA has a single-stranded nucleotide overhang of 1 to 4, generally 1 or 2 nucleotides. In some embodiments, dsRNAs having at least one nucleotide overhang have superior inhibitory properties relative to their blunt-ended counterparts. In some embodiments, the RNA of an iRNA (*e.g.,* a dsRNA) is chemically modified to enhance stability or other beneficial characteristics. The nucleic acids featured in the disclosure may be synthesized and/or modified by methods well established in the art, such as those described in "Current protocols in nucleic acid chemistry," Beaucage, S.L. *et al.* (Edrs.), John Wiley & Sons, Inc., New York, NY, USA, which is hereby incorporated herein by reference. Modifications include, for example, (a) end modifications, *e.g.,* 5' end modifications (phosphorylation, conjugation, inverted linkages, *etc.*) 3' end modifications (conjugation, DNA nucleotides, inverted linkages, *etc.*), (b) base modifications, *e.g.,* replacement with stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, removal of bases (abasic nucleotides), or conjugated bases, (c) sugar

modifications (*e.g.,* at the 2' position or 4' position, or having an acyclic sugar) or replacement of the sugar, as well as (d) backbone modifications, including modification or replacement of the phosphodiester linkages. Specific examples of RNA compounds useful in this disclosure include, but are not limited to, RNAs containing modified backbones or no natural internucleoside linkages. RNAs having modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In particular embodiments, the modified RNA will have a phosphorus atom in its internucleoside backbone.

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

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

Modified RNA backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatoms and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

Representative U.S. patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Patent Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,64,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307;

5,561,225; 5,596,086; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and, 5,677,439, each of which is herein incorporated by reference.

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

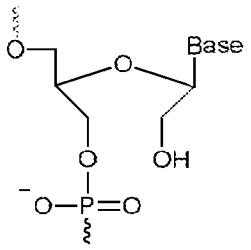
Some embodiments featured in the disclosure include RNAs with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular --CH_2--NH--CH_2--, --CH_2--N(CH_3)--O--CH_2--[known as a methylene (methylimino) or MMI backbone], --CH_2--O--N(CH_3)--CH_2--, --CH_2--N(CH_3)--N(CH_3)--CH_2-- and --N(CH_3)--CH_2----[wherein the native phosphodiester backbone is represented as --O--P--O--CH_2--] of the above-referenced U.S. Patent No. 5,489,677, and the amide backbones of the above-referenced U.S. Patent No. 5,602,240. In some embodiments, the RNAs featured herein have morpholino backbone structures of the above-referenced U.S. Patent No. 5,034,506.

Modified RNAs may also contain one or more substituted sugar moieties. The iRNAs, *e.g.*, dsRNAs, featured herein can include one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Exemplary suitable modifications include O[$(CH_2)_nO$]$_mCH_3$, O$(CH_2)_nOCH_3$, O$(CH_2)_nNH_2$, O$(CH_2)_nCH_3$, O$(CH_2)_nONH_2$, and O$(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. In other embodiments, dsRNAs include one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an iRNA, or a group for improving the pharmacodynamic properties of an iRNA, and other substituents having similar properties. In some embodiments, the modification includes a 2'-methoxyethoxy (2'-O--$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*, 1995, 78:486-504) *i.e.*, an alkoxy-alkoxy group. Another exemplary modification is 2'-dimethylaminooxyethoxy, *i.e.*, a O$(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, and 2'-

dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), *i.e.*, 2'-O--CH_2--O--CH_2--N(CH_2)$_2$.

In other embodiments, an iRNA agent comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides (or nucleosides). In certain embodiments, the sense strand or the antisense strand, or both sense strand and antisense strand, include less than five acyclic nucleotides per strand (*e.g.*, four, three, two or one acyclic nucleotides per strand). The one or more acyclic nucleotides can be found, for example, in the double-stranded region, of the sense or antisense strand, or both strands; at the 5'-end, the 3'-end, both of the 5' and 3'-ends of the sense or antisense strand, or both strands, of the iRNA agent. In some embodiments, one or more acyclic nucleotides are present at positions 1 to 8 of the sense or antisense strand, or both. In some embodiments, one or more acyclic nucleotides are found in the antisense strand at positions 4 to 10 (*e.g.*, positions 6-8) from the 5'-end of the antisense strand. In some embodiments, the one or more acyclic nucleotides are found at one or both 3'-terminal overhangs of the iRNA agent.

The term "acyclic nucleotide" or "acyclic nucleoside" as used herein refers to any nucleotide or nucleoside having an acyclic sugar, *e.g.*, an acyclic ribose. An exemplary acyclic nucleotide or nucleoside can include a nucleobase, *e.g.*, a naturally occurring or a modified nucleobase (*e.g.*, a nucleobase as described herein). In certain embodiments, a bond between any of the ribose carbons (C1, C2, C3, C4, or C5), is independently or in combination absent from the nucleotide. In some embodiments, the bond between C2-C3 carbons of the ribose ring is absent, *e.g.*, an acyclic 2'-3'-seco-nucleotide monomer. In other embodiments, the bond between C1-C2, C3-C4, or C4-C5 is absent (*e.g.*, a 1'-2', 3'-4' or 4'-5'-seco nucleotide monomer). Exemplary acyclic nucleotides are disclosed in US 8,314,227, incorporated herein by reference in its entirely. For example, an acyclic nucleotide can include any of monomers D-J in Figures 1-2 of US 8,314,227. In some embodiments, the acyclic nucleotide includes the following monomer:



wherein Base is a nucleobase, *e.g.*, a naturally occurring or a modified nucleobase (*e.g.*, a nucleobase as described herein).

In certain embodiments, the acyclic nucleotide can be modified or derivatized, *e.g.*, by coupling the acyclic nucleotide to another moiety, *e.g.*, a ligand (*e.g.*, a GalNAc, a cholesterol ligand), an alkyl, a polyamine, a sugar, a polypeptide, among others.

In other embodiments, the iRNA agent includes one or more acyclic nucleotides and one or more LNAs (*e.g.*, an LNA as described herein). For example, one or more acyclic nucleotides and/or one or more LNAs can be present in the sense strand, the antisense strand, or both. The number of

acyclic nucleotides in one strand can be the same or different from the number of LNAs in the opposing strand. In certain embodiments, the sense strand and/or the antisense strand comprises less than five LNAs (*e.g.,* four, three, two or one LNAs) located in the double stranded region or a 3'-overhang. In other embodiments, one or two LNAs are located in the double stranded region or the 3'-overhang of the sense strand. Alternatively, or in combination, the sense strand and/or antisense strand comprises less than five acyclic nucleotides (*e.g.,* four, three, two or one acyclic nucleotides) in the double-stranded region or a 3'-overhang. In some embodiments, the sense strand of the iRNA agent comprises one or two LNAs in the 3'-overhang of the sense strand, and one or two acyclic nucleotides in the double-stranded region of the antisense strand (*e.g.,* at positions 4 to 10 (*e.g.,* positions 6-8) from the 5'-end of the antisense strand) of the iRNA agent.

In other embodiments, inclusion of one or more acyclic nucleotides (alone or in addition to one or more LNAs) in the iRNA agent results in one or more (or all) of: (i) a reduction in an off-target effect; (ii) a reduction in passenger strand participation in RNAi; (iii) an increase in specificity of the guide strand for its target mRNA; (iv) a reduction in a microRNA off-target effect; (v) an increase in stability; or (vi) an increase in resistance to degradation, of the iRNA molecule.

Other modifications include 2'-methoxy (2'-OCH3), 2'-5 aminopropoxy (2'-OCH2CH2CH2NH2) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the RNA of an iRNA, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked dsRNAs and the 5' position of 5' terminal nucleotide. iRNAs may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative U.S. patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Patent Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, certain of which are commonly owned with the instant application, and each of which is herein incorporated by reference.

An iRNA may also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl anal other 8-substituted adenines and guanines, 5-halo, particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-daazaadenine and 3-deazaguanine and 3-deazaadenine.

Further nucleobases include those disclosed in U.S. Patent No. 3,687,808, those disclosed in Modified Nucleosides in Biochemistry, Biotechnology and Medicine, Herdewijn, P. ed. Wiley-VCH, 2008; those disclosed in The Concise Encyclopedia of Polymer Science and Engineering, pages 858-859, Kroschwitz, J. L, ed. John Wiley & Sons, 1990, these disclosed by Englisch *et al.*, *Angewandte Chemie*, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y S., Chapter 15, *dsRNA Research and Applications*, pages 289-302, Crooke, S. T. and Lebleu, B., Ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds featured in the disclosure. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y. S., Crooke, S. T. and Lebleu, B., Eds., dsRNA Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are exemplary base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative U.S. patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. Patent No. 3,687,808, as well as U.S. Patent Nos. 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,681,941; 6,015,886; 6,147,200; 6,166,197; 6,222,025; 6,235,887; 6,380,368; 6,528,640; 6,639,062; 6,617,438; 7,045,610; 7,427,672; and 7,495,088, each of which is herein incorporated by reference, and U.S. Patent No. 5,750,692, also herein incorporated by reference.

The RNA of an iRNA can also be modified to include one or more (*e.g.,* about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) bicyclic sugar moieties. A "bicyclic sugar" is a furanosyl ring modified by the bridging of two atoms. A "bicyclic nucleoside" ("BNA") is a nucleoside having a sugar moiety comprising a bridge connecting two carbon atoms of the sugar ring, thereby forming a bicyclic ring system. In certain embodiments, the bridge connects the 4'-carbon and the 2'-carbon of the sugar ring. Thus, in some embodiments an agent of the disclosure may include one or more locked nucleic acids (LNAs) (also referred to herein as "locked nucleotides"). In some embodiments, a locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting, *e.g.,* the 2' and 4' carbons. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, increase thermal stability, and to reduce off-target effects (Elmen, J. *et al.*, 2005 *Nucleic Acids Research* 33(1):439-447; Mook, OR. *et al.*, 2007 *Mol. Canc. Ther.* 6(3):833-843; Grunweller, A. *et al.*, 2003 *Nucleic Acids Research* 31(12):3185-3193).

Examples of bicyclic nucleosides for use in the polynucleotides of the disclosure include without limitation nucleosides comprising a bridge between the 4'and the 2' ribosyl ring atoms. In certain embodiments, the antisense polynucleotide agents of the disclosure include one or more

bicyclic nucleosides comprising a 4' to 2' bridge. Examples of such 4' to 2' bridged bicyclic nucleosides, include but are not limited to 4'-(CH2)—O-2' (LNA); 4'-(CH2)—S-2'; 4'-(CH2)2—O-2' (ENA); 4'-CH(CH3)—O-2' (also referred to as "constrained ethyl" or "cEt") and 4'-CH(CH2OCH3)—O-2' (and analogs thereof; see, *e.g.,* U.S. Patent No. 7,399,845); 4'-C(CH3)(CH3)—O-2' (and analogs thereof; see *e.g.,* U.S. Patent No. 8,278,283); 4'-CH2—N(OCH3)-2' (and analogs thereof; see *e.g.,* U.S. Patent No. 8,278,425); 4'-CH2—O—N(CH3)-2' (see, *e.g.*, U.S. Patent Publication No. 2004/0171570); 4'-CH2—N(R)—O-2', wherein R is H, C1-C12 alkyl, or a protecting group (see, *e.g.,* U.S. Patent No. 7,427,672); 4'-CH2—C(H)(CH3)-2' (see, *e.g.,* Chattopadhyaya *et al., J. Org. Chem.*, 2009, 74, 118-134); and 4'-CH2—C(=CH2)-2' (and analogs thereof; see, *e.g.,* U.S. Patent No. 8,278,426). The contents of each of the foregoing are incorporated herein by reference for the methods provided therein. Representative U.S. Patents that teach the preparation of locked nucleic acids include, but are not limited to, the following: U.S. Patent Nos. 6,268,490; 6,670,461; 6,794,499; 6,998,484; 7,053,207; 7,084,125; 7,399,845, and 8,314,227, each of which is herein incorporated by reference in its entirety. Exemplary LNAs include but are not limited to, a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.,* International PCT 5 Publication No. WO 00/66604 and WO 99/14226).

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

A RNAi agent of the disclosure can also be modified to include one or more constrained ethyl nucleotides. As used herein, a "constrained ethyl nucleotide" or "cEt" is a locked nucleic acid comprising a bicyclic sugar moiety comprising a 4'-CH(CH3)-0-2' bridge. In some embodiments, a constrained ethyl nucleotide is in the S conformation referred to herein as "S-cEt."

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

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

In some embodiments, a RNAi agent of the disclosure comprises one or more monomers that are UNA (unlocked nucleic acid) nucleotides. UNA is unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked "sugar" residue. In one example, UNA also encompasses monomer with bonds between C1'-C4' have been removed (*i.e.* the covalent carbon-oxygen-carbon bond between the C1' and C4' carbons). In another example, the C2'-C3' bond (*i.e.* the covalent carbon-carbon bond between the C2' and C3' carbons) of the sugar has been

removed (see 2008 *Nuc. Acids Symp. Series* 52:133-134 and Fluiter *et al.*, 2009 *Mol. Biosyst.* 10:1039).

Representative U.S. publications that teach the preparation of UNA include, but are not limited to, US8,314,227; and U.S. Patent Publication Nos. 2013/0096289; 2013/0011922; and 2011/0313020, the contents of each of which are hereby incorporated herein by reference for the methods provided therein.

In other embodiments, the iRNA agents include one or more (*e.g.,* about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998 *J. Am. Chem. Soc.* 120:8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in the iRNA molecules can result in enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands.

Potentially stabilizing modifications to the ends of RNA molecules can include N-(acetylaminocaproyl)-4-hydroxyprolinol (Hyp-C6-NHAc), N-(caproyl-4-hydroxyprolinol (Hyp- C6), N-(acetyl-4-hydroxyprolinol (Hyp-NHAc), thymidine-2'-O-deoxythymidine (ether), N-(aminocaproyl)-4-hydroxyprolinol (Hyp-C6-amino), 2-docosanoyl-uridine-3"- phosphate, inverted base dT(idT) and others. Disclosure of this modification can be found in PCT Publication No. WO 2011/005861.

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

A. iRNA Motifs

In certain aspects of the disclosure, the double-stranded RNAi agents of the disclosure include agents with chemical modifications as disclosed, for example, in WO 2013/075035, the contents of which are incorporated herein by reference for the methods provided therein. As shown herein and in WO 2013/075035, a superior result may be obtained by introducing one or more motifs of three identical modifications on three consecutive nucleotides into a sense strand or antisense strand of an RNAi agent, particularly at or near the cleavage site. In some embodiments, the sense strand and antisense strand of the RNAi agent may otherwise be completely modified. The introduction of these motifs interrupts the modification pattern, if present, of the sense or antisense strand. The RNAi agent may be optionally conjugated with a lipophilic moiety or ligand, *e.g.,* a C16 moiety or ligand, for instance on the sense strand. The RNAi agent may be optionally modified with a (*S*)-glycol nucleic

acid (GNA) modification, for instance on one or more residues of the antisense strand. The resulting RNAi agents present superior gene silencing activity.

In some embodiments, the sense strand sequence may be represented by formula (I):

5' np-Na-(X)i-Nb-Y Y -Nb-(Z Z)j-Na-nq 3' (I)

wherein:

i and j are each independently 0 or 1;

p and q are each independently 0-6;

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

each Nb independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

each np and nq independently represent an overhang nucleotide;

wherein Nb and Y do not have the same modification; and

XXX, YYY and ZZZ each independently represent one motif of three identical modifications on three consecutive nucleotides. In some embodiments, YYY is all 2'-F modified nucleotides.

In some embodiments, the Na and/or Nb comprise modifications of alternating pattern.

In some embodiments, the YYY motif occurs at or near the cleavage site of the sense strand. For example, when the RNAi agent has a duplex region of 17-23 nucleotides in length, the YYY motif can occur at or the vicinity of the cleavage site (*e.g.*: can occur at positions 6, 7, 8; 7, 8, 9; 8, 9, 10; 9, 10, 11; 10, 11,12 or 11, 12, 13) of the sense strand, the count starting from the 1st nucleotide, from the 5'-end; or optionally, the count starting at the 1st paired nucleotide within the duplex region, from the 5'-end.

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

5' np-Na-YYY-Nb-ZZZ-Na-nq 3' (Ib);

5' np-Na-XXX-Nb-YYY-Na-nq 3' (Ic); or

5' np-Na-XXX-Nb-YYY-Nb-ZZZ-Na-nq 3' (Id).

When the sense strand is represented by formula (Ib), Nb represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each Na independently can represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the sense strand is represented as formula (Ic), Nb represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each Na can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the sense strand is represented as formula (Id), each Nb independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. In some embodiments, Nb is 0, 1, 2, 3, 4, 5 or 6. Each Na can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

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

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

5' n_p-N_a-YYY- N_a-n_q 3' (Ia).

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

In some embodiments, the antisense strand sequence of the RNAi may be represented by formula (Ie):

5' $n_{q'}$-N_a'-(Z'Z'Z')$_k$-N_b'-Y'Y'Y'-N_b'-(X'X'X')$_l$-N'$_a$-n_p' 3' (Ie)

wherein:

k and l are each independently 0 or 1;

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

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

each Nb' independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

each n_p' and n_q' independently represent an overhang nucleotide;

wherein N_b' and Y' do not have the same modification;

and

X'X'X', Y'Y'Y', and Z'Z'Z' each independently represent one of three identical modification on three consecutive nucleotides.

In some embodiments, the N_a' and/or N_b' comprise modification of alternating pattern.

The Y'Y'Y' motif occurs at or near the cleavage site of the antisense strand. For example, when the RNAi agent has a duplex region of 17-23 nucleotides in length, the Y'Y'Y' motif can occur at positions 9, 10, 11; 10, 11, 12; 11, 12, 13; 12, 13, 14; or 13, 14, 15 of the antisense strand, with the count starting from the 1st nucleotide, from the 5'-end; or optionally, the count starting at the 1st paired nucleotide within the duplex region, from the 5'- end. In some embodiments, the Y'Y'Y' motif occurs at positions 11, 12, 13.

In some embodiments, Y'Y'Y' motif is all 2'-Ome modified nucleotides.

In on embodiment, k is 1 and l is 0, or k is 0 and l is 1, or both 5 k and l are 1.

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

5' n_q'-N_a'-Z'Z'Z'-N_b'-Y'Y'Y'-N_a'-n_p' 3' (If);

5' n_q'-N_a'-Y'Y'Y'-N_b'-X'X'X'-n_p' 3' (Ig); or

5' n_q'-N_a'- Z'Z'Z'-N_b'-Y'Y'Y'-N_b'- X'X'X'-N_a'-n_p' 3' (Ih).

When the antisense strand is represented by formula (If), Nb' represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each Na' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the antisense strand is represented as formula (Ig), each Nb' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each Na' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. In some embodiments, Nb is 0, 1, 2, 3, 4, 5 or 6.

When the antisense strand is represented as formula (Ih), each N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. Preferably, N_b is 0, 1, 2, 3, 4, 5 or 6.

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

5' np'-Na'-Y'Y'Y'- Na'-nq' 3' (Ia).

When the antisense strand is represented as formula (Ie), each Na' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

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

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

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

In some embodiments the antisense strand may Y'Y'Y' motif occurring at positions 11, 12, 13 of the strand, the count starting from the 1st nucleotide from the 5'-end, or optionally, the count starting at the 1st paired nucleotide within the duplex region, from the 5'- end; and Y' represents 2'-O-methyl modification. The antisense strand may additionally contain X'X'X' motif or Z'Z'Z' motifs as wing modifications at the opposite end of the duplex region; and X'X'X' and Z'Z'Z' each independently represents a 2'-OMe modification or 2'-F modification.

The sense strand represented by any one of the above formulas (Ia), (Ib), (Ic), and (Id) forms a duplex with an antisense strand being represented by any one of formulas (Ie), (If), (Ig), and (Ih), respectively.

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

sense: 5' n_p -N_a-(XXX)i -N_b- YYY -N_b -(ZZZ)j-N_a-n_q 3'

antisense: 3' n_p'-Na'-(X'X'X')k-N_b'-Y'Y'Y'-N_b'-(Z'Z'Z')$_l$-N_a'-n_q' 5' (Ii)

wherein,

i, j, k, and l are each independently 0 or 1;

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

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

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 modified nucleotides;

wherein

each n_p', n_p, n_q', and n_q, each of which may or may not be present independently represents an overhang nucleotide; and

XXX, YYY, ZZZ, X'X'X', Y'Y'Y', and Z'Z'Z' each independently represent one motif of three identical modification on three consecutive nucleotides.

In some embodiments, i is 0 and j is 0; or i is 1 and j is 0; or i is 0 and j is 1; or both i and j are 0; or both i and j are 1. In some embodiments, k is 0 and l is 0; or k is 1 and l is 0; k is 0 and l is 1; or both k and l are 0; or both k and l are 1.

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

5' n_p -N_a-Y Y Y-N_a-n_q 3'

3' n_p' -N_a'- Y'Y'Y'-N_a'n_q' 5' (Ij)

5' n_p -N_a -Y -N_b -Z -N_a-n_q 3'

3' n_p -N_a'- Y'Y'Y'-N_b'- Z'Z'Z'- Na'-nq' 5' (Ik)

5' n_p -N_a - X -N_b- Y -N_a-n_q 3'

3' n_p -N_a'- X'X'X' -N_b'- Y'Y'Y'- Na'-n_q' 5' (Il)

5' n_p -N_a - X -N_b -Y - N_b- Z Z-N_a-n_q 3'

3' n_p -N_a'- X'X'X'-N_b'- Y'Y'Y'-N_b'- Z'Z'Z'-Na'-n_q' 5' (Im)

When the RNAi agent is represented by formula (Ij), each N_a independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the RNAi agent is represented by formula (Ik), each N_b independently represents an oligonucleotide sequence comprising 1-10, 1-7, 1-5 or 1-4 modified nucleotides. Each N_a independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the RNAi agent is represented as formula (II), each Nb, Nb' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N_a independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the RNAi agent is represented as formula (Im), each N_b, N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each N_a, N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. Each of N_a, N_a', N_b and N_b' independently comprises modifications of alternating pattern.

Each of X, Y and Z in formulas (Ii), (Ij), (Ik), (Il), and (Im) may be the same or different from each other.

When the RNAi agent is represented by formula (Ii), (Ij), (Ik), (Il), and (Im), at least one of the Y nucleotides may form a base pair with one of the Y' nucleotides. Alternatively, at least two of the Y nucleotides form base pairs with the corresponding Y' nucleotides; or all three of the Y nucleotides all form base pairs with the corresponding Y' nucleotides.

When the RNAi agent is represented by formula (Ik) or (Im), at least one of the Z nucleotides may form a base pair with one of the Z' nucleotides. Alternatively, at least two of the Z nucleotides form base pairs with the corresponding Z' nucleotides; or all three of the Z nucleotides all form base pairs with the corresponding Z' nucleotides.

When the RNAi agent is represented as formula (Il) or (Im), at least one of the X nucleotides may form a base pair with one of the X' nucleotides. Alternatively, at least two of the X nucleotides form base pairs with the corresponding X' nucleotides; or all three of the X nucleotides all form base pairs with the corresponding X' nucleotides.

In some embodiments, the modification on the Y nucleotide is different than the modification on the Y' nucleotide, the modification on the Z nucleotide is different than the modification on the Z' nucleotide, and/or the modification on the X nucleotide is different than the modification on the X' nucleotide.

In some embodiments, when the RNAi agent is represented by formula (Im), the Na modifications are 2'-O-methyl or 2'-fluoro modifications. In some embodiments, when the RNAi agent is represented by formula (Im), the Na modifications are 2'-O-methyl or 2'-fluoro modifications and np' > 0 and at least one np' is linked to a neighboring nucleotide a via phosphorothioate linkage. In some embodiments, when the RNAi agent is represented by formula (Im), the Na modifications are 2'-O-methyl or 2'-fluoro modifications, np' >0 and at least one np' is linked to a neighboring nucleotide via phosphorothioate linkage, and the sense strand is conjugated to one or more moieties or ligands (*e.g.,* one or more lipophilic moieties, optionally one or more C16 moieties, or one or more GalNAc moieties) attached through a bivalent or trivalent branched linker. In some embodiments, when the RNAi agent is represented by formula (Im), the Na modifications are 2'-O-methyl or 2'-fluoro modifications, np' >0 and at least one np' is linked to a neighboring nucleotide via

phosphorothioate linkage, the sense strand comprises at least one phosphorothioate linkage, and the sense strand is conjugated to one or more moieties or ligands (*e.g.,* one or more lipophilic moieties, optionally one or more C16 moieties, or one or more GalNAc moieties) attached through a bivalent or trivalent branched linker.

In some embodiments, when the RNAi agent is represented by formula (Ij), the Na modifications are 2'-O-methyl or 2'-fluoro modifications, np' >0 and at least one np' is linked to a neighboring nucleotide via phosphorothioate linkage, the sense strand comprises at least one phosphorothioate linkage, and the sense strand is conjugated to one or more moieties or ligands (*e.g.,* one or more lipophilic moieties, optionally one or more C16 moieties, or one or more GalNAc moieties) attached through a bivalent or trivalent branched linker.

In some embodiments, the RNAi agent is a multimer containing at least two duplexes represented by formula (Ii), (Ij), (Ik), (Il), and (Im), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable. Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

In some embodiments, the RNAi agent is a multimer containing three, four, five, six or more duplexes represented by formula (Ii), (Ij), (Ik), (Il), and (Im), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable. Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

In some embodiments, two RNAi agents represented by formula (Ii), (Ij), (Ik), (Il), and (Im) are linked to each other at the 5' end, and one or both of the 3' ends and are optionally conjugated to a ligand. Each of the agents can target the same gene or two different genes; or each of the agents can target same gene at two different target sites.

Various publications describe multimeric RNAi agents that can be used in the methods of the disclosure. Such publications include WO2007/091269, WO2010/141511, WO2007/117686, WO2009/014887, and WO2011/031520; and US 7858769, the contents of each of which are hereby incorporated herein by reference for the methods provided therein. In certain embodiments, the RNAi agents of the disclosure may include GalNAc ligands.

As described in more detail below, the RNAi agent that contains conjugations of one or more carbohydrate moieties to a RNAi agent can optimize one or more properties of the RNAi agent. In many cases, the carbohydrate moiety will be attached to a modified subunit of the RNAi agent. For example, the ribose sugar of one or more ribonucleotide subunits of a dsRNA agent can be replaced with another moiety, *e.g.,* a non-carbohydrate (preferably cyclic) carrier to which is attached a carbohydrate ligand. A ribonucleotide subunit in which the ribose sugar of the subunit has been so replaced is referred to herein as a ribose replacement modification subunit (RRMS). A cyclic carrier may be a carbocyclic ring system, *i.e.*, all ring atoms are carbon atoms, or a heterocyclic ring system,

i.e., one or more ring atoms may be a heteroatom, *e.g.,* nitrogen, oxygen, sulfur. The cyclic carrier may be a monocyclic ring system, or may contain two or more rings, *e.g.* fused rings. The cyclic carrier may be a fully saturated ring system, or it may contain one or more double bonds.

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

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

In certain specific embodiments, the RNAi agent for use in the methods of the disclosure is an agent selected from the group of agents listed in any one of Tables 2-7. These agents may further comprise a ligand. The ligand can be attached to the sense strand, antisense strand or both strands, at the 3'-end, 5'-end, or both ends. For instance, the ligand may be conjugated to the sense strand, in particular, the 3'-end of the sense strand.

B. iRNA Conjugates

The iRNA agents disclosed herein can be in the form of conjugates. The conjugate may be attached at any suitable location in the iRNA molecule, *e.g.,* at the 3' end or the 5' end of the sense or the antisense strand. The conjugates are optionally attached via a linker.

In some embodiments, an iRNA agent described herein is chemically linked to one or more ligands, moieties or conjugates, which may confer functionality, *e.g.,* by affecting (*e.g.,* enhancing) the activity, cellular distribution or cellular uptake of the iRNA. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger *et al.*, 1989 *Proc. Natl. Acid. Sci. U.S.A.* 86:6553-6556), cholic acid (Manoharan *et al.*, 1994 *Biorg. Med. Chem. Let.*, 4:1053-1060), a thioether, *e.g.,* beryl-S-tritylthiol (Manoharan *et al.*, 1992 *Ann. N.Y. Acad. Sci.*, 660:306-309;

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

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

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

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

Other examples of ligands include dyes, intercalating agents (*e.g.* acridines), cross-linkers (*e.g.* psoralene, mitomycin C), porphyrins (TPPC4, texaphyrin, Sapphyrin), polycyclic aromatic hydrocarbons (*e.g.,* phenazine, dihydrophenazine), artificial endonucleases (*e.g.* EDTA), lipophilic

molecules, *e.g.*, cholesterol, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-Bis-O(hexadecyl)glycerol, geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid,O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine)and peptide conjugates (*e.g.,* antennapedia peptide, Tat peptide), alkylating agents, phosphate, amino, mercapto, PEG (*e.g.,* PEG-40K), MPEG, $[MPEG]_2$, polyamino, alkyl, substituted alkyl, radiolabeled markers, enzymes, haptens (*e.g.* biotin), transport/absorption facilitators (*e.g.,* aspirin, vitamin E, folic acid), synthetic ribonucleases (*e.g.,* imidazole, bisimidazole, histamine, imidazole clusters, acridine-imidazole conjugates, Eu3+ complexes of tetraazamacrocycles), dinitrophenyl, HRP, or AP.

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

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

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

Ligand-conjugated oligonucleotides of the disclosure may be synthesized by the use of an oligonucleotide that bears a pendant reactive functionality, such as that derived from the attachment of a linking molecule onto the oligonucleotide (described below). This reactive oligonucleotide may be reacted directly with commercially available ligands, ligands that are synthesized bearing any of a variety of protecting groups, or ligands that have a linking moiety attached thereto.

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

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

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

1. *Lipophilic Moieties*

In certain embodiments, the lipophilic moiety is an aliphatic, cyclic such as alicyclic, or polycyclic such as polyalicyclic compound, such as a steroid (*e.g.,* sterol) or a linear or branched aliphatic hydrocarbon. The lipophilic moiety may generally comprise a hydrocarbon chain, which may be cyclic or acyclic. The hydrocarbon chain may comprise various substituents or one or more heteroatoms, such as an oxygen or nitrogen atom. Such lipophilic aliphatic moieties include, without limitation, saturated or unsaturated C_4-C_{30} hydrocarbon (*e.g.,* C_6-C_{18} hydrocarbon), saturated or unsaturated fatty acids, waxes (*e.g.,* monohydric alcohol esters of fatty acids and fatty diamides), terpenes (*e.g.,* C_{10} terpenes, C_{15} sesquiterpenes, C_{20} diterpenes, C_{30} triterpenes, and C_{40} tetraterpenes), and other polyalicyclic hydrocarbons. For instance, the lipophilic moiety may contain a C_4-C_{30} hydrocarbon chain (*e.g.,* C_4-C_{30} alkyl or alkenyl). In some embodiments the lipophilic moiety contains a saturated or unsaturated C_6-C_{18} hydrocarbon chain (*e.g.,* a linear C_6-C_{18} alkyl or alkenyl). In some embodiments, the lipophilic moiety contains a saturated or unsaturated C16 hydrocarbon chain (*e.g.,* a linear C16 alkyl or alkenyl).

The lipophilic moiety may be attached to the RNAi agent by any method known in the art, including via a functional grouping already present in the lipophilic moiety or introduced into the RNAi agent, such as a hydroxy group (*e.g.,* —CO—CH_2—OH). The functional groups already

present in the lipophilic moiety or introduced into the RNAi agent include, but are not limited to, hydroxyl, amine, carboxylic acid, sulfonate, phosphate, thiol, azide, and alkyne.

Conjugation of the RNAi agent and the lipophilic moiety may occur, for example, through formation of an ether or a carboxylic or carbamoyl ester linkage between the hydroxy and an alkyl group R—, an alkanoyl group RCO— or a substituted carbamoyl group RNHCO—. The alkyl group R may be cyclic (*e.g.,* cyclohexyl) or acyclic (*e.g.,* straight-chained or branched; and saturated or unsaturated). Alkyl group R may be a butyl, pentyl, hexyl, heptyl, octyl, nonyl, decyl, undecyl, dodecyl, tridecyl, tetradecyl, pentadecyl, hexadecyl, heptadecyl or octadecyl group, or the like.

In some embodiments, the lipophilic moiety is conjugated to the double-stranded RNAi agent via a linker a linker containing an ether, thioether, urea, carbonate, amine, amide, maleimide-thioether, disulfide, phosphodiester, sulfonamide linkage, a product of a click reaction (*e.g.,* a triazole from the azide-alkyne cycloaddition), or carbamate.

In another embodiment, the lipophilic moiety is a steroid, such as sterol. Steroids are polycyclic compounds containing a perhydro-1,2-cyclopentanophenanthrene ring system. Steroids include, without limitation, bile acids (*e.g.,* cholic acid, deoxycholic acid and dehydrocholic acid), cortisone, digoxigenin, testosterone, cholesterol, and cationic steroids, such as cortisone. A "cholesterol derivative" refers to a compound derived from cholesterol, for example by substitution, addition or removal of substituents.

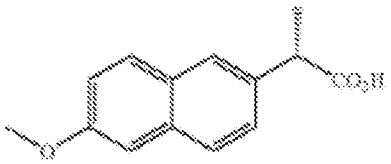
In another embodiment, the lipophilic moiety is an aromatic moiety. In this context, the term "aromatic" refers broadly to mono- and polyaromatic hydrocarbons. Aromatic groups include, without limitation, C_6-C_{14} aryl moieties comprising one to three aromatic rings, which may be optionally substituted; "aralkyl" or "arylalkyl" groups comprising an aryl group covalently linked to an alkyl group, either of which may independently be optionally substituted or unsubstituted; and "heteroaryl" groups. As used herein, the term "heteroaryl" refers to groups having 5 to 14 ring atoms, preferably 5, 6, 9, or 10 ring atoms; having 6, 10, or 14π electrons shared in a cyclic array, and having, in addition to carbon atoms, one to about three heteroatoms selected from the group consisting of nitrogen (N), oxygen (O), and sulfur (S).

As employed herein, a "substituted" alkyl, cycloalkyl, aryl, heteroaryl, or heterocyclic group is one having one to about four, preferably one to about three, more preferably one or two, non-hydrogen substituents. Suitable substituents include, without limitation, halo, hydroxy, nitro, haloalkyl, alkyl, alkaryl, aryl, aralkyl, alkoxy, aryloxy, amino, acylamino, alkylcarbamoyl, arylcarbamoyl, aminoalkyl, alkoxycarbonyl, carboxy, hydroxyalkyl, alkanesulfonyl, arenesulfonyl, alkanesulfonamido, arenesulfonamido, aralkylsulfonamido, alkylcarbonyl, acyloxy, cyano, and ureido groups.

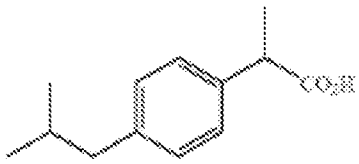
In some embodiments, the lipophilic moiety is an aralkyl group, *e.g.,* a 2-arylpropanoyl moiety. The structural features of the aralkyl group are selected so that the lipophilic moiety will bind to at least one protein in vivo. In certain embodiments, the structural features of the aralkyl group are

selected so that the lipophilic moiety binds to serum, vascular, or cellular proteins. In certain embodiments, the structural features of the aralkyl group promote binding to albumin, an immunoglobulin, a lipoprotein, α-2-macroglubulin, or α-1-glycoprotein.

In certain embodiments, the ligand is naproxen or a structural derivative of naproxen. Procedures for the synthesis of naproxen can be found in U.S. Patent No. 3,904,682 and U.S. Patent No. 4,009,197, which are hereby incorporated by reference in their entirety. Naproxen has the chemical name (S)-6-Methoxy-α-methyl-2-naphthaleneacetic acid and the structure is



In certain embodiments, the ligand is ibuprofen or a structural derivative of ibuprofen. Procedures for the synthesis of ibuprofen can be found in US3,228,831, which is incorporated herein by reference for the methods provided therein. The structure of ibuprofen is



Additional exemplary aralkyl groups are illustrated in US 7,626,014, which is incorporated herein by reference for the methods provided therein.

In another embodiment, suitable lipophilic moieties include lipid, cholesterol, retinoic acid, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-bis-O(hexadecyl)glycerol, geranyloxyhexyanol, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, ibuprofen, naproxen, dimethoxytrityl, or phenoxazine.

In certain embodiments, more than one lipophilic moiety can be incorporated into the double-strand RNAi agent, particularly when the lipophilic moiety has a low lipophilicity or hydrophobicity. In some embodiments, two or more lipophilic moieties are incorporated into the same strand of the double-strand RNAi agent. In some embodiments, each strand of the double-strand RNAi agent has one or more lipophilic moieties incorporated. In some embodiments, two or more lipophilic moieties are incorporated into the same position (*i.e.*, the same nucleobase, same sugar moiety, or same internucleosidic linkage) of the double-strand RNAi agent. This can be achieved by, *e.g.,* conjugating the two or more lipophilic moieties via a carrier, or conjugating the two or more lipophilic moieties via a branched linker, or conjugating the two or more lipophilic moieties via one or more linkers, with one or more linkers linking the lipophilic moieties consecutively.

The lipophilic moiety may be conjugated to the RNAi agent via a direct attachment to the ribosugar of the RNAi agent. Alternatively, the lipophilic moiety may be conjugated to the double-strand RNAi agent via a linker or a carrier.

In certain embodiments, the lipophilic moiety may be conjugated to the RNAi agent via one or more linkers (tethers).

In some embodiments, the lipophilic moiety is conjugated to the double-stranded RNAi agent via a linker containing an ether, thioether, urea, carbonate, amine, amide, maleimide-thioether, disulfide, phosphodiester, sulfonamide linkage, a product of a click reaction (*e.g.,* a triazole from the azide-alkyne cycloaddition), or carbamate.

2. *Lipid Conjugates*

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

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

In some embodiments, the lipid-based ligand binds HSA. For example, the ligand can bind HSA with a sufficient affinity such that distribution of the conjugate to a non-kidney tissue is enhanced. However, the affinity is typically not so strong that the HSA-ligand binding cannot be reversed.

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

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

3. *Cell Permeation Agents*

In another aspect, the ligand is a cell-permeation agent, such as a helical cell-permeation agent. In some embodiments, the agent is amphipathic. An exemplary agent is a peptide such as tat or

antennopedia. If the agent is a peptide, it can be modified, including a peptidylmimetic, invertomers, non-peptide or pseudo-peptide linkages, and use of D-amino acids. The helical agent is typically an α-helical agent, and can have a lipophilic and a lipophobic phase.

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

A peptide or peptidomimetic can be, for example, a cell permeation peptide, cationic peptide, amphipathic peptide, or hydrophobic peptide (*e.g.,* consisting primarily of Tyr, Trp or Phe). The peptide moiety can be a dendrimer peptide, constrained peptide or crosslinked peptide. In another alternative, the peptide moiety can include a hydrophobic membrane translocation sequence (MTS). An exemplary hydrophobic MTS-containing peptide is RFGF having the amino acid sequence AAVALLPAVLLALLAP (SEQ ID NO: 9). An RFGF analogue (*e.g.,* amino acid sequence AALLPVLLAAP (SEQ ID NO: 10)) containing a hydrophobic MTS can also be a targeting moiety. The peptide moiety can be a "delivery" peptide, which can carry large polar molecules including peptides, oligonucleotides, and protein across cell membranes. For example, sequences from the HIV Tat protein (GRKKRRQRRRPPQ (SEQ ID NO: 11)) and the *Drosophila Antennapedia* protein (RQIKIWFQNRRMKWKK (SEQ ID NO: 12)) have been found to be capable of functioning as delivery peptides. A peptide or peptidomimetic can be encoded by a random sequence of DNA, such as a peptide identified from a phage-display library, or one-bead-one-compound (OBOC) combinatorial library (Lam *et al.*, *Nature*, 354:82-84, 1991). Typically, the peptide or peptidomimetic tethered to a dsRNA agent via an incorporated monomer unit is a cell targeting peptide such as an arginine-glycine-aspartic acid (RGD)-peptide, or RGD mimic. A peptide moiety can range in length from about 5 amino acids to about 40 amino acids. The peptide moieties can have a structural modification, such as to increase stability or direct conformational properties. Any of the structural modifications described below can be utilized.

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

An RGD peptide moiety can be used to target a particular cell type, *e.g.,* a tumor cell, such as an endothelial tumor cell or a breast cancer tumor cell (Zitzmann *et al.*, *Cancer Res.*, 62:5139-43, 2002). An RGD peptide can facilitate targeting of an dsRNA agent to tumors of a variety of other tissues, including the lung, kidney, spleen, or liver (Aoki *et al.*, *Cancer Gene Therapy* 8:783-787,

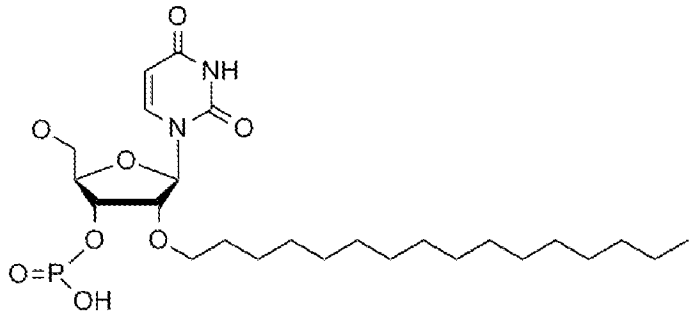
2001). Typically, the RGD peptide will facilitate targeting of an iRNA agent to the kidney. The RGD peptide can be linear or cyclic, and can be modified, *e.g.,* glycosylated or methylated to facilitate targeting to specific tissues. For example, a glycosylated RGD peptide can deliver a iRNA agent to a tumor cell expressing $\alpha_V\beta_3$ (Haubner *et al.*, *Jour. Nucl. Med.*, 42:326-336, 2001).

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

4. *Carbohydrate Conjugates and Ligands*

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

In certain embodiments, the compositions and methods of the disclosure include a C16 ligand. In exemplary embodiments, the C16 ligand of the disclosure has the following structure (exemplified here below for a uracil base, yet attachment of the C16 ligand is contemplated for a nucleotide presenting any base (C, G, A, etc.) or possessing any other modification as presented herein, provided that 2' ribo attachment is preserved) and is attached at the 2' position of the ribo within a residue that is so modified:



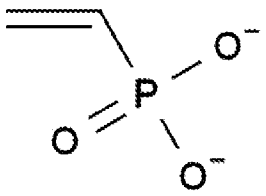
Chemical Formula: $C_{25}H_{43}N_2O_8P$
Exact Mass: 530.2757
Molecular Weight: 530.5913

As shown above, a C16 ligand-modified residue presents a straight chain alkyl at the 2'-ribo position of an exemplary residue (here, a Uracil) that is so modified.

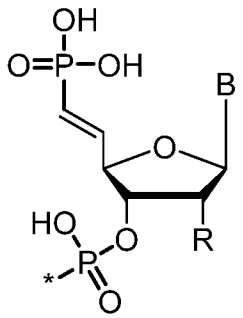
In some embodiments, a carbohydrate conjugate of a RNAi agent of the instant disclosure further comprises one or more additional ligands as described above, such as, but not limited to, a PK modulator or a cell permeation peptide.

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

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



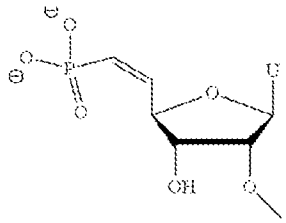
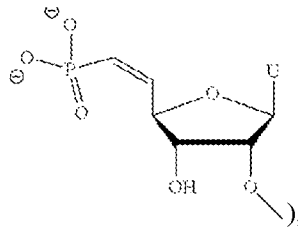
For example, when the phosphate mimic is a 5'-E-vinyl phosphonate (VP), the 5'-terminal nucleotide can have the following structure,



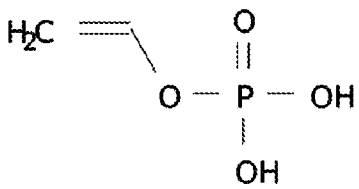
wherein * indicates the location of the bond to 5'-position of the adjacent nucleotide;

R is hydrogen, hydroxy, methoxy, fluoro (e.g., hydroxy or methoxy), or another modification described herein; and

B is a nucleobase or a modified nucleobase, optionally where B is adenine, guanine, cytosine, thymine or uracil.

A vinyl phosponate of the instant disclosure may be attached to either the antisense or the sense strand of a dsRNA of the disclosure. In certain embodiments, a vinyl phosphonate of the instant disclosure is attached to the antisense strand of a dsRNA, optionally at the 5' end of the antisense strand of the dsRNA. The dsRNA agent can comprise a phosphorus-containing group at the 5'-end of the sense strand or antisense strand. The 5'-end phosphorus-containing group can be 5'-end phosphate (5'-P), 5'-end phosphorothioate (5'-PS), 5'-end phosphorodithioate (5'-PS2), 5'-end vinylphosphonate (5'-VP), 5'-end methylphosphonate (MePhos), or 5'-deoxy-5'-C-malonyl. When the 5'-end phosphorus-containing group is 5'-end vinylphosphonate (5'-VP), the 5'-VP can be either 5'-E-VP isomer (i.e., trans-vinylphosphonate, ), 5'-Z-VP isomer (i.e., cis-vinylphosphonate, ), or mixtures thereof.

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



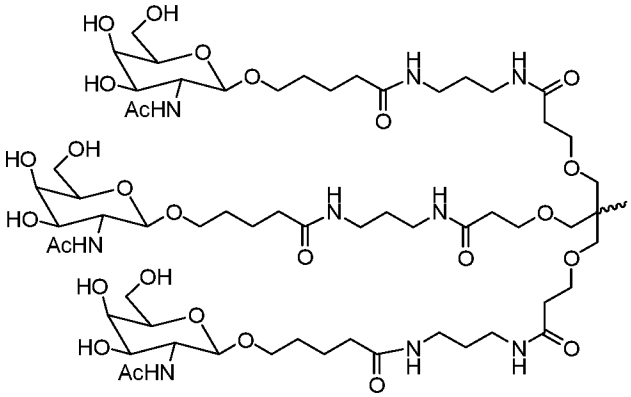
For example, when the phosphate mimic is a 5'-vinyl phosphate, the 5'-terminal nucleotide can have the immediately structure, where the phosphonate group is replaced by a phosphate.

In some embodiments, a carbohydrate conjugate comprises a monosaccharide. In some embodiments, the monosaccharide is an N-acetylgalactosamine (GalNAc). GalNAc conjugates, which comprise one or more N-acetylgalactosamine (GalNAc) derivatives, are described, for example, in U.S. Patent No. 8,106,022, the entire content of which is hereby incorporated herein by reference. In some embodiments, the GalNAc conjugate serves as a ligand that targets the iRNA to particular cells.

In some embodiments, the GalNAc conjugate targets the iRNA to liver cells, *e.g.,* by serving as a ligand for the asialoglycoprotein receptor of liver cells (*e.g.,* hepatocytes).

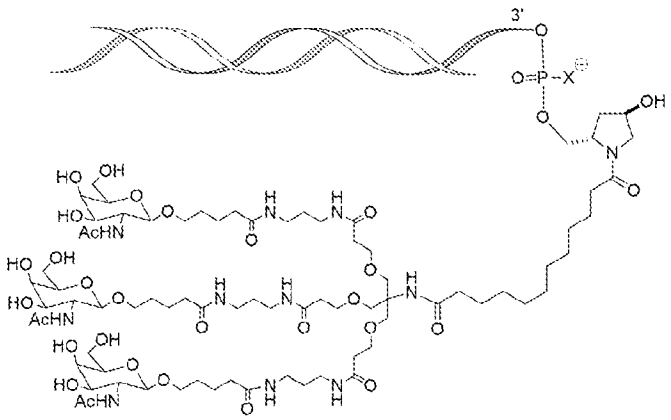
In some embodiments, the carbohydrate conjugate comprises one or more GalNAc derivatives. The GalNAc derivatives may be attached via a linker, *e.g.,* a bivalent or trivalent branched linker. In some embodiments the GalNAc conjugate is conjugated to the 3' end of the sense strand. In some embodiments,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

In some embodiments, the GalNAc conjugate is

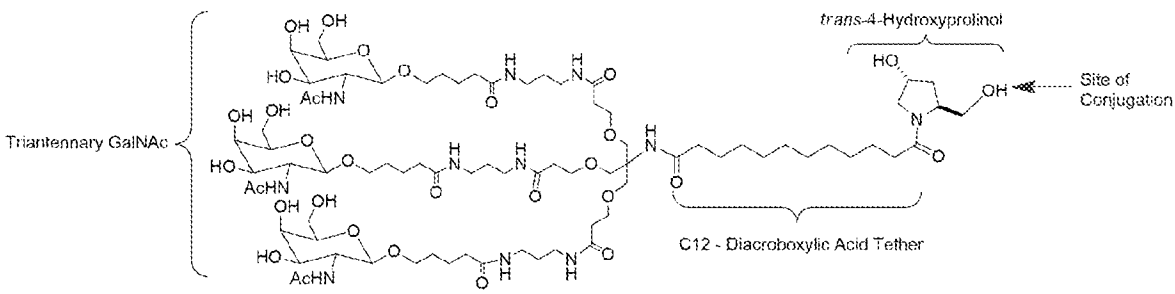


Formula II.

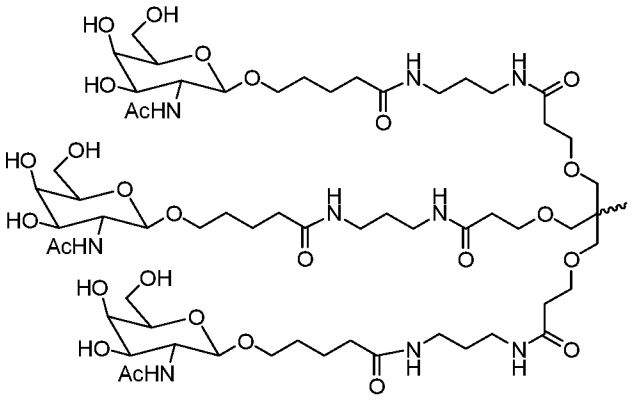
In some embodiments, the RNAi agent is attached to the carbohydrate conjugate via a linker as shown in the following schematic, wherein X is O or S:



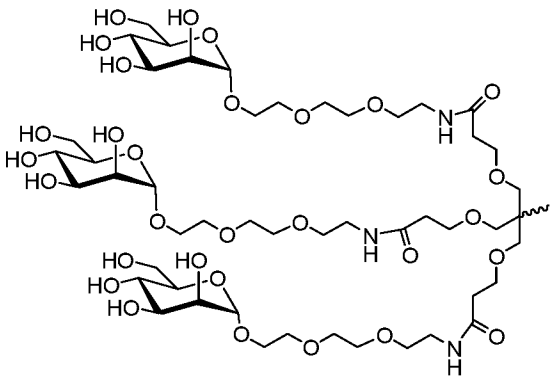
In some embodiments, the RNAi agent is conjugated to L96 as defined in Table 1 and shown below:



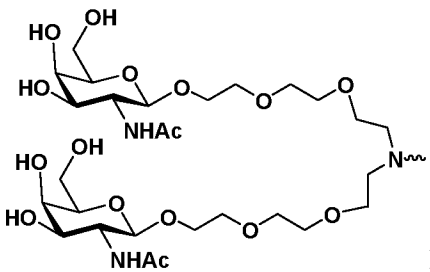
In some embodiments, a carbohydrate conjugate for use in the compositions and methods of the disclosure is selected from the group consisting of:



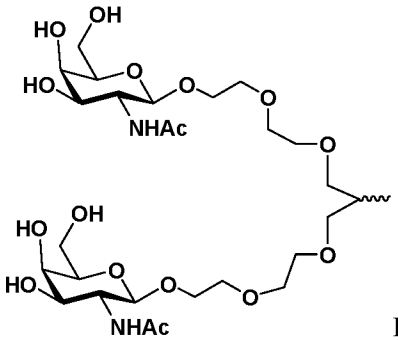
Formula II,



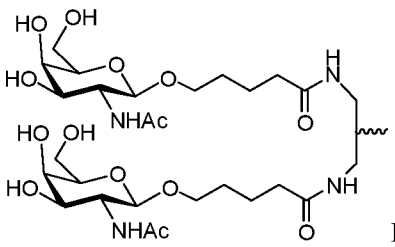
Formula III,



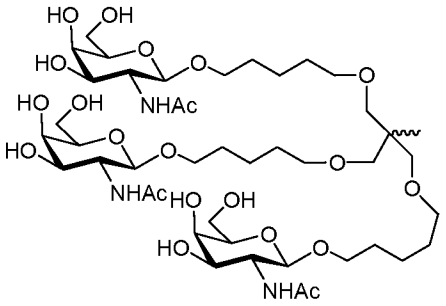
Formula IV,



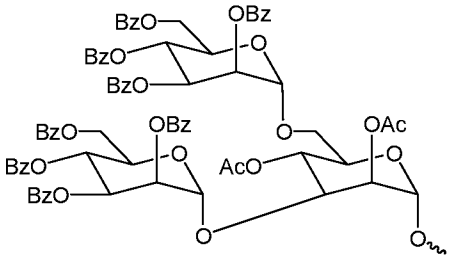
Formula V,



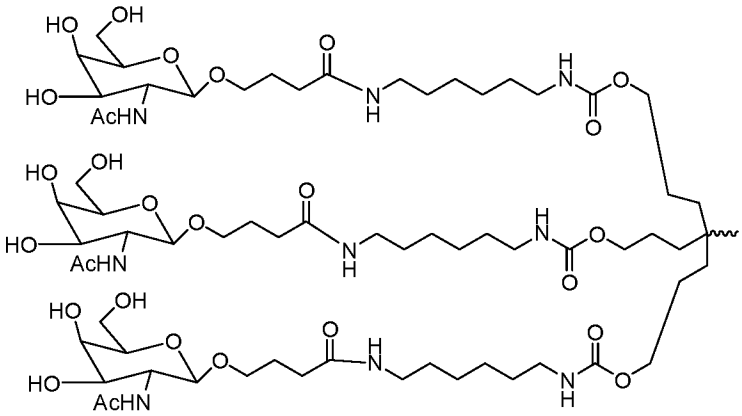
Formula VI,



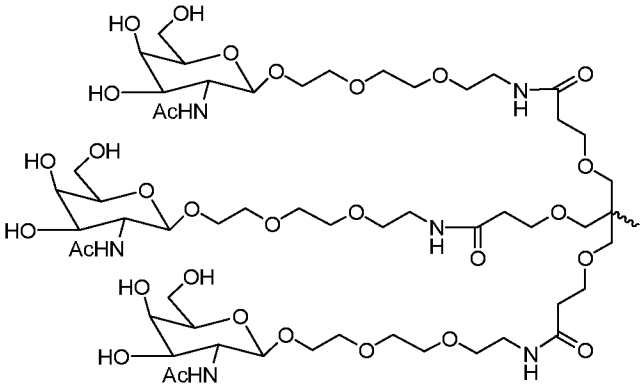
Formula VII,



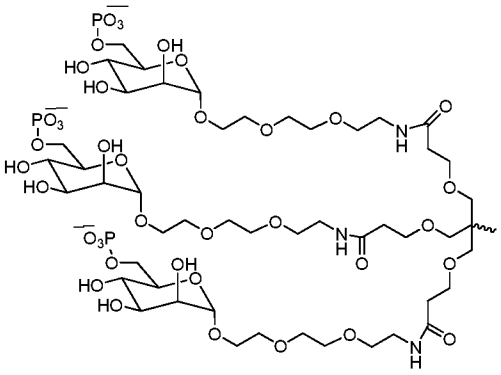
Formula VIII,



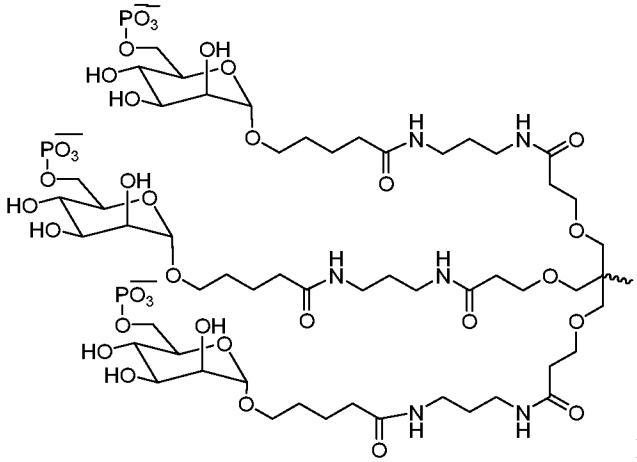
Formula IX,



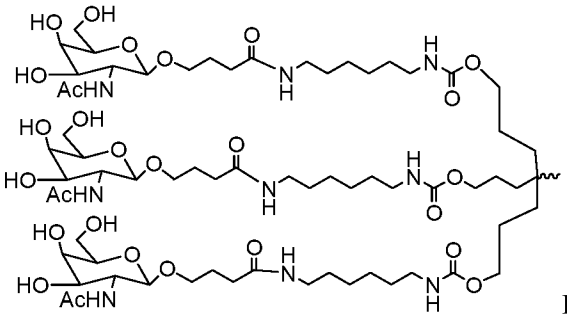
Formula X,



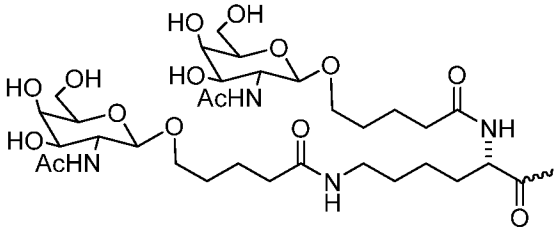
Formula XI,



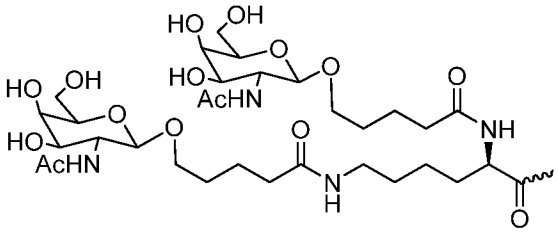
Formula XII,



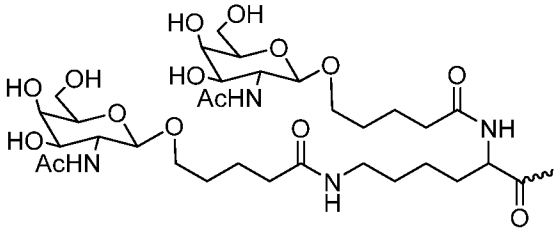
Formula XIII,



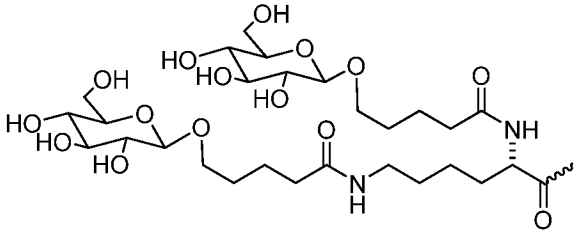
Formula XIV,



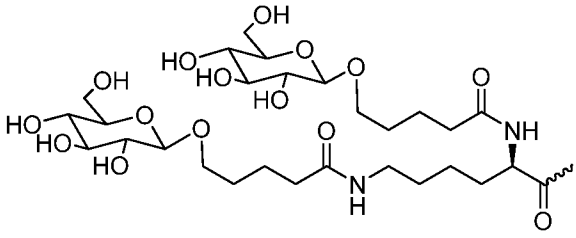
Formula XV,



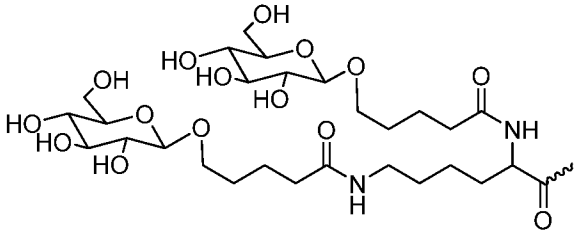
Formula XVI,



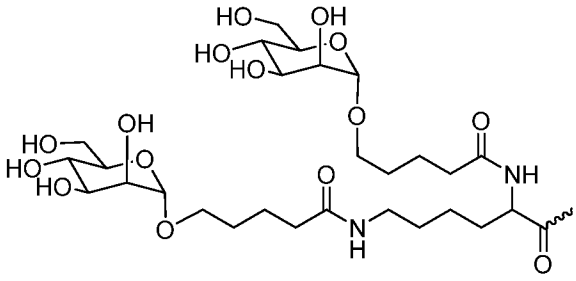
Formula XVII,



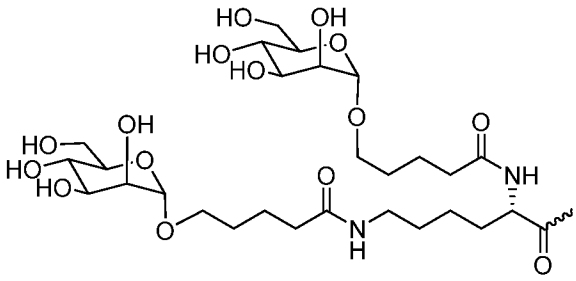
Formula XVIII,



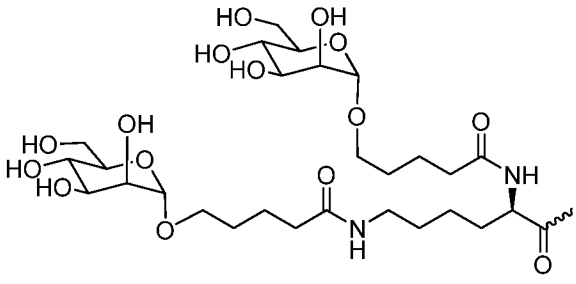
Formula XIX,



Formula XX,

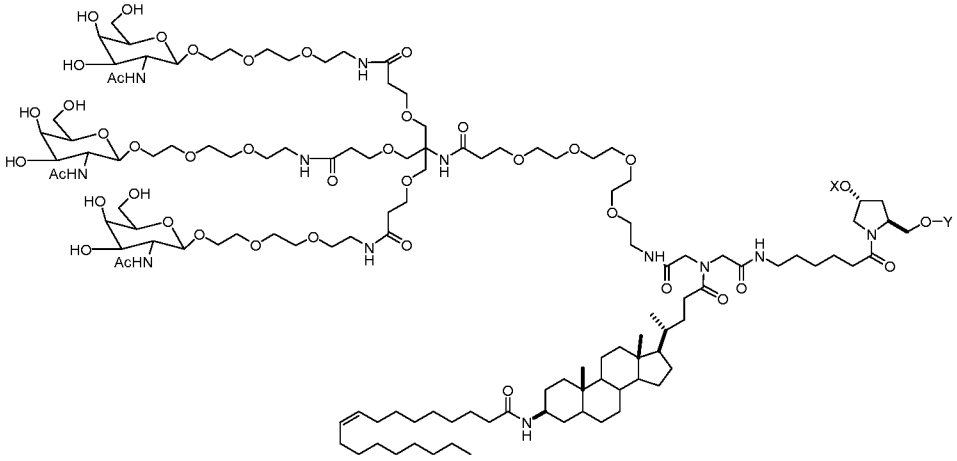


Formula XXI,



Formula XXII.

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

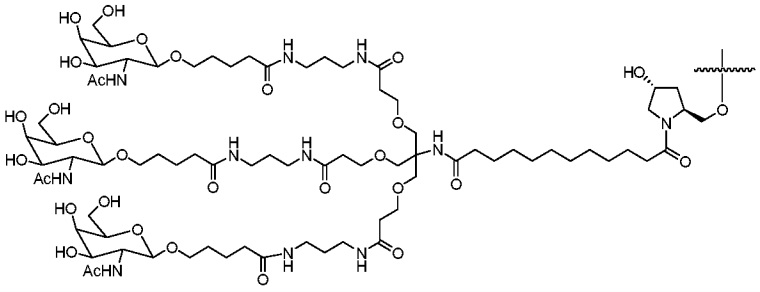


(Formula XXIII),

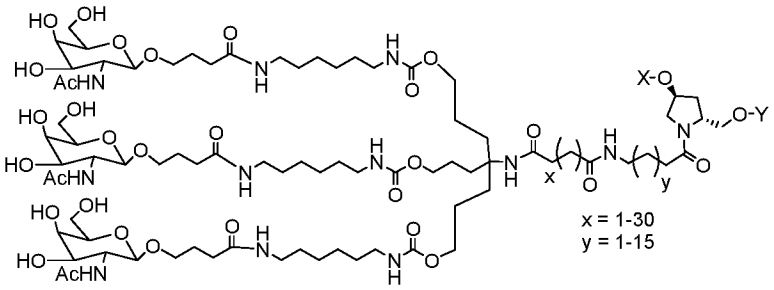
when one of X or Y is an oligonucleotide, the other is a hydrogen.

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

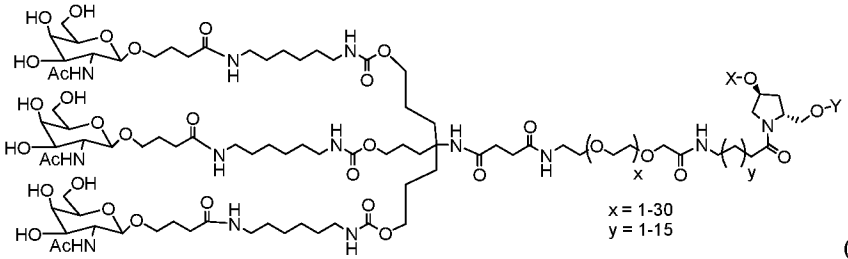
In some embodiments, an iRNA of the disclosure is conjugated to a carbohydrate through a linker. Non-limiting examples of iRNA carbohydrate conjugates with linkers of the compositions and methods of the disclosure include, but are not limited to,



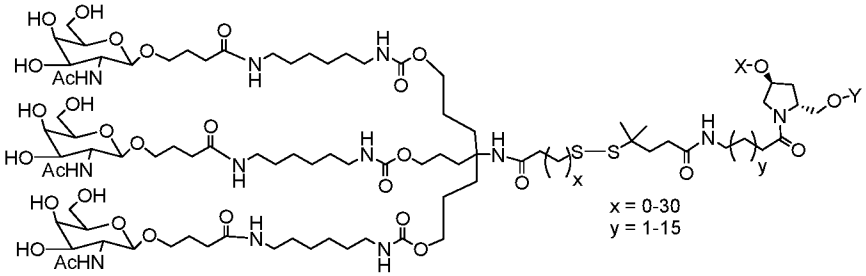
(Formula XXIV),



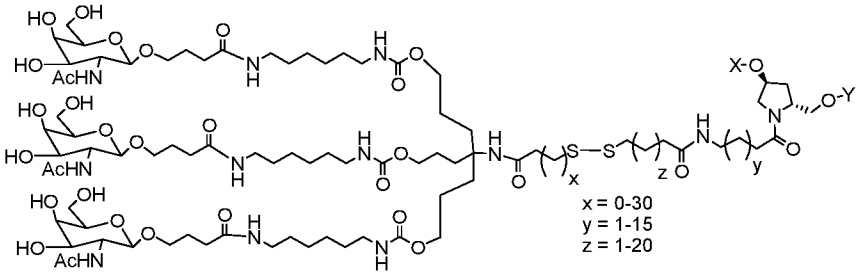
(Formula XXV),



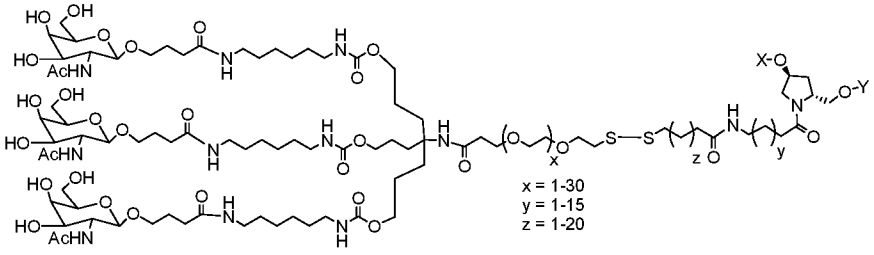
(Formula XXVI),



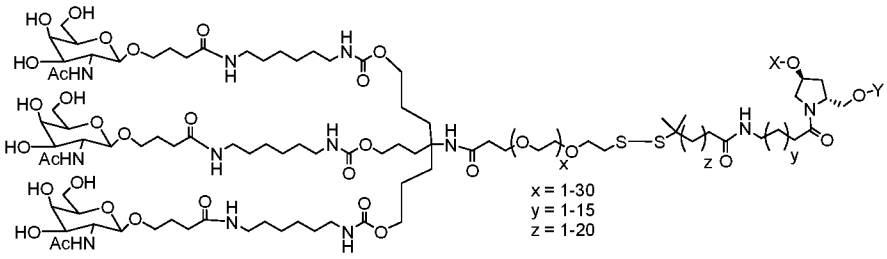
(Formula XXVII),



(Formula XXVIII),



(Formula XXIX), and



(Formula XXX),

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

5. *Thermally Destabilizing Modifications*

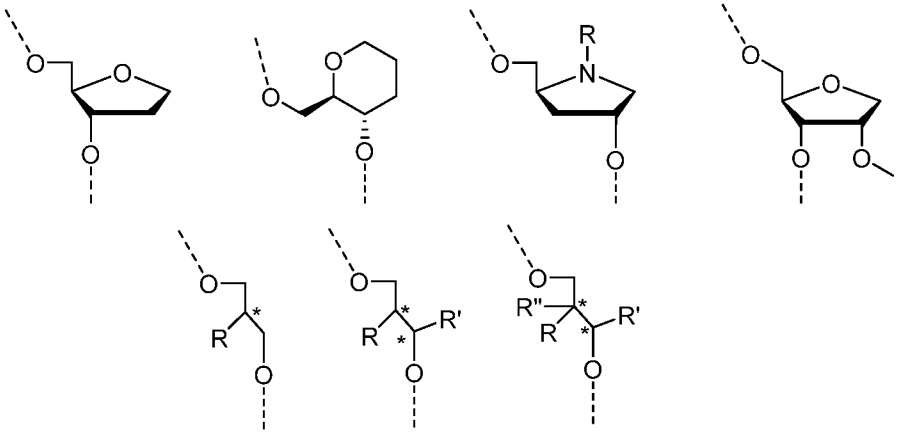
In certain embodiments, a dsRNA molecule can be optimized for RNA interference by incorporating thermally destabilizing modifications in the seed region of the antisense strand. As used herein "seed region" means at positions 2-9 of the 5'-end of the referenced strand. For example, thermally destabilizing modifications can be incorporated in the seed region of the antisense strand to reduce or inhibit off-target gene silencing.

The term "thermally destabilizing modification(s)" includes modification(s) that would result with a dsRNA with a lower overall melting temperature (Tm) than the Tm of the dsRNA without having such modification(s). For example, the thermally destabilizing modification(s) can decrease the T_m of the dsRNA by 1 – 4 °C, such as one, two, three or four degrees Celcius. And, the term "thermally destabilizing nucleotide" refers to a nucleotide containing one or more thermally destabilizing modifications.

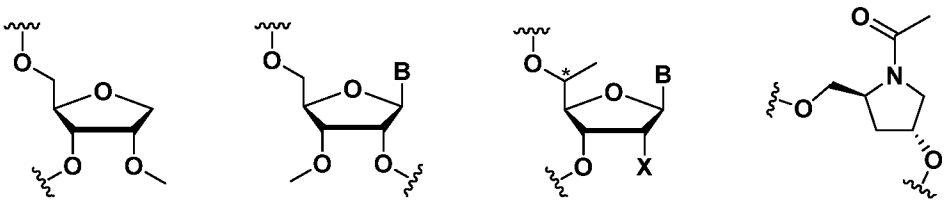
It has been discovered that dsRNAs with an antisense strand comprising at least one thermally destabilizing modification of the duplex within the first 9 nucleotide positions, counting from the 5' end, of the antisense strand have reduced off-target gene silencing activity. Accordingly, in some embodiments, the antisense strand comprises at least one (*e.g.,* one, two, three, four, five, or more) thermally destabilizing modification of the duplex within the first 9 nucleotide positions of the 5' region of the antisense strand. In some embodiments, one or more thermally destabilizing modification(s) of the duplex is/are located in positions 2-9, or preferably positions 4-8, from the 5'-end of the antisense strand. In some further embodiments, the thermally destabilizing modification(s) of the duplex is/are located at position 6, 7, or 8 from the 5'-end of the antisense strand. In still some further embodiments, the thermally destabilizing modification of the duplex is located at position 7 from the 5'-end of the antisense strand. In some embodiments, the thermally destabilizing modification of the duplex is located at position 2, 3, 4, 5, or 9 from the 5'-end of the antisense strand.

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

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

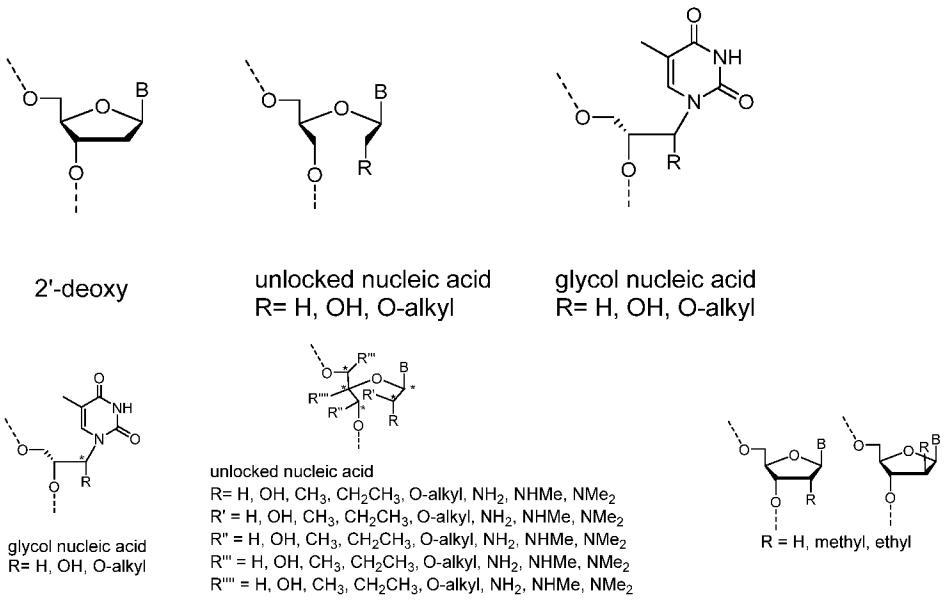


Wherein R = H, Me, Et or OMe; R' = H, Me, Et or OMe; R" = H, Me, Et or OMe



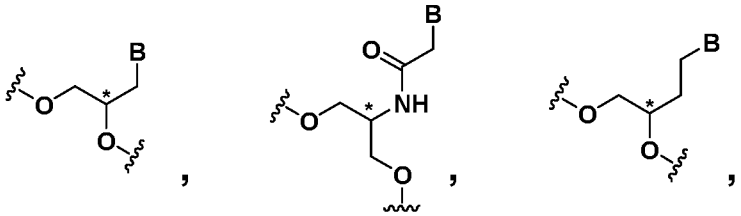
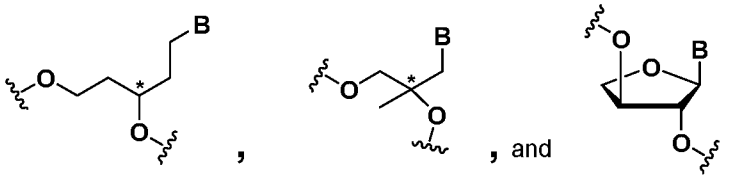
wherein B is a modified or unmodified nucleobase.

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

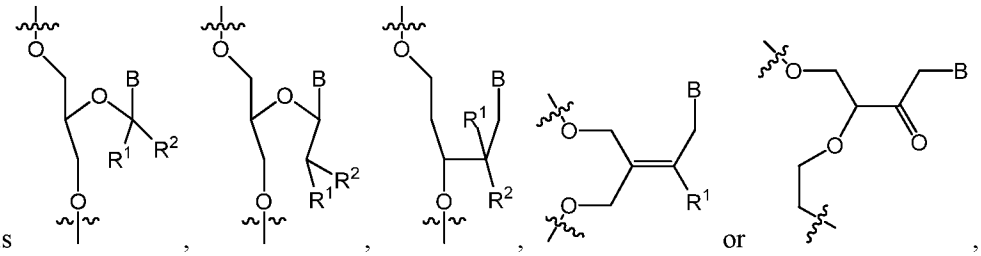


wherein B is a modified or unmodified nucleobase.

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

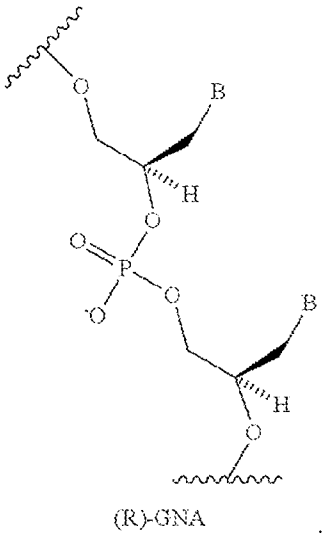



wherein B is a modified or unmodified nucleobase and the asterisk on each structure represents either *R*, *S* or *racemic*.

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

wherein B is a modified or unmodified nucleobase, R^1 and R^2 independently are H, halogen, OR_3, or alkyl; and R_3 is H, alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or sugar). The term "UNA" refers to unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked "sugar" residue. In one example, UNA also encompasses monomers with bonds between C1'-C4' being removed (*i.e.* the covalent carbon-oxygen-carbon bond between the C1' and C4' carbons). In another example, the C2'-C3' bond (*i.e.* the covalent carbon-carbon bond between the C2' and C3' carbons) of the sugar is removed (see Mikhailov *et al.*, 1985 *Tetrahedron Letters* 26 (17):2059; and Fluiter *et al.*, 2009 *Mol. Biosyst.*, 10:1039, which are hereby incorporated by reference in their entirety). The acyclic derivative provides greater backbone flexibility without affecting the Watson-Crick pairings. The acyclic nucleotide can be linked via 2'-5' or 3'-5' linkage.

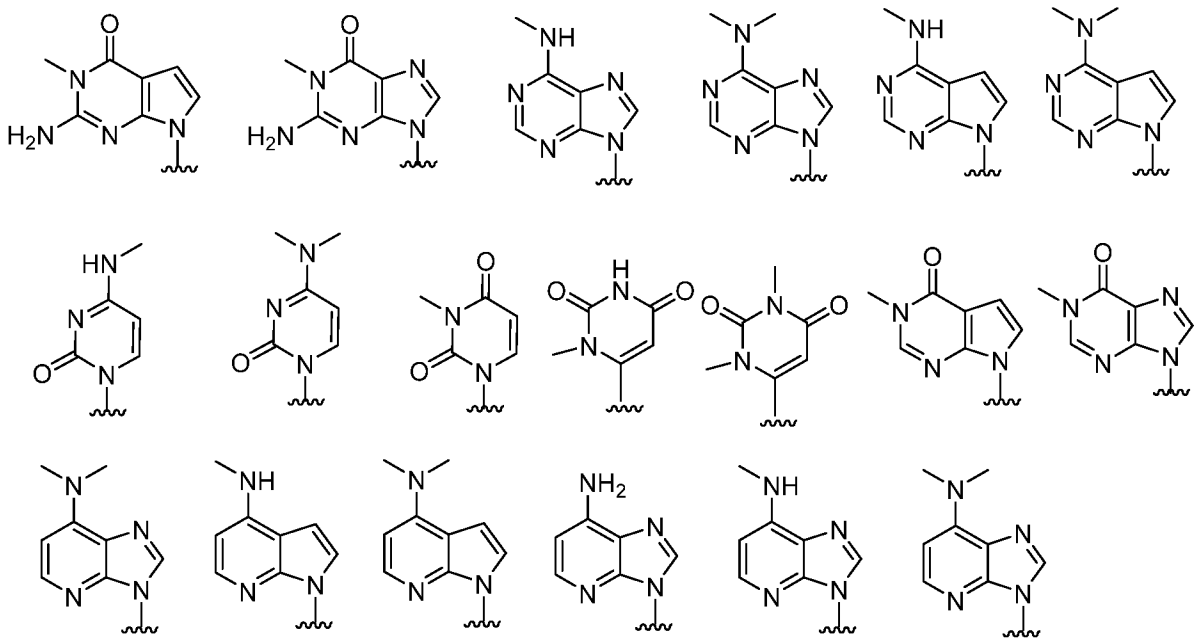
The term 'GNA' refers to glycol nucleic acid which is a polymer similar to DNA or RNA but differing in the composition of its "backbone" in that is composed of repeating glycerol units linked by phosphodiester bonds:



(R)-GNA

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

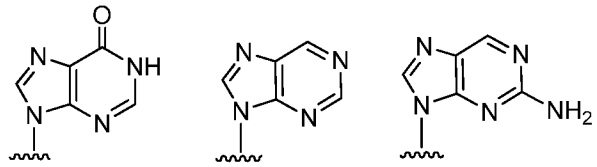
In some embodiments, the thermally destabilizing modification of the duplex in the seed region of the antisense strand includes nucleotides with impaired W-C H-bonding to complementary base on the target mRNA, such as:



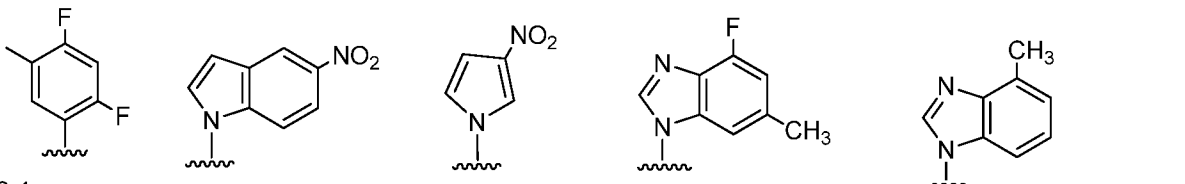
More examples of abasic nucleotide, acyclic nucleotide modifications (including UNA and GNA), and mismatch modifications have been described in detail in WO 2011/133876, which is herein incorporated by reference in its entirety.

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

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

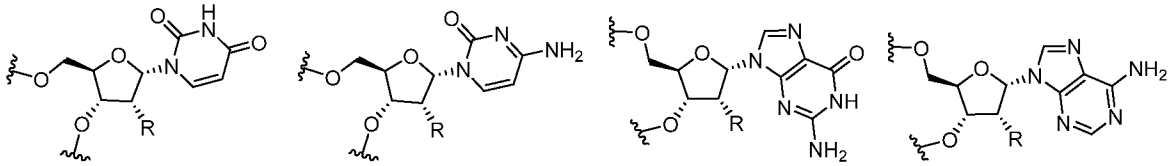


inosine nebularine 2-aminopurine



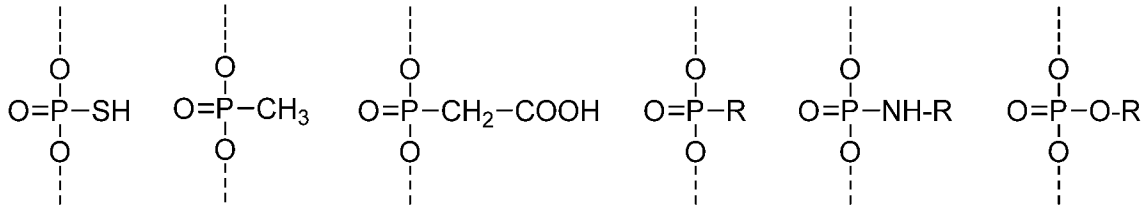
2,4-difluorotoluene 5-nitroindole 3-nitropyrrole 4-Fluoro-6-methylbenzimidazole 4-Methylbenzimidazole.

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



wherein R is H, OH, OCH_3, F, NH_2, NHMe, NMe_2 or O-alkyl.

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



R = alkyl

The alkyl for the R group can be a C_1-C_6alkyl. Specific alkyls for the R group include, but are not limited to methyl, ethyl, propyl, isopropyl, butyl, pentyl and hexyl.

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

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

stabilizing modifications on the sense strand can have a shift relative to the alternating pattern of the stabilizing modifications on the antisense strand.

In some embodiments, the antisense strand comprises at least two (*e.g.,* two, three, four, five, six, seven, eight, nine, ten, or more) stabilizing modifications. Without limitations, a stabilizing modification in the antisense strand can be present at any positions.

In some embodiments, the antisense strand comprises stabilizing modifications at positions 2, 6, 8, 9, 14, and 16 from the 5'-end. In some other embodiments, the antisense strand comprises stabilizing modifications at positions 2, 6, 14, and 16 from the 5'-end. In still some other embodiments, the antisense strand comprises stabilizing modifications at positions 2, 14, and 16 from the 5'-end.

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

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

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

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

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

In some embodiments, the dsRNA of the disclosure comprises at least four (*e.g.,* four, five, six, seven, eight, nine, ten, or more) 2'-fluoro nucleotides. Without limitations, the 2'-fluoro

nucleotides all can be present in one strand. In some embodiments, both the sense and the antisense strands comprise at least two 2'-fluoro nucleotides. The 2'-fluoro modification can occur on any nucleotide of the sense strand or antisense strand. For instance, the 2'-fluoro modification can occur on every nucleotide on the sense strand or antisense strand; each 2'-fluoro modification can occur in an alternating pattern on the sense strand or antisense strand; or the sense strand or antisense strand comprises both 2'-fluoro modifications in an alternating pattern. The alternating pattern of the 2'-fluoro modifications on the sense strand may be the same or different from the antisense strand, and the alternating pattern of the 2'-fluoro modifications on the sense strand can have a shift relative to the alternating pattern of the 2'-fluoro modifications on the antisense strand.

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

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

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

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

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

In some embodiments, the dsRNA molecule of the disclosure comprises a 21 nucleotides (nt) sense strand and a 23 nucleotides (nt) antisense, wherein the antisense strand contains at least one thermally destabilizing nucleotide, where the at least one thermally destabilizing nucleotide occurs in the seed region of the antisense strand (*i.e.*, at position 2-9 of the 5'-end of the antisense strand), wherein one end of the dsRNA is blunt, while the other end is comprises a 2 nt overhang, and wherein the dsRNA optionally further has at least one (*e.g.*, one, two, three, four, five, six, or all seven) of the following characteristics: (i) the antisense comprises 2, 3, 4, 5, or 6 2'-fluoro modifications; (ii) the antisense comprises 1, 2-7 phosphorothioate internucleotide linkages; (iii) the sense strand is conjugated with a ligand; (iv) the sense strand comprises 2-7 2'-fluoro modifications; (v) the sense strand comprises 1, 2-7 phosphorothioate internucleotide linkages; (vi) the dsRNA comprises at least four 2'-fluoro modifications; and (vii) the dsRNA comprises a blunt end at 5'-end of the antisense strand. Preferably, the 2 nt overhang is at the 3'-end of the antisense.

In some embodiments, every nucleotide in the sense strand and antisense strand of the dsRNA molecule may be modified. Each nucleotide may be modified with the same or different modification which can include one or more alteration of one or both of the non-linking phosphate oxygens or of one or more of the linking phosphate oxygens; alteration of a constituent of the ribose sugar, *e.g.*, of the 2′ hydroxyl on the ribose sugar; wholesale replacement of the phosphate moiety with "dephospho" linkers; modification or replacement of a naturally occurring base; and replacement or modification of the ribose-phosphate backbone.

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

It may be possible, *e.g.*, to enhance stability, to include particular bases in overhangs, or to include modified nucleotides or nucleotide surrogates, in single strand overhangs, *e.g.*, in a 5' or 3' overhang, or in both. *E.g.*, it can be desirable to include purine nucleotides in overhangs. In some

embodiments all or some of the bases in a 3' or 5' overhang may be modified, *e.g.,* with a modification described herein. Modifications can include, *e.g.,* the use of modifications at the 2' position of the ribose sugar with modifications that are known in the art, *e.g.,* the use of deoxyribonucleotides, 2'-deoxy-2'-fluoro (2'-F) or 2'-O-methyl modified instead of the ribosugar of the nucleobase, and modifications in the phosphate group, *e.g.,* phosphorothioate modifications. Overhangs need not be homologous with the target sequence.

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

At least two different modifications are typically present on the sense strand and antisense strand. Those two modifications may be the 2'-deoxy, 2'- O-methyl, or 2'-fluoro modifications, acyclic nucleotides or others. In some embodiments, the sense strand and antisense strand each comprises two differently modified nucleotides selected from 2'-O-methyl or 2'-deoxy. In some embodiments, each residue of the sense strand and antisense strand is independently modified with 2'-O-methyl nucleotide, 2'-deoxy nucleotide, 2′-deoxy-2'-fluoro nucleotide, 2'-O-N-methylacetamido (2'-O-NMA) nucleotide, a 2'-O-dimethylaminoethoxyethyl (2'-O-DMAEOE) nucleotide, 2'-O-aminopropyl (2'-O-AP) nucleotide, or 2'-ara-F nucleotide. Again, it is to be understood that these modifications are in addition to the at least one thermally destabilizing modification of the duplex present in the antisense strand.

In some embodiments, the dsRNA molecule of the disclosure comprises modifications of an alternating pattern, particular in the B1, B2, B3, B1', B2', B3', B4' regions. The term "alternating motif" or "alternative pattern" as used herein refers to a motif having one or more modifications, each modification occurring on alternating nucleotides of one strand. The alternating nucleotide may refer to one per every other nucleotide or one per every three nucleotides, or a similar pattern. For example, if A, B and C each represent one type of modification to the nucleotide, the alternating motif can be "ABABABABABAB…," "AABBAABBAABB…," "AABAABAABAAB…," "AAABAAABAAAB…," "AAABBBAAABBB…," or "ABCABCABCABC…," etc.

The type of modifications contained in the alternating motif may be the same or different. For example, if A, B, C, D each represent one type of modification on the nucleotide, the alternating pattern, *i.e.*, modifications on every other nucleotide, may be the same, but each of the sense strand or antisense strand can be selected from several possibilities of modifications within the alternating motif such as "ABABAB…", "ACACAC…" "BDBDBD…" or "CDCDCD…," etc.

In some embodiments, the dsRNA molecule of the disclosure comprises the modification pattern for the alternating motif on the sense strand relative to the modification pattern for the

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

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

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

In some embodiments, the sense strand of the dsRNA molecule comprises 1-10 blocks of two to ten phosphorothioate or methylphosphonate internucleotide linkages separated by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 phosphate internucleotide linkages, wherein one of the phosphorothioate or methylphosphonate internucleotide linkages is placed at any position in the

oligonucleotide sequence and the said sense strand is paired with an antisense strand comprising any combination of phosphorothioate, methylphosphonate, and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

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

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

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

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

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

phosphorothioate, methylphosphonate, and phosphate internucleotide linkages or an antisense strand comprising either phosphorothioate or methylphosphonate or phosphate linkage.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

In some embodiments, the dsRNA molecule of the disclosure further comprises two phosphorothioate internucleotide linkage modifications at position 1 and 2, and two phosphorothioate internucleotide linkage modifications at position 20 and 21 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and one at position 21 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises one phosphorothioate internucleotide linkage modification at position 1, and one phosphorothioate internucleotide linkage modification at position 21 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications at positions 20 and 21 the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises two phosphorothioate internucleotide linkage modifications at position 1 and 2, and two phosphorothioate internucleotide linkage modifications at position 21 and 22 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and one phosphorothioate internucleotide linkage modification at position 21 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises one phosphorothioate internucleotide linkage modification at position 1, and one phosphorothioate internucleotide linkage modification at position 21 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications at positions 21 and 22 the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises two phosphorothioate internucleotide linkage modifications at position 1 and 2, and two phosphorothioate internucleotide linkage modifications at position 22 and 23 of the sense strand (counting from the 5'-end), and one phosphorothioate internucleotide linkage modification at positions 1 and one phosphorothioate internucleotide linkage modification at position 21 of the antisense strand (counting from the 5'-end).

In some embodiments, the dsRNA molecule of the disclosure further comprises one phosphorothioate internucleotide linkage modification at position 1, and one phosphorothioate internucleotide linkage modification at position 21 of the sense strand (counting from the 5'-end), and two phosphorothioate internucleotide linkage modifications at positions 1 and 2 and two phosphorothioate internucleotide linkage modifications at positions 23 and 23 the antisense strand (counting from the 5'-end).

In some embodiments, compound of the disclosure comprises a pattern of backbone chiral centers. In some embodiments, a common pattern of backbone chiral centers comprises at least 5 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 6 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 7 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 8 internucleotidic linkages in the Sp configuration. In some embodiments, a

common pattern of backbone chiral centers comprises at least 9 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 10 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 11 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 12 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 13 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 14 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 15 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 16 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 17 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 18 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises at least 19 internucleotidic linkages in the Sp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 8 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 7 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 6 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 5 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 4 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 3 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 2 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 1 internucleotidic linkages in the Rp configuration. In some embodiments, a common pattern of backbone chiral centers comprises no more than 8 internucleotidic linkages which are not chiral (as a non-limiting example, a phosphodiester). In some embodiments, a common pattern of backbone chiral centers comprises no more than 7 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 6 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 5 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 4 internucleotidic linkages which are not chiral. In some embodiments, a common pattern of backbone chiral centers comprises no more than 3 internucleotidic linkages which are not chiral. In

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

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

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

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

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

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

In some embodiments, the dsRNA molecule of the disclosure comprises at least one of the first 1, 2-7 base pairs within the duplex regions from the 5'- end of the antisense strand can be chosen independently from the group of: A:U, G:U, I:C, and mismatched pairs, *e.g.,* non-canonical or other than canonical pairings or pairings which include a universal base, to promote the dissociation of the antisense strand at the 5'-end of the duplex.

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

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

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

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

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

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

In some embodiments, 4'-*O*-alkylated nucleoside is introduced at any position on the sense strand or antisense strand of a dsRNA, and such modification maintains or improves potency of the

dsRNA. The 5'-alkyl can be either racemic or chirally pure *R* or *S* isomer. An exemplary 4'-*O*-alkylated nucleoside is 4'-*O*-methyl nucleoside. The 4'-*O*-methyl can be either racemic or chirally pure *R* or *S* isomer.

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

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

Various publications describe multimeric siRNA which can all be used with the dsRNA of the disclosure. Such publications include WO2007/091269, US 7858769, WO2010/141511, WO2007/117686, WO2009/014887, and WO2011/031520 which are hereby incorporated by their entirely.

In some embodiments dsRNA molecules of the disclosure are 5' phosphorylated or include a phosphoryl analog at the 5' prime terminus. 5'-phosphate modifications include those which are compatible with RISC mediated gene silencing. Suitable modifications include: 5'-monophosphate ($(HO)_2(O)P$-O-5'); 5'-diphosphate ($(HO)_2(O)P$-O-P(HO)(O)-O-5'); 5'-triphosphate ($(HO)_2(O)P$-O-(HO)(O)P-O-P(HO)(O)-O-5'); 5'-guanosine cap (7-methylated or non-methylated) (7m-G-O-5'-(HO)(O)P-O-(HO)(O)P-O-P(HO)(O)-O-5'); 5'-adenosine cap (Appp), and any modified or unmodified nucleotide cap structure (N-O-5'-(HO)(O)P-O-(HO)(O)P-O-P(HO)(O)-O-5'); 5'-monothiophosphate (phosphorothioate; $(HO)_2(S)P$-O-5'); 5'-monodithiophosphate (phosphorodithioate; (HO)(HS)(S)P-O-5'), 5'-phosphorothiolate ((HO)2(O)P-S-5'); any additional combination of oxygen/sulfur replaced monophosphate, diphosphate and triphosphates (*e.g.* 5'-alpha-thiotriphosphate, 5'-gamma-thiotriphosphate, etc.), 5'-phosphoramidates ($(HO)_2(O)P$-NH-5', $(HO)(NH_2)(O)P$-O-5'), 5'-alkylphosphonates (R=alkyl=methyl, ethyl, isopropyl, propyl, etc., *e.g.* RP(OH)(O)-O-5'-, 5'-alkenylphosphonates (*i.e.* vinyl, substituted vinyl), $(OH)_2(O)P$-5'-CH2-), 5'-alkyletherphosphonates (R=alkylether=methoxymethyl (MeOCH2-), ethoxymethyl, etc., *e.g.* RP(OH)(O)-O-5'-). In one example, the modification can in placed in the antisense strand of a dsRNA molecule.

6. *Linkers*

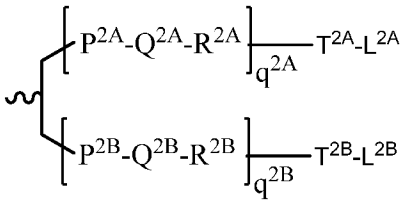
In some embodiments, the conjugate or ligand described herein can be attached to an iRNA oligonucleotide with various linkers that can be cleavable or non-cleavable.

Linkers typically comprise a direct bond or an atom such as oxygen or sulfur, a unit such as NR8, C(O), C(O)NH, SO, SO_2, SO_2NH or a chain of atoms, such as, but not limited to, substituted or unsubstituted alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl,

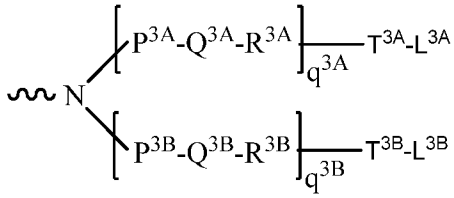
arylalkyl, arylalkenyl, arylalkynyl, heteroarylalkyl, heteroarylalkenyl, heteroarylalkynyl, heterocyclylalkyl, heterocyclylalkenyl, heterocyclylalkynyl, aryl, heteroaryl, heterocyclyl, cycloalkyl, cycloalkenyl, alkylarylalkyl, alkylarylalkenyl, alkylarylalkynyl, alkenylarylalkyl, alkenylarylalkenyl, alkenylarylalkynyl, alkynylarylalkyl, alkynylarylalkenyl, alkynylarylalkynyl, alkylheteroarylalkyl, alkylheteroarylalkenyl, alkylheteroarylalkynyl, alkenylheteroarylalkyl, alkenylheteroarylalkenyl, alkenylheteroarylalkynyl, alkynylheteroarylalkyl, alkynylheteroarylalkenyl, alkynylheteroarylalkynyl, alkylheterocyclylalkyl, alkylheterocyclylalkenyl, alkylhererocyclylalkynyl, alkenylheterocyclylalkyl, alkenylheterocyclylalkenyl, alkenylheterocyclylalkynyl, alkynylheterocyclylalkyl, alkynylheterocyclylalkenyl, alkynylheterocyclylalkynyl, alkylaryl, alkenylaryl, alkynylaryl, alkylheteroaryl, alkenylheteroaryl, alkynylhereroaryl, which one or more methylenes can be interrupted or terminated by O, S, S(O), SO_2, N(R8), C(O), substituted or unsubstituted aryl, substituted or unsubstituted heteroaryl, substituted or unsubstituted heterocyclic; where R8 is hydrogen, acyl, aliphatic or substituted aliphatic. In some embodiments, the linker is between about 1-24 atoms, 2-24, 3-24, 4-24, 5-24, 6-24, 6-18, 7-18, 8-18 atoms, 7-17, 8-17, 6-16, 7-16, or 8-16 atoms.

In some embodiments, a dsRNA of the disclosure is conjugated to a bivalent or trivalent branched linker selected from the group of structures shown in any of formula (XXXI) – (XXXIV):

Formula XXXI

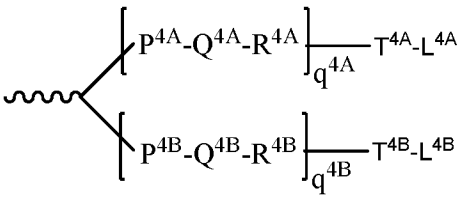


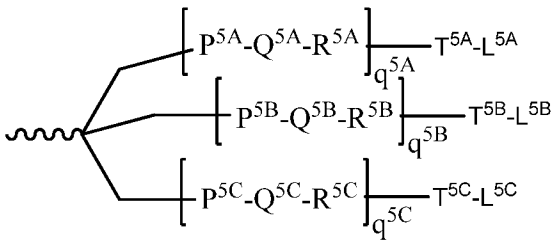
Formula XXXII



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Formula XXXIII , Formula XXXIV;

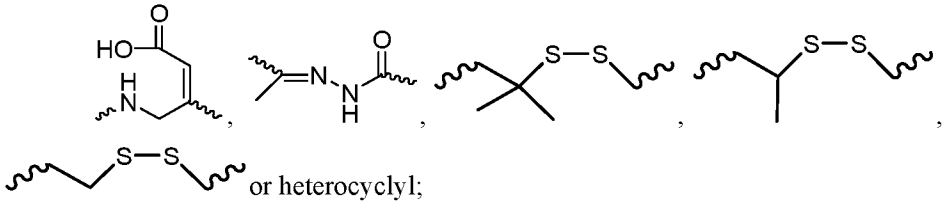
wherein:

q2A, q2B, q3A, q3B, q4A, q4B, q5A, q5B and q5C represent independently for each occurrence 0-20 and wherein the repeating unit can be the same or different;

P^{2A}, P^{2B}, P^{3A}, P^{3B}, P^{4A}, P^{4B}, P^{5A}, P^{5B}, P^{5C}, T^{2A}, T^{2B}, T^{3A}, T^{3B}, T^{4A}, T^{4B}, T^{4A}, T^{5B}, T^{5C} are each independently for each occurrence absent, CO, NH, O, S, OC(O), NHC(O), CH_2, CH_2NH or CH_2O;

Q^{2A}, Q^{2B}, Q^{3A}, Q^{3B}, Q^{4A}, Q^{4B}, Q^{5A}, Q^{5B}, Q^{5C} are independently for each occurrence absent, alkylene, substituted alkylene wherein one or more methylenes can be interrupted or terminated by one or more of O, S, S(O), SO_2, $N(R^N)$, C(R')=C(R''), C≡C or C(O);

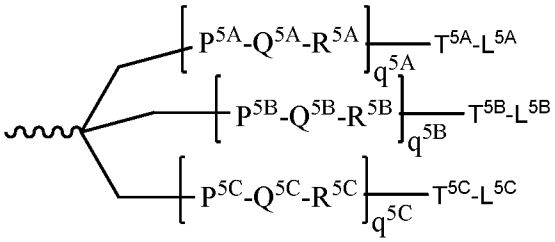
R^{2A}, R^{2B}, R^{3A}, R^{3B}, R^{4A}, R^{4B}, R^{5A}, R^{5B}, R^{5C} are each independently for each occurrence absent, NH, O, S, CH_2, C(O)O, C(O)NH, $NHCH(R^a)C(O)$, -C(O)-$CH(R^a)$-NH-, CO, CH=N-O,



or heterocyclyl;

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

Formula XXXV



,

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

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

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

Cleavable linking groups are susceptible to cleavage agents, *e.g.,* pH, redox potential or the presence of degradative molecules. Generally, cleavage agents are more prevalent or found at higher levels or activities inside cells than in serum or blood. Examples of such degradative agents include: redox agents which are selected for particular substrates or which have no substrate specificity,

including, *e.g.,* oxidative or reductive enzymes or reductive agents such as mercaptans, present in cells, that can degrade a redox cleavable linking group by reduction; esterases; endosomes or agents that can create an acidic environment, *e.g.,* those that result in a pH of five or lower; enzymes that can hydrolyze or degrade an acid cleavable linking group by acting as a general acid, peptidases (which can be substrate specific), and phosphatases.

A cleavable linkage group, such as a disulfide bond can be susceptible to pH. The pH of human serum is 7.4, while the average intracellular pH is slightly lower, ranging from about 7.1-7.3. Endosomes have a more acidic pH, in the range of 5.5-6.0, and lysosomes have an even more acidic pH at around 5.0. Some linkers will have a cleavable linking group that is cleaved at a suitable pH, thereby releasing a cationic lipid from the ligand inside the cell, or into the desired compartment of the cell.

A linker can include a cleavable linking group that is cleavable by a particular enzyme. The type of cleavable linking group incorporated into a linker can depend on the cell to be targeted.

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

Redox cleavable linking groups

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

60, 70, 80, 90, or about 100 times faster in the cell (or under *in vitro* conditions selected to mimic intracellular conditions) as compared to blood (or under *in vitro* conditions selected to mimic extracellular conditions). The rate of cleavage of candidate compounds can be determined using standard enzyme kinetics assays under conditions chosen to mimic intracellular media and compared to conditions chosen to mimic extracellular media.

Phosphate-based cleavable linking groups

In some embodiments, a cleavable linker comprises a phosphate-based cleavable linking group. A phosphate-based cleavable linking group is cleaved by agents that degrade or hydrolyze the phosphate group. An example of an agent that cleaves phosphate groups in cells are enzymes such as phosphatases in cells. Examples of phosphate-based linking groups are -O-P(O)(ORk)-O-, -O-P(S)(ORk)-O-, -O-P(S)(SRk)-O-, -S-P(O)(ORk)-O-, -O-P(O)(ORk)-S-, -S-P(O)(ORk)-S-, -O-P(S)(ORk)-S-, -S-P(S)(ORk)-O-, -O-P(O)(Rk)-O-, -O-P(S)(Rk)-O-, -S-P(O)(Rk)-O-, -S-P(S)(Rk)-O-, -S-P(O)(Rk)-S-, -O-P(S)(Rk)-S-, wherein Rk at each occurrence can be, independently, C1-C20 alkyl, C1-C20 haloalkyl, C6-C10 aryl, or C7-C12 aralkyl. In some additional embodiments, phosphate-based linking groups are -O-P(O)(OH)-O-, -O-P(S)(OH)-O-, -O-P(S)(SH)-O-, -S-P(O)(OH)-O-, -O-P(O)(OH)-S-, -S-P(O)(OH)-S-, -O-P(S)(OH)-S-, -S-P(S)(OH)-O-, -O-P(O)(H)-O-, -O-P(S)(H)-O-, -S-P(O)(H)-O, -S-P(S)(H)-O-, -S-P(O)(H)-S-, -O-P(S)(H)-S-. In some embodiments, a phosphate-based linking group is -O-P(O)(OH)-O-. These candidates can be evaluated using methods analogous to those described above.

Acid cleavable linking groups

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

Ester-based cleavable linking groups

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

Peptide-based cleavable linking groups

In some embodiments, a cleavable linker comprises a peptide-based cleavable linking group. A peptide-based cleavable linking group is cleaved by enzymes such as peptidases and proteases in cells. Peptide-based cleavable linking groups are peptide bonds formed between amino acids to yield oligopeptides (*e.g.,* dipeptides, tripeptides *etc.*) and polypeptides. Peptide-based cleavable groups do not include the amide group (-C(O)NH-). The amide group can be formed between any alkylene, alkenylene or alkynelene. A peptide bond is a special type of amide bond formed between amino acids to yield peptides and proteins. The peptide-based cleavage group is generally limited to the peptide bond (*i.e.*, the amide bond) formed between amino acids yielding peptides and proteins and does not include the entire amide functional group. Peptide-based cleavable linking groups have the general formula – NHCHRAC(O)NHCHRBC(O)-, where RA and RB are the R groups of the two adjacent amino acids. These candidates can be evaluated using methods analogous to those described above. Representative U.S. patents that teach the preparation of RNA conjugates include, but are not limited to, U.S. Patent Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941; 6,294,664; 6,320,017; 6,576,752; 6,783,931; 6,900,297; 7,037,646; 8,106,022, the entire contents of each of which is herein incorporated by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an iRNA. The present disclosure also includes iRNA compounds that are chimeric compounds.

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

the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

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

C. Delivery of iRNA

The delivery of an iRNA to a subject in need thereof can be achieved in a number of different ways. *In vivo* delivery can be performed directly by administering a composition comprising an iRNA, *e.g.* a dsRNA, to a subject. Alternatively, delivery can be performed indirectly by administering one or more vectors that encode and direct the expression of the iRNA. These alternatives are discussed further below.

1. *Direct delivery*

In general, any method of delivering a nucleic acid molecule can be adapted for use with an iRNA (*see, e.g.,* Akhtar S. and Julian RL., 1992 *Trends Cell. Biol.* 2(5):139-144 and WO94/02595, which are incorporated herein by reference in their entireties). However, there are three factors that are important to consider in order to successfully deliver an iRNA molecule *in vivo*: (a) biological stability of the delivered molecule, (2) preventing non-specific effects, and (3) accumulation of the

delivered molecule in the target tissue. The non-specific effects of an iRNA can be minimized by local administration, for example by direct injection or implantation into a tissue (as a non-limiting example, the eye) or topically administering the preparation. Local administration to a treatment site maximizes local concentration of the agent, limits the exposure of the agent to systemic tissues that may otherwise be harmed by the agent or that may degrade the agent, and permits a lower total dose of the iRNA molecule to be administered. Several studies have shown successful knockdown of gene products when an iRNA is administered locally. For example, intraocular delivery of a dsRNA by intravitreal injection in cynomolgus monkeys (Tolentino, MJ. *et al.*, 2004 *Retina* 24:132-138) and subretinal injections in mice (Reich, SJ. *et al.*, 2003 *Mol. Vis.* 9:210-216) were both shown to prevent neovascularization in an experimental model of age-related macular degeneration. In addition, direct intratumoral injection of a dsRNA in mice reduces tumor volume (Pille, J. *et al.*, 2005 *Mol. Ther.*11:267-274) and can prolong survival of tumor-bearing mice (Kim, WJ. *et al.*, 2006 *Mol. Ther.* 14:343-350; Li, S. *et al.*, 2007 *Mol. Ther.* 15:515-523). RNA interference has also shown success with local delivery to the CNS by direct injection (Dorn, G. *et al.*, 2004 *Nucleic Acids* 32:e49; Tan, PH. *et al.*, 2005 *Gene Ther.* 12:59-66; Makimura, H. *et al.*, 2002 *BMC Neurosci.* 3:18; Shishkina, GT. *et al.*, 2004 *Neuroscience* 129:521-528; Thakker, ER. *et al.*, 2004 *Proc. Natl. Acad. Sci. U.S.A.* 101:17270-17275; Akaneya,Y. *et al.*, 2005 *J. Neurophysiol.* 93:594-602) and to the lungs by intranasal administration (Howard, KA. *et al.*, 2006 *Mol. Ther.* 14:476-484; Zhang, X. *et al.*, 2004 *J. Biol. Chem.* 279:10677-10684; Bitko, V. *et al.*, 2005 *Nat. Med.* 11:50-55). For administering an iRNA systemically for the treatment of a disease, the RNA can be modified or alternatively delivered using a drug delivery system; both methods act to prevent the rapid degradation of the dsRNA by endo- and exo-nucleases *in vivo*.

Modification of the RNA or the pharmaceutical carrier can also permit targeting of the iRNA composition to the target tissue and avoid undesirable off-target effects. iRNA molecules can be modified by chemical conjugation to other groups, *e.g.,* a lipid or carbohydrate group as described herein. Such conjugates can be used to target iRNA to particular cells, *e.g.,* liver cells, *e.g.,* hepatocytes. For example, GalNAc conjugates or lipid (*e.g.,* LNP) formulations can be used to target iRNA to particular cells, *e.g.,* liver cells, *e.g.,* hepatocytes.

iRNA molecules can also be modified by chemical conjugation to lipophilic groups such as cholesterol to enhance cellular uptake and prevent degradation. For example, an iRNA directed against ApoB conjugated to a lipophilic cholesterol moiety was injected systemically into mice and resulted in knockdown of apoB mRNA in both the liver and jejunum (Soutschek, J. *et al.*, 2004 *Nature* 432:173-178). Conjugation of an iRNA to an aptamer has been shown to inhibit tumor growth and mediate tumor regression in a mouse model of prostate cancer (McNamara, JO. *et al.*, 2006 *Nat. Biotechnol.* 24:1005-1015). In an alternative embodiment, the iRNA can be delivered using drug delivery systems such as a nanoparticle, a dendrimer, a polymer, liposomes, or a cationic delivery system. Positively charged cationic delivery systems facilitate binding of an iRNA molecule

(negatively charged) and also enhance interactions at the negatively charged cell membrane to permit efficient uptake of an iRNA by the cell. Cationic lipids, dendrimers, or polymers can either be bound to an iRNA, or induced to form a vesicle or micelle (*see e.g.,* Kim SH. *et al.*, 2008 *Journal of Controlled Release* 129(2):107-116) that encases an iRNA. The formation of vesicles or micelles further prevents degradation of the iRNA when administered systemically. Methods for making and administering cationic- iRNA complexes are well within the abilities of one skilled in the art (*see e.g.,* Sorensen, DR. *et al.*, 2003 *J. Mol. Biol.* 327:761-766; Verma, UN. *et al.*, 2003 *Clin. Cancer Res.* 9:1291-1300; Arnold, AS *et al.*, 2007) *J. Hypertens.* 25:197-205, which are incorporated herein by reference in their entirety). Some non-limiting examples of drug delivery systems useful for systemic delivery of iRNAs include DOTAP (Sorensen, DR. *et al.*, 2003 *supra*; Verma, UN. *et al.*, 2003 *supra*), Oligofectamine, "solid nucleic acid lipid particles" (Zimmermann, TS. *et al.*, 2006 *Nature* 441:111-114), cardiolipin (Chien, PY. *et al.*, 2005 *Cancer Gene Ther.* 12:321-328; Pal, A. *et al.*, 2005 *Int J. Oncol.* 26:1087-1091), polyethyleneimine (Bonnet ME. *et al.*, 2008 *Pharm. Res.* Aug 16 Epub ahead of print; Aigner, A., 2006 *J. Biomed. Biotechnol.* 71659), Arg-Gly-Asp (RGD) peptides (Liu, S., 2006 *Mol. Pharm.* 3:472-487), and polyamidoamines (Tomalia, DA. *et al.*, 2007 *Biochem. Soc. Trans.* 35:61-67; Yoo, H. *et al.*, 1999 *Pharm. Res.* 16:1799-1804). In some embodiments, an iRNA forms a complex with cyclodextrin for systemic administration. Methods for administration and pharmaceutical compositions of iRNAs and cyclodextrins can be found in U.S. Patent No. 7,427,605, which is herein incorporated by reference in its entirety.

2. *Vector encoded iRNAs*

In another aspect, iRNA targeting ANGPTL7 can be expressed from transcription units inserted into DNA or RNA vectors (*see, e.g.,* Couture, A *et al.*, *TIG.* 1996 12:5-10; Skillern, A. *et al.*, International PCT Publication No. WO 00/22113, Conrad, International PCT Publication No. WO 00/22114, and Conrad, U.S. Patent No. 6,054,299). Expression can be transient (on the order of hours to weeks) or sustained (weeks to months or longer), depending upon the specific construct used and the target tissue or cell type. These transgenes can be introduced as a linear construct, a circular plasmid, or a viral vector, which can be an integrating or non-integrating vector. The transgene can also be constructed to permit it to be inherited as an extrachromosomal plasmid (Gassmann *et al.*, 1995 *Proc. Natl. Acad. Sci. U.S.A.* 92:1292).

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

An iRNA expression vector is typically a DNA plasmid or viral vector. An expression vector compatible with eukaryotic cells, *e.g.,* with vertebrate cells, can be used to produce recombinant constructs for the expression of an iRNA as described herein. Eukaryotic cell expression vectors are well known in the art and are available from a number of commercial sources. Typically, such vectors contain convenient restriction sites for insertion of the desired nucleic acid segment. Delivery of iRNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that allows for introduction into a desired target cell.

An iRNA expression plasmid can be transfected into a target cell as a complex with a cationic lipid carrier (*e.g.,* Oligofectamine) or a non-cationic lipid-based carrier (*e.g.,* Transit-TKO™). Multiple lipid transfections for iRNA-mediated knockdowns targeting different regions of a target RNA over a period of a week or more are also contemplated by the disclosure. Successful introduction of vectors into host cells can be monitored using various known methods. For example, transient transfection can be signaled with a reporter, such as a fluorescent marker, such as Green Fluorescent Protein (GFP). Stable transfection of cells *ex vivo* can be ensured using markers that provide the transfected cell with resistance to specific environmental factors (*e.g.,* antibiotics and drugs), such as hygromycin B resistance.

Viral vector systems which can be utilized with the methods and compositions described herein include, but are not limited to, (a) adenovirus vectors; (b) retrovirus vectors, including but not limited to lentiviral vectors, moloney murine leukemia virus, *etc.*; (c) adeno-associated virus vectors; (d) herpes simplex virus vectors; (e) SV40 vectors; (f) polyoma virus vectors; (g) papilloma virus vectors; (h) picornavirus vectors; (i) pox virus vectors such as an orthopox, *e.g.,* vaccinia virus vectors or avipox, *e.g.* canary pox or fowl pox; and (j) a helper-dependent or gutless adenovirus. Replication-defective viruses can also be advantageous. Different vectors will or will not become incorporated into the cells' genome. The constructs can include viral sequences for transfection, if desired. Alternatively, the construct may be incorporated into vectors capable of episomal replication, *e.g.,* EPV and EBV vectors. Constructs for the recombinant expression of an iRNA will generally require regulatory elements, *e.g.,* promoters, enhancers, *etc.*, to ensure the expression of the iRNA in target cells. Other aspects to consider for vectors and constructs are further described below.

Vectors useful for the delivery of an iRNA will include regulatory elements (promoter, enhancer, *etc.*) sufficient for expression of the iRNA in the desired target cell or tissue. The regulatory elements can be chosen to provide either constitutive or regulated/inducible expression.

Expression of the iRNA can be precisely regulated, for example, by using an inducible regulatory sequence that is sensitive to certain physiological regulators, *e.g.,* circulating glucose levels, or hormones (Docherty *et al.*, 1994 *FASEB J.* 8:20-24). Such inducible expression systems, suitable for the control of dsRNA expression in cells or in mammals include, for example, regulation by ecdysone, by estrogen, progesterone, tetracycline, chemical inducers of dimerization, and

isopropyl-β-D1-thiogalactopyranoside (IPTG). A person skilled in the art would be able to choose the appropriate regulatory/promoter sequence based on the intended use of the iRNA transgene.

In a specific embodiment, viral vectors that contain nucleic acid sequences encoding an iRNA can be used. For example, a retroviral vector can be used (see Miller *et al.*, 1993 *Meth. Enzymol.* 217:581-599). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the host cell DNA. The nucleic acid sequences encoding an iRNA are cloned into one or more vectors, which facilitates delivery of the nucleic acid into a patient. More detail about retroviral vectors can be found, for example, in Boesen *et al.*, 1994 *Biotherapy* 6:291-302, which describes the use of a retroviral vector to deliver the mdr1 gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes *et al.*, 1994 *J. Clin. Invest.* 93:644-651; Kiem *et al.*, 1994 *Blood* 83:1467-1473; Salmons and Gunzberg, 1993 *Human Gene Therapy* 4:129-141; and Grossman and Wilson, 1993 *Curr. Opin. in Genetics and Devel.* 3:110-114. Lentiviral vectors contemplated for use include, for example, the HIV based vectors described in U.S. Patent Nos. 6,143,520; 5,665,557; and 5,981,276, which are herein incorporated by reference.

Adenoviruses are also contemplated for use in delivery of iRNAs. Adenoviruses are especially attractive vehicles, *e.g.,* for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993 *Current Opinion in Genetics and Development* 3:499-503 present a review of adenovirus-based gene therapy. Bout *et al.*, 1994 *Human Gene Therapy* 5:3-10 demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld *et al.*, 1991 *Science* 252:431-434; Rosenfeld *et al.*, 1992 *Cell* 68:143-155; Mastrangeli *et al.*, 1993 *J. Clin. Invest.* 91:225-234; PCT Publication WO94/12649; and Wang *et al.*, 1995 *Gene Therapy* 2:775-783. A suitable AV vector for expressing an iRNA featured in the disclosure, a method for constructing the recombinant AV vector, and a method for delivering the vector into target cells, are described in Xia H *et al.*, 2002 *Nat. Biotech.* 20:1006-1010.

Use of Adeno-associated virus (AAV) vectors is also contemplated (Walsh *et al.*, 1993 *Proc. Soc. Exp. Biol. Med.* 204:289-300; U.S. Patent No. 5,436,146). In some embodiments, the iRNA can be expressed as two separate, complementary single-stranded RNA molecules from a recombinant AAV vector having, for example, either the U6 or H1 RNA promoters, or the cytomegalovirus (CMV) promoter. Suitable AAV vectors for expressing the dsRNA featured in the disclosure, methods for constructing the recombinant AV vector, and methods for delivering the vectors into target cells are described in Samulski R *et al.*, 1987 *J. Virol.* 61:3096-3101; Fisher K J *et al.*, 1996 *J. Virol.* 70:520-532; Samulski R *et al.*, 1989 *J. Virol.* 63:3822-3826; U.S. Patent No. 5,252,479; U.S.

Patent No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641, the entire disclosures of which are herein incorporated by reference.

Another typical viral vector is a pox virus such as a vaccinia virus, for example an attenuated vaccinia such as Modified Virus Ankara (MVA) or NYVAC, an avipox such as fowl pox or canary pox.

The tropism of viral vectors can be modified by pseudotyping the vectors with envelope proteins or other surface antigens from other viruses, or by substituting different viral capsid proteins, as appropriate. For example, lentiviral vectors can be pseudotyped with surface proteins from vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. AAV vectors can be made to target different cells by engineering the vectors to express different capsid protein serotypes; *see*, *e.g.*, Rabinowitz J.E. *et al.*, 2002 *J Virol* 76:791-801, the entire disclosure of which is herein incorporated by reference.

The pharmaceutical preparation of a vector can include the vector in an acceptable diluent, or can include a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

III. Pharmaceutical compositions containing iRNA

In some embodiments, the disclosure provides pharmaceutical compositions containing an iRNA, as described herein, and a pharmaceutically acceptable carrier. The pharmaceutical composition containing the iRNA is useful for treating a disease or disorder related to the expression or activity of ANGPTL7 (*e.g.,* glaucoma or conditions associated with glaucoma). Such pharmaceutical compositions are formulated based on the mode of delivery. In some embodiments, compositions can be formulated for localized delivery, *e.g.,* by intraocular delivery (*e.g.,* intravitreal administration, *e.g.*, intravitreal injection; transscleral administration, *e.g.*, transscleral injection; subconjunctival administration, *e.g.*, subconjunctival injection; retrobulbar administration, *e.g.*, retrobulbar injection; intracameral administration, *e.g.*, intracameral injection; or subretinal administration, *e.g.*, subretinal injection). In other embodiments, compositions can be formulated for topical delivery. In another example, compositions can be formulated for systemic administration via parenteral delivery, *e.g.,* by intravenous (IV) delivery. In some embodiments, a composition provided herein (*e.g.,* a composition comprising a GalNAc conjugate or an LNP formulation) is formulated for intravenous delivery.

The pharmaceutical compositions featured herein are administered in a dosage sufficient to inhibit expression of ANGPTL7. In general, a suitable dose of iRNA will be in the range of 0.01 to 200.0 milligrams per kilogram body weight of the recipient per day. The pharmaceutical composition may be administered once daily, or the iRNA may be administered as two, three, or more sub-doses at appropriate intervals throughout the day or even using continuous infusion or delivery through a

controlled release formulation. In that case, the iRNA contained in each sub-dose must be correspondingly smaller in order to achieve the total daily dosage. The dosage unit can also be compounded for delivery over several days, *e.g.,* using a conventional sustained release formulation which provides sustained release of the iRNA over a several day period. Sustained release formulations are well known in the art and are particularly useful for delivery of agents at a particular site, such as can be used with the agents of the present disclosure. In this embodiment, the dosage unit contains a corresponding multiple of the daily dose.

The effect of a single dose on ANGPTL7 levels can be long lasting, such that subsequent doses are administered at not more than 3, 4, or 5-day intervals, or at not more than 1, 2, 3, 4, 12, 24, or 36-week intervals.

The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a composition can include a single treatment or a series of treatments. Estimates of effective dosages and *in vivo* half-lives for the individual iRNAs encompassed by the disclosure can be made using conventional methodologies or on the basis of *in vivo* testing using a suitable animal model.

A suitable animal model, *e.g.,* a mouse or a cynomolgus monkey, *e.g.*, an animal containing a transgene expressing human ANGPTL7, can be used to determine the therapeutically effective dose and/or an effective dosage regimen administration of ANGPTL7 siRNA.

The present disclosure also includes pharmaceutical compositions and formulations that include the iRNA compounds featured herein. The pharmaceutical compositions of the present disclosure may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be local (*e.g.,* by intraocular injection), topical (*e.g.,* by an eye drop solution), or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; subdermal, *e.g.,* via an implanted device; or intracranial, *e.g.,* by intraparenchymal, intrathecal, or intraventricular administration.

Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful. Suitable topical formulations include those in which the iRNAs featured in the disclosure are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Suitable lipids and liposomes include neutral (*e.g.,* dioleoylphosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearolyphosphatidyl choline) negative (*e.g.,* dimyristoylphosphatidyl glycerol DMPG) and cationic (*e.g.,*

dioleoyltetramethylaminopropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA). iRNAs featured in the disclosure may be encapsulated within liposomes or may form complexes thereto, in particular to cationic liposomes. Alternatively, iRNAs may be complexed to lipids, in particular to cationic lipids. Suitable fatty acids and esters include but are not limited to arachidonic acid, oleic acid, eicosanoic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a C_{1-20} alkyl ester (*e.g.*, isopropylmyristate IPM), monoglyceride, diglyceride or pharmaceutically acceptable salt thereof. Topical formulations are described in detail in U.S. Patent No. 6,747,014, which is incorporated herein by reference.

A. Liposomal formulations

There are many organized surfactant structures besides microemulsions that have been studied and used for the formulation of drugs. These include monolayers, micelles, bilayers and vesicles. Vesicles, such as liposomes, have attracted great interest because of their specificity and the duration of action they offer from the standpoint of drug delivery. As used in the present disclosure, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers.

Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the composition to be delivered. Cationic liposomes possess the advantage of being able to fuse to the cell wall. Non-cationic liposomes, although not able to fuse as efficiently with the cell wall, are taken up by macrophages *in vivo*.

In order to traverse intact mammalian skin, lipid vesicles must pass through a series of fine pores, each with a diameter less than 50 nm, under the influence of a suitable transdermal gradient. Therefore, it is desirable to use a liposome which is highly deformable and able to pass through such fine pores.

Further advantages of liposomes include; liposomes obtained from natural phospholipids are biocompatible and biodegradable; liposomes can incorporate a wide range of water and lipid soluble drugs; liposomes can protect encapsulated drugs in their internal compartments from metabolism and degradation (Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Important considerations in the preparation of liposome formulations are the lipid surface charge, vesicle size and the aqueous volume of the liposomes.

Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a tissue, the liposomes start to merge with the cellular membranes and as the merging of the

liposome and cell progresses, the liposomal contents are emptied into the cell where the active agent may act.

Liposomal formulations have been the focus of extensive investigation as the mode of delivery for many drugs. There is growing evidence that for topical administration, liposomes present several advantages over other formulations. Such advantages include reduced side-effects related to high systemic absorption of the administered drug, increased accumulation of the administered drug at the desired target, and the ability to administer a wide variety of drugs, both hydrophilic and hydrophobic, into the skin.

Several reports have detailed the ability of liposomes to deliver agents including high-molecular weight DNA into the skin. Compounds including analgesics, antibodies, hormones and high-molecular weight DNAs have been administered to the skin. The majority of applications resulted in the targeting of the upper epidermis

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

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

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

Several studies have assessed the topical delivery of liposomal drug formulations to the skin. Application of liposomes containing interferon to guinea pig skin resulted in a reduction of skin herpes sores while delivery of interferon via other means (*e.g.,* as a solution or as an emulsion) were ineffective (Weiner *et al.*, 1992 *Journal of Drug Targeting* 2:405-410). Further, an additional study tested the efficacy of interferon administered as part of a liposomal formulation to the administration

of interferon using an aqueous system, and concluded that the liposomal formulation was superior to aqueous administration (du Plessis *et al.*, 1992 *Antiviral Research*, 18:259-265).

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

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

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

Many liposomes comprising lipids derivatized with one or more hydrophilic polymers, and methods of preparation thereof, are known in the art. Sunamoto *et al.* (Bull. *Chem.* 1980 *Soc. Jpn.* 53:2778) described liposomes comprising a nonionic detergent, $2C_{1215G}$, that contains a PEG moiety. Illum *et al.* (1984 *FEBS Lett.* 167:79) noted that hydrophilic coating of polystyrene particles with polymeric glycols results in significantly enhanced blood half-lives. Synthetic phospholipids modified by the attachment of carboxylic groups of polyalkylene glycols (*e.g.,* PEG) are described by Sears (U.S. Patent Nos. 4,426,330 and 4,534,899). Klibanov *et al.* (1990 *FEBS Lett.* 268:235) described experiments demonstrating that liposomes comprising phosphatidylethanolamine (PE) derivatized

with PEG or PEG stearate have significant increases in blood circulation half-lives. Blume *et al.* (1990 *Biochimica et Biophysica Acta*, 1990 1029:91) extended such observations to other PEG-derivatized phospholipids, *e.g.,* DSPE-PEG, formed from the combination of distearoylphosphatidylethanolamine (DSPE) and PEG. Liposomes having covalently bound PEG moieties on their external surface are described in European Patent No. EP 0 445 131 B1 and WO 90/04384 to Fisher. Liposome compositions containing 1-20 mole percent of PE derivatized with PEG, and methods of use thereof, are described by Woodle *et al.* (U.S. Patent Nos. 5,013,556 and 5,356,633) and Martin *et al.* (U.S. Patent No. 5,213,804 and European Patent No. EP 0 496 813 B1). Liposomes comprising a number of other lipid-polymer conjugates are disclosed in WO 91/05545 and U.S. Patent No. 5,225,212 (both to Martin *et al.*) and in WO 94/20073 (Zalipsky *et al.*). Liposomes comprising PEG-modified ceramide lipids are described in WO 96/10391 (Choi *et al*). U.S. Patent No. 5,540,935 (Miyazaki *et al.*) and U.S. Patent No. 5,556,948 (Tagawa *et al.*) describe PEG-containing liposomes that can be further derivatized with functional moieties on their surfaces.

A number of liposomes comprising nucleic acids are known in the art. WO 96/40062 to Thierry *et al.* discloses methods for encapsulating high molecular weight nucleic acids in liposomes. U.S. Patent No. 5,264,221 to Tagawa *et al.* discloses protein-bonded liposomes and asserts that the contents of such liposomes may include a dsRNA. U.S. Patent No. 5,665,710 to Rahman *et al.* describes certain methods of encapsulating oligodeoxynucleotides in liposomes. WO 97/04787 to Love *et al.* discloses liposomes comprising dsRNAs targeted to the raf gene.

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

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

If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are usable over a wide range of pH values. In general, their HLB values range from 2 to about 18 depending on their

structure. Nonionic surfactants include nonionic esters such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

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

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

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

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

1. *Nucleic acid lipid particles*

In some embodiments, an ANGPTL7 dsRNA featured in the disclosure is fully encapsulated in the lipid formulation, *e.g.,* to form a SPLP, pSPLP, SNALP, or other nucleic acid-lipid particle. SNALPs and SPLPs typically contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (*e.g.,* a PEG-lipid conjugate). SNALPs and SPLPs are extremely useful for systemic applications, as they exhibit extended circulation lifetimes following intravenous (i.v.) injection and accumulate at distal sites (*e.g.,* sites physically separated from the administration site). SPLPs include "pSPLP," which include an encapsulated condensing agent-nucleic acid complex as set forth in PCT Publication No. WO 00/03683. The particles of the present disclosure typically have a mean diameter of about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 nm to about 90 nm, and are substantially nontoxic. In addition, the nucleic acids when present in the nucleic acid- lipid particles of the present disclosure are resistant in aqueous solution to degradation with a nuclease. Nucleic acid-lipid particles and their method of preparation are disclosed in, *e.g.,* U.S. Patent Nos. 5,976,567; 5,981,501; 6,534,484; 6,586,410; 6,815,432; and PCT Publication No. WO 96/40964.

In some embodiments, the lipid to drug ratio (mass/mass ratio) (*e.g.,* lipid to dsRNA ratio) will be in the range of from about 1:1 to about 50:1, from about 1:1 to about 25:1, from about 3:1 to about 15:1, from about 4:1 to about 10:1, from about 5:1 to about 9:1, or about 6:1 to about 9:1.

The cationic lipid may be, for example, N,N-dioleyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), N-(I -(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(I -(2,3- dioleyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), N,N-dimethyl-2,3- dioleyloxy)propylamine (DODMA), 1,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA), l,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA), 1,2-Dilinoleylcarbamoyloxy-3-dimethylaminopropane (DLin-C-DAP), 1,2-Dilinoleyoxy-3-(dimethylamino)acetoxypropane (DLin-DAC), 1,2-Dilinoleyoxy-3-morpholinopropane (DLin-MA), 1,2-Dilinoleoyl-3-dimethylaminopropane (DLinDAP), 1,2-Dilinoleylthio-3-dimethylaminopropane (DLin-S-DMA), 1-Linoleoyl-2-linoleyloxy-3-dimethylaminopropane (DLin-2-DMAP), 1,2-Dilinoleyloxy-3-trimethylaminopropane chloride salt (DLin-TMA.Cl), 1,2-Dilinoleoyl-3-trimethylaminopropane chloride salt (DLin-TAP.Cl), 1,2-Dilinoleyloxy-3-(N-methylpiperazino)propane (DLin-MPZ), or 3-(N,N-Dilinoleylamino)-1,2-propanediol (DLinAP), 3-(N,N-Dioleylamino)-1,2-propanedio (DOAP), 1,2-Dilinoleyloxo-3-(2-N,N-dimethylamino)ethoxypropane (DLin-EG-DMA), l,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA), 2,2-Dilinoleyl-4-dimethylaminomethyl-[1,3]-dioxolane (DLin-K-DMA) or analogs thereof, (3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-cyclopenta[d][1,3]dioxol-5-amine (ALN100), (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3), 1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (Tech G1), or a mixture thereof. The cationic lipid may comprise from about 20 mol % to about 50 mol % or about 40 mol % of the total lipid present in the particle.

In some embodiments, the compound 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane can be used to prepare lipid-siRNA nanoparticles. Synthesis of 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane is described in United States provisional patent application number 61/107,998 filed on October 23, 2008, which is herein incorporated by reference.

In some embodiments, the lipid-siRNA particle includes 40% 2, 2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane: 10% DSPC: 40% Cholesterol: 10% PEG-C-DOMG (mole percent) with a particle size of 63.0 ± 20 nm and a 0.027 siRNA/Lipid Ratio.

The non-cationic lipid may be an anionic lipid or a neutral lipid including, but not limited to, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoylphosphatidylethanolamine (POPE), dioleoyl- phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-l- carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1 -trans PE, 1 -stearoyl-2-oleoyl- phosphatidyethanolamine (SOPE), cholesterol, or a mixture thereof. The

non-cationic lipid may be from about 5 mol % to about 90 mol %, about 10 mol %, or about 58 mol % if cholesterol is included, of the total lipid present in the particle.

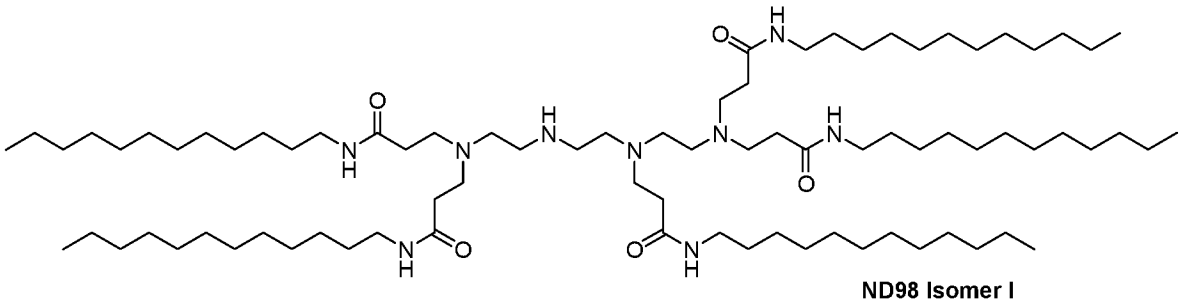
The conjugated lipid that inhibits aggregation of particles may be, for example, a polyethyleneglycol (PEG)-lipid including, without limitation, a PEG-diacylglycerol (DAG), a PEG-dialkyloxypropyl (DAA), a PEG-phospholipid, a PEG-ceramide (Cer), or a mixture thereof. The PEG-DAA conjugate may be, for example, a PEG-dilauryloxypropyl (Ci_2), a PEG-dimyristyloxypropyl (Ci_4), a PEG-dipalmityloxypropyl (Ci_6), or a PEG- distearyloxypropyl ($C]_8$). The conjugated lipid that prevents aggregation of particles may be from 0 mol % to about 20 mol % or about 2 mol % of the total lipid present in the particle.

In some embodiments, the nucleic acid-lipid particle further includes cholesterol at, *e.g.*, about 10 mol % to about 60 mol % or about 48 mol % of the total lipid present in the particle.

In some embodiments, the iRNA is formulated in a lipid nanoparticle (LNP).

LNP01

In some embodiments, the lipidoid ND98·4HCl (MW 1487) (*see* U.S. Patent Application No. 12/056,230, filed 3/26/2008, which is herein incorporated by reference), Cholesterol (Sigma-Aldrich), and PEG-Ceramide C16 (Avanti Polar Lipids) can be used to prepare lipid-dsRNA nanoparticles (*e.g.*, LNP01 particles). Stock solutions of each in ethanol can be prepared as follows: ND98, 133 mg/ml; Cholesterol, 25 mg/ml, PEG-Ceramide C16, 100 mg/ml. The ND98, Cholesterol, and PEG-Ceramide C16 stock solutions can then be combined in a, *e.g.*, 42:48:10 molar ratio. The combined lipid solution can be mixed with aqueous dsRNA (*e.g.*, in sodium acetate pH 5) such that the final ethanol concentration is about 35-45% and the final sodium acetate concentration is about 100-300 mM. Lipid-dsRNA nanoparticles typically form spontaneously upon mixing. Depending on the desired particle size distribution, the resultant nanoparticle mixture can be extruded through a polycarbonate membrane (*e.g.*, 100 nm cut-off) using, for example, a thermobarrel extruder, such as Lipex Extruder (Northern Lipids, Inc). In some cases, the extrusion step can be omitted. Ethanol removal and simultaneous buffer exchange can be accomplished by, for example, dialysis or tangential flow filtration. Buffer can be exchanged with, for example, phosphate buffered saline (PBS) at about pH 7, *e.g.*, about pH 6.9, about pH 7.0, about pH 7.1, about pH 7.2, about pH 7.3, or about pH 7.4.



Formula 1

LNP01 formulations are described, *e.g.,* in International Application Publication No. WO 2008/042973, which is hereby incorporated by reference.

Additional exemplary lipid-dsRNA formulations are provided in the following Table A.

Table A: **Exemplary lipid formulations**

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

	Cationic Lipid	cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
LNP14	MC3	MC3/DSPC/Chol/PEG-DMG 40/15/40/5 Lipid:siRNA: 11:1
LNP15	MC3	MC3/DSPC/Chol/PEG-DSG/GalNAc-PEG-DSG 50/10/35/4.5/0.5 Lipid:siRNA: 11:1
LNP16	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP17	MC3	MC3/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP18	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 12:1
LNP19	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/35/5 Lipid:siRNA: 8:1
LNP20	MC3	MC3/DSPC/Chol/PEG-DPG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP21	C12-200	C12-200/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP22	XTC	XTC/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1

DSPC: distearoylphosphatidylcholine

DPPC: dipalmitoylphosphatidylcholine

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

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

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

SNALP (l,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA)) comprising formulations are described in International Publication No. WO2009/127060, filed April 15, 2009, which is hereby incorporated by reference.

XTC comprising formulations are described, *e.g.,* in U.S. Provisional Serial No. 61/148,366, filed January 29, 2009; U.S. Provisional Serial No. 61/156,851, filed March 2, 2009; U.S. Provisional Serial No. 61/185,712, filed June 10, 2009; U.S. Provisional Serial No. 61/228,373, filed July 24, 2009; U.S. Provisional Serial No. 61/239,686, filed September 3, 2009, and International Application No. PCT/US2010/022614, filed January 29, 2010, which are hereby incorporated by reference.

MC3 comprising formulations are described, *e.g.,* in U.S. Provisional Serial No. 61/244,834, filed September 22, 2009, U.S. Provisional Serial No. 61/185,800, filed June 10, 2009, and International Application No. PCT/US10/28224, filed June 10, 2010, which are hereby incorporated by reference.

ALNY-100 comprising formulations are described, *e.g.,* International patent application number PCT/US09/63933, filed on November 10, 2009, which is hereby incorporated by reference.

C12-200 comprising formulations are described in U.S. Provisional Serial No. 61/175,770, filed May 5, 2009 and International Application No. PCT/US10/33777, filed May 5, 2010, which are hereby incorporated by reference.

2. *Synthesis of cationic lipids*

Any of the compounds, *e.g.,* cationic lipids and the like, used in the nucleic acid-lipid particles featured in the disclosure may be prepared by known organic synthesis techniques. All substituents are as defined below unless indicated otherwise.

"Alkyl" means a straight chain or branched, noncyclic or cyclic, saturated aliphatic hydrocarbon containing from 1 to 24 carbon atoms. Representative saturated straight chain alkyls include methyl, ethyl, n-propyl, n-butyl, n-pentyl, n-hexyl, and the like; while saturated branched alkyls include isopropyl, *sec*-butyl, isobutyl, *tert*-butyl, isopentyl, and the like. Representative saturated cyclic alkyls include cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, and the like; while unsaturated cyclic alkyls include cyclopentenyl and cyclohexenyl, and the like.

"Alkenyl" means an alkyl, as defined above, containing at least one double bond between adjacent carbon atoms. Alkenyls include both cis and trans isomers. Representative straight chain and branched alkenyls include ethylenyl, propylenyl, 1-butenyl, 2-butenyl, isobutylenyl, 1-pentenyl, 2-pentenyl, 3-methyl-1-butenyl, 2-methyl-2-butenyl, 2,3-dimethyl-2-butenyl, and the like.

"Alkynyl" means any alkyl or alkenyl, as defined above, which additionally contains at least one triple bond between adjacent carbons. Representative straight chain and branched alkynyls include acetylenyl, propynyl, 1-butynyl, 2-butynyl, 1-pentynyl, 2-pentynyl, 3-methyl-1 butynyl, and the like.

"Acyl" means any alkyl, alkenyl, or alkynyl wherein the carbon at the point of attachment is substituted with an oxo group, as defined below. For example, -C(=O)alkyl, -C(=O)alkenyl, and -C(=O)alkynyl are acyl groups.

"Heterocycle" means a 5- to 7-membered monocyclic, or 7- to 10-membered bicyclic, heterocyclic ring which is either saturated, unsaturated, or aromatic, and which contains from 1 or 2 heteroatoms independently selected from nitrogen, oxygen and sulfur, and wherein the nitrogen and sulfur heteroatoms may be optionally oxidized, and the nitrogen heteroatom may be optionally quaternized, including bicyclic rings in which any of the above heterocycles are fused to a benzene ring. The heterocycle may be attached via any heteroatom or carbon atom. Heterocycles include heteroaryls as defined below. Heterocycles include morpholinyl, pyrrolidinonyl, pyrrolidinyl,

piperidinyl, piperizynyl, hydantoinyl, valerolactamyl, oxiranyl, oxetanyl, tetrahydrofuranyl, tetrahydropyranyl, tetrahydropyridinyl, tetrahydroprimidinyl, tetrahydrothiophenyl, tetrahydrothiopyranyl, tetrahydropyrimidinyl, tetrahydrothiophenyl, tetrahydrothiopyranyl, and the like.

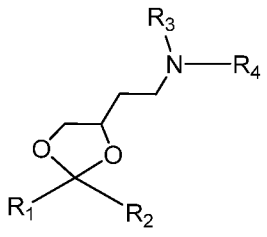
The terms "optionally substituted alkyl", "optionally substituted alkenyl", "optionally substituted alkynyl", "optionally substituted acyl", and "optionally substituted heterocycle" means that, when substituted, at least one hydrogen atom is replaced with a substituent. In the case of an oxo substituent (=O) two hydrogen atoms are replaced. In this regard, substituents include oxo, halogen, heterocycle, -CN, -OR^x, -NR^xR^y, -$NR^xC(=O)R^y$, -$NR^xSO_2R^y$, -$C(=O)R^x$, -$C(=O)OR^x$, -$C(=O)NR^xR^y$, -SO_nR^x and -$SO_nNR^xR^y$, wherein n is 0, 1 or 2, R^x and R^y are the same or different and independently hydrogen, alkyl or heterocycle, and each of said alkyl and heterocycle substituents may be further substituted with one or more of oxo, halogen, -OH, -CN, alkyl, -OR^x, heterocycle, -NR^xR^y, -$NR^xC(=O)R^y$, -$NR^xSO_2R^y$, -$C(=O)R^x$, -$C(=O)OR^x$, -$C(=O)NR^xR^y$, -SO_nR^x and -$SO_nNR^xR^y$.

"Halogen" means fluoro, chloro, bromo and iodo.

In some embodiments, the methods featured in the disclosure may require the use of protecting groups. Protecting group methodology is well known to those skilled in the art (*see, for example*, PROTECTIVE GROUPS IN ORGANIC SYNTHESIS, Green, T.W. *et al.*, Wiley-Interscience, New York City, 1999). Briefly, protecting groups within the context of this disclosure are any group that reduces or eliminates unwanted reactivity of a functional group. A protecting group can be added to a functional group to mask its reactivity during certain reactions and then removed to reveal the original functional group. In some embodiments an "alcohol protecting group" is used. An "alcohol protecting group" is any group which decreases or eliminates unwanted reactivity of an alcohol functional group. Protecting groups can be added and removed using techniques well known in the art.

Synthesis of Formula A

In some embodiments, nucleic acid-lipid particles featured in the disclosure are formulated using a cationic lipid of formula A:

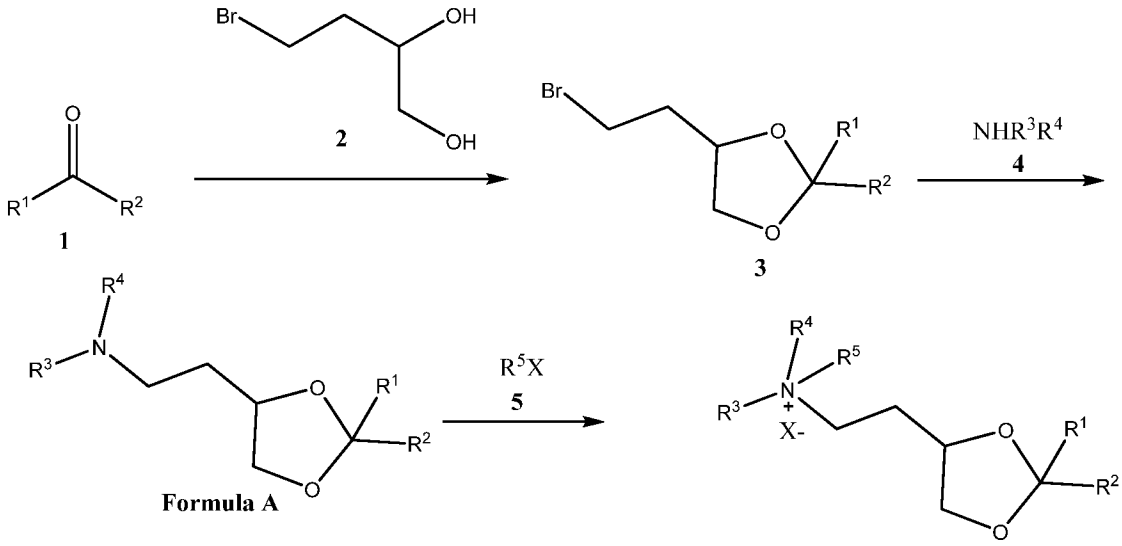


,

where R1 and R2 are independently alkyl, alkenyl or alkynyl, each can be optionally substituted, and R3 and R4 are independently lower alkyl or R3 and R4 can be taken together to form an optionally substituted heterocyclic ring. In some embodiments, the cationic lipid is XTC (2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane). In general, the lipid of formula A above may be made by the

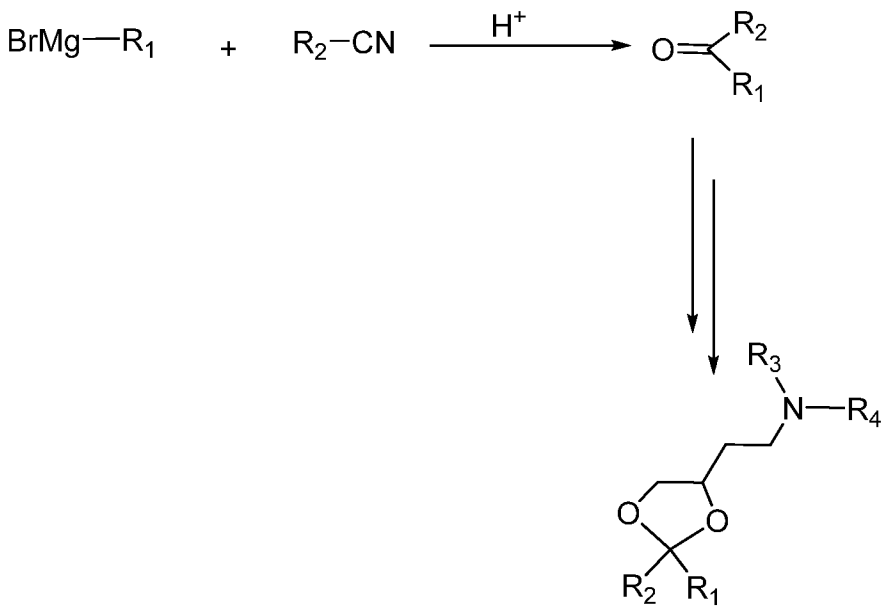
following Reaction Schemes 1 or 2, wherein all substituents are as defined above unless indicated otherwise.

Scheme 1



Lipid A, where R_1 and R_2 are independently alkyl, alkenyl or alkynyl, each can be optionally substituted, and R_3 and R_4 are independently lower alkyl or R_3 and R_4 can be taken together to form an optionally substituted heterocyclic ring, can be prepared according to Scheme 1. Ketone 1 and bromide 2 can be purchased or prepared according to methods known to those of ordinary skill in the art. Reaction of 1 and 2 yields ketal 3. Treatment of ketal 3 with amine 4 yields lipids of formula A. The lipids of formula A can be converted to the corresponding ammonium salt with an organic salt of formula 5, where X is anion counter ion selected from halogen, hydroxide, phosphate, sulfate, or the like.

Scheme 2



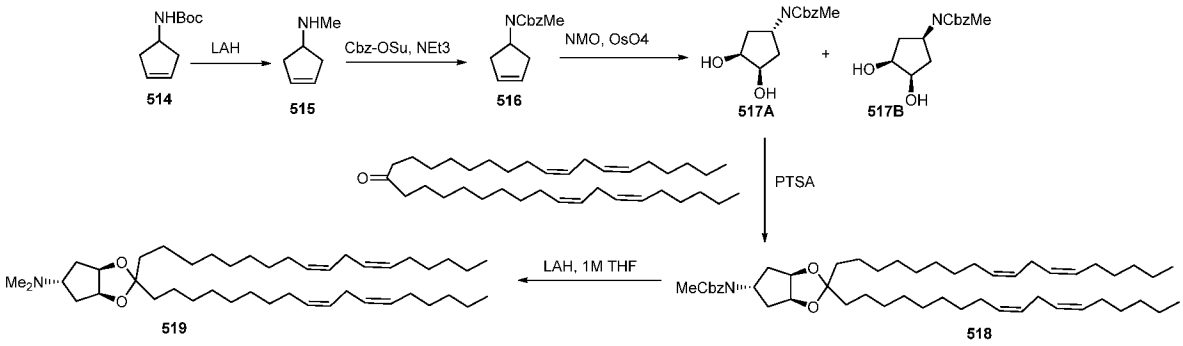
Alternatively, the ketone 1 starting material can be prepared according to Scheme 2. Grignard reagent 6 and cyanide 7 can be purchased or prepared according to methods known to those of ordinary skill in the art. Reaction of 6 and 7 yields ketone 1. Conversion of ketone 1 to the corresponding lipids of formula A is as described in Scheme 1.

Synthesis of MC3

Preparation of DLin-M-C3-DMA (*i.e.*, (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate) was as follows. A solution of (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-ol (0.53 g), 4-N,N-dimethylaminobutyric acid hydrochloride (0.51 g), 4-N,N-dimethylaminopyridine (0.61g) and 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide hydrochloride (0.53 g) in dichloromethane (5 mL) was stirred at room temperature overnight. The solution was washed with dilute hydrochloric acid followed by dilute aqueous sodium bicarbonate. The organic fractions were dried over anhydrous magnesium sulphate, filtered and the solvent removed on a rotovap. The residue was passed down a silica gel column (20 g) using a 1-5% methanol/dichloromethane elution gradient. Fractions containing the purified product were combined and the solvent removed, yielding a colorless oil (0.54 g).

Synthesis of ALNY-100

Synthesis of ketal 519 [ALNY-100] was performed using the following scheme 3:



Synthesis of 515

To a stirred suspension of LiAlH4 (3.74 g, 0.09852 mol) in 200 ml anhydrous THF in a two neck RBF (1L), was added a solution of 514 (10g, 0.04926mol) in 70 mL of THF slowly at 0 0C under nitrogen atmosphere. After complete addition, reaction mixture was warmed to room temperature and then heated to reflux for 4 h. Progress of the reaction was monitored by TLC. After completion of reaction (by TLC) the mixture was cooled to 0 0C and quenched with careful addition of saturated Na2SO4 solution. Reaction mixture was stirred for 4 h at room temperature and filtered off. Residue was washed well with THF. The filtrate and washings were mixed and diluted with 400 mL dioxane and 26 mL conc. HCl and stirred for 20 minutes at room temperature. The volatilities were stripped off under vacuum to furnish the hydrochloride salt of 515 as a white solid. Yield: 7.12 g

1H-NMR (DMSO, 400MHz): δ= 9.34 (broad, 2H), 5.68 (s, 2H), 3.74 (m, 1H), 2.66-2.60 (m, 2H), 2.50-2.45 (m, 5H).

Synthesis of 516

To a stirred solution of compound 515 in 100 mL dry DCM in a 250 mL two neck RBF, was added NEt3 (37.2 mL, 0.2669 mol) and cooled to 0 0C under nitrogen atmosphere. After a slow addition of N-(benzyloxy-carbonyloxy)-succinimide (20 g, 0.08007 mol) in 50 mL dry DCM, reaction mixture was allowed to warm to room temperature. After completion of the reaction (2-3 h by TLC) mixture was washed successively with 1N HCl solution (1 x 100 mL) and saturated NaHCO3 solution (1 x 50 mL). The organic layer was then dried over anhyd. Na2SO4 and the solvent was evaporated to give crude material which was purified by silica gel column chromatography to get 516 as sticky mass. Yield: 11g (89%). 1H-NMR (CDCl3, 400MHz): δ = 7.36-7.27(m, 5H), 5.69 (s, 2H), 5.12 (s, 2H), 4.96 (br., 1H) 2.74 (s, 3H), 2.60(m, 2H), 2.30-2.25(m, 2H). LC-MS [M+H] -232.3 (96.94%).

Synthesis of 517A and 517B

The cyclopentene 516 (5 g, 0.02164 mol) was dissolved in a solution of 220 mL acetone and water (10:1) in a single neck 500 mL RBF and to it was added N-methyl morpholine-N-oxide (7.6 g, 0.06492 mol) followed by 4.2 mL of 7.6% solution of OsO4 (0.275 g, 0.00108 mol) in tert-butanol at room temperature. After completion of the reaction (~ 3 h), the mixture was quenched with addition of solid Na2SO3 and resulting mixture was stirred for 1.5 h at room temperature. Reaction mixture was diluted with DCM (300 mL) and washed with water (2 x 100 mL) followed by saturated NaHCO3 (1 x 50 mL) solution, water (1 x 30 mL) and finally with brine (1x 50 mL). Organic phase was dried over anhyd. Na2SO4 and solvent was removed in vacuum. Silica gel column chromatographic purification of the crude material was afforded a mixture of diastereomers, which were separated by prep HPLC. Yield: - 6 g crude

517A - Peak-1 (white solid), 5.13 g (96%). 1H-NMR (DMSO, 400MHz): δ= 7.39-7.31(m, 5H), 5.04(s, 2H), 4.78-4.73 (m, 1H), 4.48-4.47(d, 2H), 3.94-3.93(m, 2H), 2.71(s, 3H), 1.72- 1.67(m, 4H). LC-MS - [M+H]-266.3, [M+NH4 +]-283.5 present, HPLC-97.86%. Stereochemistry confirmed by X-ray.

Synthesis of 518

Using a procedure analogous to that described for the synthesis of compound 505, compound 518 (1.2 g, 41%) was obtained as a colorless oil. 1H-NMR (CDCl3, 400MHz): δ= 7.35-7.33(m, 4H), 7.30-7.27(m, 1H), 5.37-5.27(m, 8H), 5.12(s, 2H), 4.75(m,1H), 4.58-4.57(m,2H), 2.78-2.74(m,7H), 2.06-2.00(m,8H), 1.96-1.91(m, 2H), 1.62(m, 4H), 1.48(m, 2H), 1.37-1.25(br m, 36H), 0.87(m, 6H). HPLC-98.65%.

General Procedure for the Synthesis of Compound 519:

A solution of compound 518 (1 eq) in hexane (15 mL) was added in a drop-wise fashion to an ice-cold solution of LAH in THF (1 M, 2 eq). After complete addition, the mixture was heated at 40°C over 0.5 h then cooled again on an ice bath. The mixture was carefully hydrolyzed with saturated

aqueous Na2SO4 then filtered through celite and reduced to an oil. Column chromatography provided the pure 519 (1.3 g, 68%) which was obtained as a colorless oil. 13C NMR = 130.2, 130.1 (x2), 127.9 (x3), 112.3, 79.3, 64.4, 44.7, 38.3, 35.4, 31.5, 29.9 (x2), 29.7, 29.6 (x2), 29.5 (x3), 29.3 (x2), 27.2 (x3), 25.6, 24.5, 23.3, 226, 14.1; Electrospray MS (+ve): Molecular weight for C44H80NO2 (M + H)+ Calc. 654.6, Found 654.6.

Formulations prepared by either the standard or extrusion-free method can be characterized in similar manners. For example, formulations are typically characterized by visual inspection. They should be whitish translucent solutions free from aggregates or sediment. Particle size and particle size distribution of lipid-nanoparticles can be measured by light scattering using, for example, a Malvern Zetasizer Nano ZS (Malvern, USA). Particles should be about 20-300 nm, such as 40-100 nm in size. The particle size distribution should be unimodal. The total dsRNA concentration in the formulation, as well as the entrapped fraction, is estimated using a dye exclusion assay. A sample of the formulated dsRNA can be incubated with an RNA-binding dye, such as Ribogreen (Molecular Probes) in the presence or absence of a formulation disrupting surfactant, *e.g.,* 0.5% Triton-X100. The total dsRNA in the formulation can be determined by the signal from the sample containing the surfactant, relative to a standard curve. The entrapped fraction is determined by subtracting the "free" dsRNA content (as measured by the signal in the absence of surfactant) from the total dsRNA content. Percent entrapped dsRNA is typically >85%. For SNALP formulation, the particle size is at least 30 nm, at least 40 nm, at least 50 nm, at least 60 nm, at least 70 nm, at least 80 nm, at least 90 nm, at least 100 nm, at least 110 nm, and at least 120 nm. The suitable range is typically about at least 50 nm to about at least 110 nm, about at least 60 nm to about at least 100 nm, or about at least 80 nm to about at least 90 nm.

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. In some embodiments, oral formulations are those in which dsRNAs featured in the disclosure are administered in conjunction with one or more penetration enhancers surfactants and chelators. Suitable surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Suitable bile acids/salts include chenodeoxycholic acid (CDCA) and ursodeoxychenodeoxycholic acid (UDCA), cholic acid, dehydrocholic acid, deoxycholic acid, glucholic acid, glycholic acid, glycodeoxycholic acid, taurocholic acid, taurodeoxycholic acid, sodium tauro-24,25-dihydro-fusidate and sodium glycodihydrofusidate. Suitable fatty acids include arachidonic acid, undecanoic acid, oleic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a monoglyceride, a diglyceride or a pharmaceutically acceptable salt thereof (*e.g.,* sodium). In some embodiments, combinations of penetration enhancers are used, for example, fatty acids/salts in

combination with bile acids/salts. One exemplary combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. DsRNAs featured in the disclosure may be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. DsRNA complexing agents include poly-amino acids; polyimines; polyacrylates; polyalkylacrylates, polyoxethanes, polyalkylcyanoacrylates; cationized gelatins, albumins, starches, acrylates, polyethyleneglycols (PEG) and starches; polyalkylcyanoacrylates; DEAE-derivatized polyimines, pollulans, celluloses and starches. Suitable complexing agents include chitosan, N-trimethylchitosan, poly-L-lysine, polyhistidine, polyornithine, polyspermines, protamine, polyvinylpyridine, polythiodiethylaminomethylethylene P(TDAE), polyaminostyrene (*e.g.,* p-amino), poly(methylcyanoacrylate), poly(ethylcyanoacrylate), poly(butylcyanoacrylate), poly(isobutylcyanoacrylate), poly(isohexylcynaoacrylate), DEAE-methacrylate, DEAE-hexylacrylate, DEAE-acrylamide, DEAE-albumin and DEAE-dextran, polymethylacrylate, polyhexylacrylate, poly(D,L-lactic acid), poly(DL-lactic-co-glycolic acid (PLGA), alginate, and polyethyleneglycol (PEG). Oral formulations for dsRNAs and their preparation are described in detail in U.S. Patent 6,887,906, U.S. Publication No. 20030027780, and U.S. Patent No. 6,747,014, each of which is incorporated herein by reference.

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

Pharmaceutical compositions of the present disclosure include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids.

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

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

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

B. Additional Formulations

1. *Emulsions*

The compositions of the present disclosure may be prepared and formulated as emulsions. Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter (*see e.g.,* Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi *et al.*, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 301). Emulsions are often biphasic systems comprising two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions may be of either the water-in-oil (w/o) or the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase, the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase, the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions may contain additional components in addition to the dispersed phases, and the active drug which may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants may also be present in emulsions as needed. Pharmaceutical emulsions may also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise, a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion may be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that may be incorporated into either phase of the emulsion. Emulsifiers may broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (*see e.g.,* Ansel's *Pharmaceutical Dosage Forms and Drug Delivery Systems,* Allen,

LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Synthetic surfactants, also known as surface active agents, have found wide applicability in the formulation of emulsions and have been reviewed in the literature (*see e.g.,* Ansel's *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rieger, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199). Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The ratio of the hydrophilic to the hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants may be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic and amphoteric (*see e.g.,* Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY Rieger, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

Naturally occurring emulsifiers used in emulsion formulations include lanolin, beeswax, phosphatides, lecithin and acacia. Absorption bases possess hydrophilic properties such that they can soak up water to form w/o emulsions yet retain their semisolid consistencies, such as anhydrous lanolin and hydrophilic petrolatum. Finely divided solids have also been used as good emulsifiers especially in combination with surfactants and in viscous preparations. These include polar inorganic solids, such as heavy metal hydroxides, nonswelling clays such as bentonite, attapulgite, hectorite, kaolin, montmorillonite, colloidal aluminum silicate and colloidal magnesium aluminum silicate, pigments and nonpolar solids such as carbon or glyceryl tristearate.

A large variety of non-emulsifying materials are also included in emulsion formulations and contribute to the properties of emulsions. These include fats, oils, waxes, fatty acids, fatty alcohols, fatty esters, humectants, hydrophilic colloids, preservatives and antioxidants (Block, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

Hydrophilic colloids or hydrocolloids include naturally occurring gums and synthetic polymers such as polysaccharides (for example, acacia, agar, alginic acid, carrageenan, guar gum, karaya gum, and tragacanth), cellulose derivatives (for example, carboxymethylcellulose and carboxypropylcellulose), and synthetic polymers (for example, carbomers, cellulose ethers, and carboxyvinyl polymers). These disperse or swell in water to form colloidal solutions that stabilize

emulsions by forming strong interfacial films around the dispersed-phase droplets and by increasing the viscosity of the external phase.

Since emulsions often contain a number of ingredients such as carbohydrates, proteins, sterols and phosphatides that may readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation. Antioxidants used may be free radical scavengers such as tocopherols, alkyl gallates, butylated hydroxyanisole, butylated hydroxytoluene, or reducing agents such as ascorbic acid and sodium metabisulfite, and antioxidant synergists such as citric acid, tartaric acid, and lecithin.

The application of emulsion formulations via dermatological, oral and parenteral routes and methods for their manufacture have been reviewed in the literature (*see e.g.,* Ansel's *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Emulsion formulations for oral delivery have been very widely used because of ease of formulation, as well as efficacy from an absorption and bioavailability standpoint (*see e.g.,* Ansel's *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Idson, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Mineral-oil base laxatives, oil-soluble vitamins and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

In some embodiments of the present disclosure, the compositions of iRNAs and nucleic acids are formulated as microemulsions. A microemulsion may be defined as a system of water, oil and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (*see e.g.,* Ansel's *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically, microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotopically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: *Controlled Release of Drugs*: *Polymers and Aggregate Systems*, Rosoff, M., Ed., 1989,

VCH Publishers, New York, pages 185-215). Microemulsions commonly are prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used and on the structure and geometric packing of the polar heads and hydrocarbon tails of the surfactant molecules (Schott, in Remington's *Pharmaceutical Sciences*, Mack Publishing Co., Easton, Pa., 1985, p. 271).

The phenomenological approach utilizing phase diagrams has been extensively studied and has yielded a comprehensive knowledge, to one skilled in the art, of how to formulate microemulsions (*see e.g.,* Ansel's *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Block, in *Pharmaceutical Dosage Forms*, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335). Compared to conventional emulsions, microemulsions offer the advantage of solubilizing water-insoluble drugs in a formulation of thermodynamically stable droplets that are formed spontaneously.

Surfactants used in the preparation of microemulsions include, but are not limited to, ionic surfactants, non-ionic surfactants, Brij 96, polyoxyethylene oleyl ethers, polyglycerol fatty acid esters, tetraglycerol monolaurate (ML310), tetraglycerol monooleate (MO310), hexaglycerol monooleate (PO310), hexaglycerol pentaoleate (PO500), decaglycerol monocaprate (MCA750), decaglycerol monooleate (MO750), decaglycerol sequioleate (SO750), decaglycerol decaoleate (DAO750), alone or in combination with cosurfactants. The cosurfactant, usually a short-chain alcohol such as ethanol, 1-propanol, and 1-butanol, serves to increase the interfacial fluidity by penetrating into the surfactant film and consequently creating a disordered film because of the void space generated among surfactant molecules. Microemulsions may, however, be prepared without the use of cosurfactants and alcohol-free self-emulsifying microemulsion systems are known in the art. The aqueous phase may typically be, but is not limited to, water, an aqueous solution of the drug, glycerol, PEG300, PEG400, polyglycerols, propylene glycols, and derivatives of ethylene glycol. The oil phase may include, but is not limited to, materials such as Captex 300, Captex 355, Capmul MCM, fatty acid esters, medium chain (C8-C12) mono, di, and tri-glycerides, polyoxyethylated glyceryl fatty acid esters, fatty alcohols, polyglycolized glycerides, saturated polyglycolized C8-C10 glycerides, vegetable oils and silicone oil.

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (*see e.g.,* U.S. Patent Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides *et al.*, 1994 *Pharmaceutical Research* 11:1385-1390; Ritschel, 1993 *Meth. Find. Exp. Clin. Pharmacol.* 13:205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of

drug absorption due to surfactant-induced alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (*see e.g.,* U.S. Patent Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides *et al.*, 1994 *Pharmaceutical Research* 11:1385; Ho *et al.*, 1996 *J. Pharm. Sci.* 85:138-143). Often microemulsions may form spontaneously when their components are brought together at ambient temperature. This may be particularly advantageous when formulating thermolabile drugs, peptides or iRNAs. Microemulsions have also been effective in the transdermal delivery of active components in both cosmetic and pharmaceutical applications. It is expected that the microemulsion compositions and formulations of the present disclosure will facilitate the increased systemic absorption of iRNAs and nucleic acids from the gastrointestinal tract, as well as improve the local cellular uptake of iRNAs and nucleic acids.

Microemulsions of the present disclosure may also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the iRNAs and nucleic acids of the present disclosure. Penetration enhancers used in the microemulsions of the present disclosure may be classified as belonging to one of five broad categories--surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p. 92). Each of these classes has been discussed above.

2. *Penetration Enhancers*

In some embodiments, the present disclosure employs various penetration enhancers to effect the efficient delivery of nucleic acids, particularly iRNAs, to the skin of animals. Most drugs are present in solution in both ionized and nonionized forms. However, usually only lipid soluble or lipophilic drugs readily cross cell membranes. It has been discovered that even non-lipophilic drugs may cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

Penetration enhancers may be classified as belonging to one of five broad categories, *i.e.*, surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (*see e.g.,* Malmsten, M. Surfactants and polymers in drug delivery, *Informa Health Care*, New York, NY, 2002; Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p.92). Each of the above-mentioned classes of penetration enhancers are described below in greater detail.

Surfactants: In connection with the present disclosure, surfactants (or "surface-active agents") are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous solution and another liquid, with the result that absorption of iRNAs through the mucosa is enhanced. In addition to bile salts and fatty acids, these penetration enhancers include, for example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether) (*see e.g.,* Malmsten, M. Surfactants and polymers in drug delivery,

Informa Health Care, New York, NY, 2002; Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p.92); and perfluorochemical emulsions, such as FC-43. Takahashi *et al.*, 1988 *J. Pharm. Pharmacol.* 40:252).

Fatty acids: Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C_{1-20} alkyl esters thereof (*e.g.,* methyl, isopropyl and t-butyl), and mono- and di-glycerides thereof (*i.e.*, oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, *etc.*) (*see e.g.,* Touitou, E. *et al. Enhancement in Drug Delivery*, CRC Press, Danvers, MA, 2006; Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p.92; Muranishi, 1990 *Critical Reviews in Therapeutic Drug Carrier Systems* 7:1-33; El Hariri *et al.*, 1992 *J. Pharm. Pharmacol.* 44:651-654).

Bile salts: The physiological role of bile includes the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (*see e.g.,* Malmsten, M. Surfactants and polymers in drug delivery, *Informa Health Care*, New York, NY, 2002; Brunton, Chapter 38 in: Goodman & Gilman's *The Pharmacological Basis of Therapeutics*, 9th Ed., Hardman *et al.* Eds., McGraw-Hill, New York, 1996, pp. 934-935). Various natural bile salts, and their synthetic derivatives, act as penetration enhancers. Thus, the term "bile salts" includes any of the naturally occurring components of bile as well as any of their synthetic derivatives. Suitable bile salts include, for example, cholic acid (or its pharmaceutically acceptable sodium salt, sodium cholate), dehydrocholic acid (sodium dehydrocholate), deoxycholic acid (sodium deoxycholate), glucholic acid (sodium glucholate), glycholic acid (sodium glycocholate), glycodeoxycholic acid (sodium glycodeoxycholate), taurocholic acid (sodium taurocholate), taurodeoxycholic acid (sodium taurodeoxycholate), chenodeoxycholic acid (sodium chenodeoxycholate), ursodeoxycholic acid (UDCA), sodium tauro-24,25-dihydro-fusidate (STDHF), sodium glycodihydrofusidate and polyoxyethylene-9-lauryl ether (POE) (*see e.g.,* Malmsten, M. Surfactants and polymers in drug delivery, *Informa Health Care*, New York, NY, 2002; Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Swinyard, Chapter 39 In: *Remington's Pharmaceutical Sciences*, 18th Ed., Gennaro, ed., Mack Publishing Co., Easton, Pa., 1990, pages 782-783; Muranishi, 1990 *Critical Reviews in Therapeutic Drug Carrier Systems* 7:1-33; Yamamoto *et al.*, 1992 *J. Pharm. Exp. Ther.* 263:25; Yamashita *et al.*, 1990 *J. Pharm. Sci.* 79:579-583).

Chelating Agents: Chelating agents, as used in connection with the present disclosure, can be defined as compounds that remove metallic ions from solution by forming complexes therewith, with the result that absorption of iRNAs through the mucosa is enhanced. With regards to their use as penetration enhancers in the present disclosure, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for

catalysis and are thus inhibited by chelating agents (Jarrett, 1993 *J. Chromatogr.* 618:315-339). Suitable chelating agents include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (*e.g.,* sodium salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of β-diketones (enamines) (*see e.g.,* Katdare, A. *et al.*, *Excipient development for pharmaceutical, biotechnology, and drug delivery*, CRC Press, Danvers, MA, 2006; Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92; Muranishi, 1990 *Critical Reviews in Therapeutic Drug Carrier Systems*, 7:1-33; Buur *et al.*, 1990 *J. Control Rel.*, 14:43-51).

Non-chelating non-surfactants: As used herein, non-chelating non-surfactant penetration enhancing compounds can be defined as compounds that demonstrate insignificant activity as chelating agents or as surfactants but that nonetheless enhance absorption of iRNAs through the alimentary mucosa (*see e.g.,* Muranishi, 1990 *Critical Reviews in Therapeutic Drug Carrier Systems* 7:1-33). This class of penetration enhancers include, for example, unsaturated cyclic ureas, 1-alkyl- and 1-alkenylazacyclo-alkanone derivatives (Lee *et al.*, *Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, page 92); and non-steroidal anti-inflammatory agents such as diclofenac sodium, indomethacin and phenylbutazone (Yamashita *et al.*, 1987 *J. Pharm. Pharmacol.* 39:621-626).

Agents that enhance uptake of iRNAs at the cellular level may also be added to the pharmaceutical and other compositions of the present disclosure. For example, cationic lipids, such as lipofectin (Junichi *et al*, U.S. Patent No. 5,705,188), cationic glycerol derivatives, and polycationic molecules, such as polylysine (Lollo *et al.*, PCT Application WO 97/30731), are also known to enhance the cellular uptake of dsRNAs. Examples of commercially available transfection reagents include, for example Lipofectamine™ (Invitrogen; Carlsbad, CA), Lipofectamine 2000™ (Invitrogen; Carlsbad, CA), 293fectin™ (Invitrogen; Carlsbad, CA), Cellfectin™ (Invitrogen; Carlsbad, CA), DMRIE-C™ (Invitrogen; Carlsbad, CA), FreeStyle™ MAX (Invitrogen; Carlsbad, CA), Lipofectamine™ 2000 CD (Invitrogen; Carlsbad, CA), Lipofectamine™ (Invitrogen; Carlsbad, CA), RNAiMAX (Invitrogen; Carlsbad, CA), Oligofectamine™ (Invitrogen; Carlsbad, CA), Optifect™ (Invitrogen; Carlsbad, CA), X-tremeGENE Q2 Transfection Reagent (Roche; Grenzacherstrasse, Switzerland), DOTAP Liposomal Transfection Reagent (Grenzacherstrasse, Switzerland), DOSPER Liposomal Transfection Reagent (Grenzacherstrasse, Switzerland), or Fugene (Grenzacherstrasse, Switzerland), Transfectam® Reagent (Promega; Madison, WI), TransFast™ Transfection Reagent (Promega; Madison, WI), Tfx™-20 Reagent (Promega; Madison, WI), Tfx™-50 Reagent (Promega; Madison, WI), DreamFect™ (OZ Biosciences; Marseille, France), EcoTransfect (OZ Biosciences; Marseille, France), TransPass[a] D1 Transfection Reagent (New England Biolabs; Ipswich, MA, USA), LyoVec™/LipoGen™ (Invivogen; San Diego, CA, USA), PerFectin Transfection Reagent (Genlantis; San Diego, CA, USA), NeuroPORTER Transfection Reagent (Genlantis; San Diego, CA, USA), GenePORTER Transfection reagent (Genlantis; San Diego, CA, USA), GenePORTER 2 Transfection reagent (Genlantis; San Diego, CA, USA), Cytofectin Transfection Reagent (Genlantis; San Diego,

CA, USA), BaculoPORTER Transfection Reagent (Genlantis; San Diego, CA, USA), TroganPORTER™ transfection Reagent (Genlantis; San Diego, CA, USA), RiboFect (Bioline; Taunton, MA, USA), PlasFect (Bioline; Taunton, MA, USA), UniFECTOR (B-Bridge International; Mountain View, CA, USA), SureFECTOR (B-Bridge International; Mountain View, CA, USA), or HiFect™ (B-Bridge International, Mountain View, CA, USA), among others.

Other agents may be utilized to enhance the penetration of the administered nucleic acids, including glycols such as ethylene glycol and propylene glycol, pyrrols such as 2-pyrrol, azones, and terpenes such as limonene and menthone.

C. Carriers

Certain compositions of the present disclosure also incorporate carrier compounds in the formulation. As used herein, "carrier compound" can refer to a nucleic acid, or analog thereof, which is inert (*i.e.*, does not possess biological activity per se) but is recognized as a nucleic acid by *in vivo* processes that reduce the bioavailability of a nucleic acid having biological activity by, for example, degrading the biologically active nucleic acid or promoting its removal from circulation. The coadministration of a nucleic acid and a carrier compound, typically with an excess of the latter substance, can result in a substantial reduction of the amount of nucleic acid recovered in the liver, kidney or other extracirculatory reservoirs, presumably due to competition between the carrier compound and the nucleic acid for a common receptor. For example, the recovery of a partially phosphorothioate dsRNA in hepatic tissue can be reduced when it is coadministered with polyinosinic acid, dextran sulfate, polycytidic acid or 4-acetamido-4'isothiocyano-stilbene-2,2'-disulfonic acid (Miyao *et al.*, 1995 *DsRNA Res. Dev.* 5:115-121; Takakura *et al.*, 1996 *DsRNA & Nucl. Acid Drug Dev.* 6:177-183).

1. *Excipients*

In contrast to a carrier compound, a pharmaceutical carrier or excipient may comprise, *e.g.,* a pharmaceutically acceptable solvent, suspending agent or any other pharmacologically inert vehicle for delivering one or more nucleic acids to an animal. The excipient may be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, *etc.*, when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutical carriers include, but are not limited to, binding agents (*e.g.,* pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, *etc.*); fillers (*e.g.,* lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, *etc.*); lubricants (*e.g.,* magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, *etc.*); disintegrants (*e.g.,* starch, sodium starch glycolate, *etc.*); and wetting agents (*e.g.,* sodium lauryl sulphate, *etc.*).

Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can also be used to formulate the

compositions of the present disclosure. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

Formulations for topical administration of nucleic acids may include sterile and non-sterile aqueous solutions, non-aqueous solutions in common solvents such as alcohols, or solutions of the nucleic acids in liquid or solid oil bases. The solutions may also contain buffers, diluents and other suitable additives. Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can be used.

Suitable pharmaceutically acceptable excipients include, but are not limited to, water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

D. Other Components

The compositions of the present disclosure may additionally contain other adjunct components conventionally found in pharmaceutical compositions, *e.g.,* at their art-established usage levels. Thus, for example, the compositions may contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or may contain additional materials useful in physically formulating various dosage forms of the compositions of the present disclosure, such as dyes, flavoring agents, preservatives, antioxidants, opacifiers, thickening agents and stabilizers. However, such materials, when added, should not unduly interfere with the biological activities of the components of the compositions of the present disclosure. The formulations can be sterilized and, if desired, mixed with auxiliary agents, *e.g.,* lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings and/or aromatic substances and the like which do not deleteriously interact with the nucleic acid(s) of the formulation.

Aqueous suspensions may contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

In some embodiments, pharmaceutical compositions featured in the disclosure include (a) one or more iRNA compounds and (b) one or more biologic agents which function by a non-RNAi mechanism. Examples of such biologic agents include agents that interfere with an interaction of ANGPTL7 and at least one ANGPTL7 binding partner.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.,* for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it

can be expressed as the ratio LD50/ED50. Compounds that exhibit high therapeutic indices are typical.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of compositions featured in the disclosure lies generally within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods featured in the disclosure, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range of the compound or, when appropriate, of the polypeptide product of a target sequence (*e.g.,* achieving a decreased concentration of the polypeptide) that includes the IC50 (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

In addition to their administration, as discussed above, the iRNAs featured in the disclosure can be administered in combination with other known agents effective in treatment of diseases or disorders related to ANGPTL7 expression (*e.g.,* glaucoma or conditions associated with glaucoma). In any event, the administering physician can adjust the amount and timing of iRNA administration on the basis of results observed using standard measures of efficacy known in the art or described herein.

IV. Methods of treating disorders related to expression of ANGPTL7

The present disclosure relates to the use of an iRNA targeting ANGPTL7 to inhibit ANGPTL7 expression and/or to treat a disease, disorder, or pathological process that is related to ANGPTL7 expression (*e.g.,* glaucoma or conditions associated with glaucoma).

In some aspects, a method of treatment of a disorder related to expression of ANGPTL7 is provided, the method comprising administering an iRNA (*e.g.,* a dsRNA) disclosed herein to a subject in need thereof. In some embodiments, the iRNA inhibits (decreases) ANGPTL7 expression.

In some embodiments, the subject is an animal that serves as a model for a disorder related to ANGPTL7 expression, *e.g.,* glaucoma or conditions associated with glaucoma.

A. Glaucoma or Conditions Associated with Glaucoma

In some embodiments, the disorder related to ANGPTL7 expression is glaucoma or conditions associated with glaucoma. Non-limiting examples of glaucoma or conditions associated with glaucoma that are treatable using the methods described herein include glaucoma, open-angle glaucoma, primary open-angle glaucoma, angle-closure glaucoma, ocular inflammation, systemic inflammation, anterior uveitis, acute retinal necrosis, Sturge-Weber syndrome, Axenfeld-Rieger syndrome, Marfan syndrome, homocystinuria, Weill-Marchesani syndrome, and autoimmune diseases, such as juvenile rheumatoid arthritis and Marie-Strumpell ankylosing spondylitis.

Glaucoma is a group of eye disorders characterized by progressive optic nerve damage, often caused by a relative increase in intraocular pressure. Clinical and pathological features of glaucoma or conditions associated with glaucoma include, but are not limited to, an increased intraocular pressure, vision loss, a reduction in visual acuity (*e.g.,* characterized by floating spots, blurriness around the edges or center of field of vision (*e.g.,* scotoma)), ocular inflammation, ocular pain, headache, and/or optic nerve damage.

Open-angle glaucoma, the most common form of glaucoma, presents with a normal angle between the iris and the cornea, and is caused by slow clogging of the aqueous humor drainage canals. Primary open-angle glaucoma is open-angle glaucoma with no identifiable cause. Open-angle glaucoma usually develops gradually.

Angle-closure glaucoma, also known as acute glaucoma or narrow-angle glaucoma, presents with a closed or narrow angle between the iris and the cornea, and is caused by blockage of the aqueous humor drainage canals. Angle-closure glaucoma often develops rapidly with noticeable symptoms and requires immediate treatment.

In some embodiments, the subject with glaucoma or conditions associated with glaucoma is less than 18 years old. In some embodiments, the subject with glaucoma or conditions associated with glaucoma is an adult. In some embodiments, the subject has, or is identified as having, elevated levels of ANGPTL7 mRNA or protein relative to a reference level (*e.g.*, a level of ANGPTL7 that is greater than a reference level).

In some embodiments, the glaucoma or conditions associated with glaucoma is diagnosed using analysis of a sample from the subject (*e.g.,* an optic nerve sample). In some embodiments, the sample is analyzed using a method selected from one or more of: fluorescent in situ hybridization (FISH), immunohistochemistry, ANGPTL7 immunoassay, electron microscopy, laser microdissection, and mass spectrometry. In some embodiments, glaucoma or conditions associated with glaucoma is diagnosed using any suitable diagnostic test or technique, *e.g.,* tonometry, pachymetry, evaluation of the retina, gonioscopy, angiography (*e.g.,* fluorescein angiography or indocyanine green angiography), electroretinography, ultrasonography, optical coherence tomography (OCT), computed tomography (CT) and magnetic resonance imaging (MRI), color vision testing, visual field testing, slit-lamp examination, ophthalmoscopy, and physical examination (*e.g.,* to assess visual acuity (*e.g.*, by fundoscopy or optical coherence tomography (OCT)).

B. Combination Therapies

In some embodiments, an iRNA (*e.g.,* a dsRNA) disclosed herein is administered in combination with a second therapy (*e.g.,* one or more additional therapies) known to be effective in treating a disorder related to ANGPTL7 expression (*e.g.,* glaucoma) or a symptom of such a disorder. The iRNA may be administered before, after, or concurrent with the second therapy. In some embodiments, the iRNA is administered before the second therapy. In some embodiments, the iRNA

is administered after the second therapy. In some embodiments, the iRNA is administered concurrent with the second therapy.

The second therapy may be an additional therapeutic agent. The iRNA and the additional therapeutic agent can be administered in combination in the same composition or the additional therapeutic agent can be administered as part of a separate composition.

In some embodiments, the second therapy is a non-iRNA therapeutic agent that is effective to treat the disorder or symptoms of the disorder.

In some embodiments, the iRNA is administered in conjunction with a therapy. Exemplary combination therapies include, but are not limited to, medication to reduce intraocular pressure, laser treatment, surgery or trabeculectomy. In some embodiments, the additional therapeutic agent comprises a prostaglandin analog, a beta blocker, an alpha-adrenergic agonist, a carbonic anhydrase inhibitor, inhibitors of Rho kinase (ROCK), iRNA agent for ROCK, an inhibitor of Rho GTPases, an anti-Rho GTPase agent, or an anti-ANGPTL7 agent.

In some embodiments, the additional therapeutic agent is a prostaglandin analog. In some embodiments, the prostaglandin analog comprises bimatoprost (Lumigan®), latanoprost (Xalatan®), tafluprost (Zioptan™), latanoprostene bunod (Vyzulta™), or travoprost (Travatan Z®).

In some embodiments, the additional therapeutic agent is a beta blocker. In some embodiments, the beta blocker comprises betaxolol (Betoptic S®), or timolol (Betimol®, Timoptic).

In some embodiments, the additional therapeutic agent is an alpha-adrenergic agonist. In some embodiments, the alpha-adrenergic agonist comprises brimonidine (Alphagan®P) or apraclonidine (Iopidine®).

In some embodiments, the additional therapeutic agent is a carbonic anhydrase inhibitor. In some embodiments, the carbonic anhydrase inhibitor comprises dorzolamide (Trusopt®), brinzolamide (Azopt®), acetazolamide (Diamox), or methazolamide (Neptazane®).

In some embodiments, the additional therapeutic agent is a ROCK inhibitor or a ROCK iRNA agent. In some embodiments, the ROCK inhibitor is netarsudil (Rhopressa®).

In some embodiments, the additional therapeutic agent is an anti-Rho GTPase agent. In some embodiments, the anti-Rho GTPase agent is an antibody molecule. In some embodiments the antibody is a monoclonal antibody.

In some embodiments, the additional therapeutic agent is an anti-ANGPTL7 agent. In some embodiments, the anti-ANGPTL7 agent is an antibody molecule. In some embodiments the antibody is a monoclonal antibody.

C. Administration dosages, routes, and timing

A subject (*e.g.,* a human subject, *e.g.,* a patient) can be administered a therapeutic amount of iRNA. The therapeutic amount can be, *e.g.,* 0.05-50 mg/kg.

In some embodiments, the iRNA is formulated for delivery to a target organ, *e.g.,* to the eye.

In some embodiments, the iRNA is formulated as a lipid formulation, *e.g.,* an LNP formulation as described herein. In some such embodiments, the therapeutic amount is 0.05-5 mg/kg dsRNA. In some embodiments, the lipid formulation, *e.g.,* LNP formulation, is administered intravenously.

In some embodiments, the iRNA is in the form of a GalNAc conjugate *e.g.,* as described herein. In some such embodiments, the therapeutic amount is 0.5-50 mg dsRNA. In some embodiments, the *e.g.,* GalNAc conjugate is administered subcutaneously.

In some embodiments, the administration is repeated, for example, on a regular basis, such as, daily, biweekly (*i.e.*, every two weeks) for one month, two months, three months, four months, six months or longer. After an initial treatment regimen, the treatments can be administered on a less frequent basis. For example, after administration biweekly for three months, administration can be repeated once per month, for six months or a year or longer.

In some embodiments, the iRNA agent is administered in two or more doses. In some embodiments, the number or amount of subsequent doses is dependent on the achievement of a desired effect, *e.g.,* to (a) inhibit or reduce intraocular pressure; (b) inhibit or reduce the expression or activity of ANGPTL7; (c) increase drainage of aqueous humor; (d) inhibit or reduce optic nerve damage; or (e) inhibit or reduce retinal ganglion cell death, or the achievement of a therapeutic or prophylactic effect, *e.g.,* reduction or prevention of one or more symptoms associated with the disorder.

In some embodiments, the iRNA agent is administered according to a schedule. For example, the iRNA agent may be administered once per week, twice per week, three times per week, four times per week, or five times per week. In some embodiments, the schedule involves regularly spaced administrations, *e.g.,* hourly, every four hours, every six hours, every eight hours, every twelve hours, daily, every 2 days, every 3 days, every 4 days, every 5 days, weekly, biweekly, or monthly. In some embodiments, the iRNA agent is administered at the frequency required to achieve a desired effect.

In some embodiments, the schedule involves closely spaced administrations followed by a longer period of time during which the agent is not administered. For example, the schedule may involve an initial set of doses that are administered in a relatively short period of time (*e.g.,* about every 6 hours, about every 12 hours, about every 24 hours, about every 48 hours, or about every 72 hours) followed by a longer time period (*e.g.,* about 1 week, about 2 weeks, about 3 weeks, about 4 weeks, about 5 weeks, about 6 weeks, about 7 weeks, or about 8 weeks) during which the iRNA agent is not administered. In some embodiments, the iRNA agent is initially administered hourly and is later administered at a longer interval (*e.g.,* daily, weekly, biweekly, or monthly). In some embodiments, the iRNA agent is initially administered daily and is later administered at a longer interval (*e.g.,* weekly, biweekly, or monthly). In certain embodiments, the longer interval increases over time or is determined based on the achievement of a desired effect.

Before administration of a full dose of the iRNA, patients can be administered a smaller dose, such as a 5% infusion dose, and monitored for adverse effects, such as an allergic reaction, or for elevated lipid levels or blood pressure. In another example, the patient can be monitored for unwanted effects.

V. Methods for modulating expression of ANGPTL7

In some aspects, the disclosure provides a method for modulating (*e.g.,* inhibiting or activating) the expression of ANGPTL7, *e.g.,* in a cell, in a tissue, or in a subject. In some embodiments, the cell or tissue is *ex vivo*, *in vitro*, or *in vivo*. In some embodiments, the cell or tissue is in the eye (*e.g.,* an optic nerve cell, a trabecular meshwork cell, a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel). In some embodiments, the cell or tissue is in a subject (*e.g.,* a mammal, such as, for example, a human). In some embodiments, the subject (*e.g.,* the human) is at risk, or is diagnosed with a disorder related to expression of ANGPTL7 expression, as described herein.

In some embodiments, the method includes contacting the cell with an iRNA as described herein, in an amount effective to decrease the expression of ANGPTL7 in the cell. In some embodiments, contacting a cell with an RNAi agent includes contacting a cell *in vitro* with the RNAi agent or contacting a cell *in vivo* with the RNAi agent. In some embodiments, the RNAi agent is put into physical contact with the cell by the individual performing the method, or the RNAi agent may be put into a situation that will permit or cause it to subsequently come into contact with the cell. Contacting a cell in vitro may be done, for example, by incubating the cell with the RNAi agent. Contacting a cell in vivo may be done, for example, by injecting the RNAi agent into or near the tissue where the cell is located, or by injecting the RNAi agent into another area, *e.g.,* ocular tissue. For example, the RNAi agent may contain or be coupled to a ligand, *e.g.,* a lipophilic moiety or moieties as described below and further detailed, *e.g.,* in PCT/US2019/031170 which is incorporated herein by reference in its entirety, including the passages therein describing lipophilic moieties, that directs or otherwise stabilizes the RNAi agent at a site of interest. Combinations of in vitro and in vivo methods of contacting are also possible. For example, a cell may also be contacted in vitro with an RNAi agent and subsequently transplanted into a subject.

The expression of ANGPTL7 may be assessed based on the level of expression of ANGPTL7 mRNA, ANGPTL7 protein, or the level of another parameter functionally linked to the level of expression of ANGPTL7. In some embodiments, the expression of ANGPTL7 is inhibited by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95%. In some embodiments, the iRNA has an IC_{50} in the

range of 0.001-0.01 nM, 0.001-0.10 nM, 0.001-1.0 nM, 0.001-10 nM, 0.01-0.05 nM, 0.01-0.50 nM, 0.02-0.60 nM, 0.01-1.0 nM, 0.01-1.5 nM, 0.01-10 nM. The IC_{50} value may be normalized relative to an appropriate control value, *e.g.,* the IC_{50} of a non-targeting iRNA.

In some embodiments, the method includes introducing into the cell or tissue an iRNA as described herein and maintaining the cell or tissue for a time sufficient to obtain degradation of the mRNA transcript of ANGPTL7, thereby inhibiting the expression of ANGPTL7 in the cell or tissue.

In some embodiments, the method includes administering a composition described herein, *e.g.,* a composition comprising an iRNA that binds ANGPTL7, to the mammal such that expression of the target ANGPTL7 is decreased, such as for an extended duration, *e.g.,* at least two, three, four days or more, *e.g.,* one week, two weeks, three weeks, or four weeks or longer. In some embodiments, the decrease in expression of ANGPTL7 is detectable within 1 hour, 2 hours, 4 hours, 8 hours, 12 hours, or 24 hours of the first administration.

In some embodiments, the method includes administering a composition as described herein to a mammal such that expression of the target ANGPTL7 is increased by *e.g.*, at least 10% compared to an untreated animal. In some embodiments, the activation of ANGPTL7 occurs over an extended duration, *e.g.*, at least two, three, four days or more, *e.g.*, one week, two weeks, three weeks, four weeks, or more. Without wishing to be bound by theory, an iRNA can activate ANGPTL7 expression by stabilizing the ANGPTL7 mRNA transcript, interacting with a promoter in the genome, or inhibiting an inhibitor of ANGPTL7 expression.

The iRNAs useful for the methods and compositions featured in the disclosure specifically target RNAs (primary or processed) of ANGPTL7. Compositions and methods for inhibiting the expression of ANGPTL7 using iRNAs can be prepared and performed as described elsewhere herein.

In some embodiments, the method includes administering a composition containing an iRNA, where the iRNA includes a nucleotide sequence that is complementary to at least a part of an RNA transcript of ANGPTL7 of the subject, *e.g.,* the mammal, *e.g.,* the human, to be treated. The composition may be administered by any appropriate means known in the art including, but not limited to ocular (*e.g.,* intraocular), topical, and intravenous administration.

In certain embodiments, the composition is administered intraocularly (*e.g.,* by intravitreal administration, *e.g.*, intravitreal injection; transscleral administration, *e.g.*, transscleral injection; subconjunctival administration, *e.g.*, subconjunctival injection; retrobulbar administration, *e.g.*, retrobulbar injection; intracameral administration, *e.g.*, intracameral injection; or subretinal administration, *e.g.*, subretinal injection. In other embodiments, the composition is administered topically. In other embodiments, the composition is administered by intravenous infusion or injection.

In certain embodiments, the composition is administered by intravenous infusion or injection. In some such embodiments, the composition comprises a lipid formulated siRNA (*e.g.,* an LNP formulation, such as an LNP11 formulation) for intravenous infusion.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the iRNAs and methods featured in the disclosure, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

SPECIFIC EMBODIMENTS

Specific embodiments of the present disclosure are provided below.

(1) dsRNA Agents

In one aspect, the present disclosure provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of angiopoietin like 7 (ANGPTL7), wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of a coding strand of mouse ANGPTL7 and the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion of a non-coding strand of mouse ANGPTL7 such that the sense strand is complementary to the at least 15 contiguous nucleotides in the antisense strand. In one embodiment, the coding strand of mouse ANGPTL7 comprises the sequence SEQ ID NO: 1. In a further embodiment, the non-coding strand of mouse ANGPTL7 comprises the sequence of SEQ ID NO: 2.

In another aspect, the present disclosure provides a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ANGPTL7, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 such that the sense strand is complementary to the at least 15 contiguous nucleotides in the antisense strand. In one embodiment, the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1.

In a certain embodiment, the dsRNA of any of the preceding embodiments comprises a sense strand and an antisense strand, wherein the antisense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 such that the sense strand is complementary to the at least 17 contiguous nucleotides in the antisense strand. In a further embodiment, the sense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1.

In a certain embodiment, the dsRNA of any of the preceding embodiments comprises a sense strand and an antisense strand, wherein the antisense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 such that the sense strand is complementary to the at least 19 contiguous nucleotides in the antisense strand. In a further embodiment, the sense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1.

In a certain embodiment, the dsRNA of any of the preceding embodiments comprises a sense strand and an antisense strand, wherein the antisense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, of a portion of nucleotide sequence of SEQ ID NO: 2 such that the sense strand is complementary to the at least 21 contiguous nucleotides in the antisense strand. In a further embodiment, the sense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, or 1, 2, or 3 mismatches, of the corresponding portion of the nucleotide sequence of SEQ ID NO: 1.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, wherein the portion of the sense strand is a portion within a sense strand in any one of Tables 2-7.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, wherein the portion of the antisense strand is a portion within an antisense strand in any one of Tables 2-7.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the antisense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the sense strand comprises a nucleotide sequence comprising at least 17 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the antisense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0,1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the sense strand comprises a nucleotide sequence comprising at least 19 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, the antisense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the sense strand comprises a nucleotide sequence comprising at least 21 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the sense strand is at least 23 nucleotides in length, *e.g.*, 23-30 nucleotides in length.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties. In a further embodiment, the lipophilic moiety is conjugated to one or more positions in the double stranded region of the dsRNA agent. In a further embodiment, the lipophilic moiety is conjugated via a linker or carrier. In a further embodiment, lipophilicity of the lipophilic moiety, measured by logKow, exceeds 0.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, wherein the hydrophobicity of the double-stranded RNAi agent, measured by the unbound fraction in a plasma protein binding assay of the double-stranded RNAi agent, exceeds 0.2. In a further embodiment, the plasma protein binding assay is an electrophoretic mobility shift assay using human serum albumin protein.

In a certain embodiment, the dsRNA agent of any of the preceding embodiments comprises at least one modified nucleotide. In a further embodiment, no more than five of the sense strand nucleotides and not more than five of the nucleotides of the antisense strand are unmodified nucleotides. In an alternative further embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand comprise a modification. In a further embodiment of any one of these embodiments, at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic

nucleotide, a 2'-amino-modified nucleotide, a 2'-O-allyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a phosphorothioate group, a nucleotide comprising a methylphosphonate group, a nucleotide comprising a 5'-phosphate, a nucleotide comprising a 5'-phosphate mimic, a glycol modified nucleotide, and a 2-O-(N-methylacetamide) modified nucleotide; and combinations thereof. 33. The dsRNA agent of any of embodiments 29-31, wherein no more than five of the sense strand nucleotides and not more than five of the nucleotides of the antisense strand include modifications other than 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, unlocked nucleic acids (UNA) or glycerol nucleic acid (GNA).

In a certain embodiment, the dsRNA agent of any of the preceding embodiments comprises a non-nucleotide spacer (wherein optionally the non-nucleotide spacer comprises a C3-C6 alkyl) between two of the contiguous nucleotides of the sense strand or between two of the contiguous nucleotides of the antisense strand.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein each strand is no more than 30 nucleotides in length.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein at least one strand comprises a 3' overhang of at least 2 nucleotides.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the double stranded region is 15-30 nucleotide pairs in length. In a further embodiment, the double stranded region is 17-23 nucleotide pairs in length. In another further embodiment, the double stranded region is 17-25 nucleotide pairs in length. In another further embodiment, the double stranded region is 23-27 nucleotide pairs in length. In another further embodiment, the double stranded region is 19-21 nucleotide pairs in length. In another further embodiment, the double stranded region is 21-23 nucleotide pairs in length.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein each strand has 19-30 nucleotides.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein each strand has 19-23 nucleotides.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein each strand has 21-23 nucleotides.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the agent comprises at least one phosphorothioate or methylphosphonate internucleotide linkage. In a first particular embodiment, the phosphorothioate or methylphosphonate internucleotide

linkage is at the 3'-terminus of one strand. In a further embodiment, the strand is the antisense strand. In an alternative further embodiment, the strand is the sense strand. 51. In a second particular embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand. In a further embodiment, the strand is the antisense strand. In an alternative further embodiment, the strand is the sense strand. In a third particular embodiment, each of the 5'- and 3'-terminus of one strand comprises a phosphorothioate or methylphosphonate internucleotide linkage. In a further embodiment, the strand is the antisense strand. In a certain embodiment, the sense strand has a total of 21 nucleotides and the antisense strand has a total of 23 nucleotides.

In a certain embodiment, provided is the dsRNA agent of any of the preceding embodiments, wherein the base pair at the 1 position of the 5′-end of the antisense strand of the duplex is an AU base pair.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties, wherein one or more lipophilic moieties are conjugated to one or more internal positions on at least one strand. In a further embodiment, the one or more lipophilic moieties are conjugated to one or more internal positions on at least one strand via a linker or carrier. In a further embodiment, the internal positions include all positions except the terminal two positions from each end of the at least one strand. In an alternative further embodiment, the internal positions include all positions except the terminal three positions from each end of the at least one strand. In a first particular embodiment of these further embodiments, the internal positions exclude a cleavage site region of the sense strand. In a further embodiment, the internal positions include all positions except positions 9-12, counting from the 5'-end of the sense strand. In an alternative further embodiment, the internal positions include all positions except positions 11-13, counting from the 3'-end of the sense strand. In a second particular embodiment of these further embodiments, the internal positions exclude a cleavage site region of the antisense strand. In a further embodiment, the internal positions include all positions except positions 12-14, counting from the 5'-end of the antisense strand. In a third particular embodiment of these further embodiments, the internal positions include all positions except positions 11-13 on the sense strand, counting from the 3'-end, and positions 12-14 on the antisense strand, counting from the 5'-end.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties, wherein the one or more lipophilic moieties are conjugated to one or more of the internal positions selected from the group consisting of positions 4-8 and 13-18 on the sense strand, and positions 6-10 and 15-18 on the antisense strand, counting from the 5'end of each strand. In a further embodiment, the one or more lipophilic moieties are conjugated to one or more of the internal positions selected from the group consisting of positions 5, 6, 7, 15, and 17 on the sense strand, and positions 15 and 17 on the antisense strand, counting from the 5'-end of each strand.

In a certain embodiment, provided is the dsRNA agent of the preceding embodiment wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties, wherein the one or more lipophilic moieties are conjugated to one or more positions in the double stranded region of the dsRNA agent, wherein the positions in the double stranded region exclude a cleavage site region of the sense strand.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties, wherein the sense strand is 21 nucleotides in length, the antisense strand is 23 nucleotides in length, and the lipophilic moiety is conjugated to position 21, position 20, position 15, position 1, position 7, position 6, or position 2 of the sense strand or position 16 of the antisense strand. In a further embodiment, the lipophilic moiety is conjugated to position 21, position 20, position 15, position 1, or position 7 of the sense strand. In an alternative further embodiment, the lipophilic moiety is conjugated to position 21, position 20, or position 15 of the sense strand. In another further embodiment, the lipophilic moiety is conjugated to position 20 or position 15 of the sense strand. In another further embodiment, the lipophilic moiety is conjugated to position 16 of the antisense strand. In another further embodiment, wherein the lipophilic moiety is conjugated to position 6, counting from the 5'-end of the sense strand.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties, wherein the lipophilic moiety is an aliphatic, alicyclic, or polyalicyclic compound. In a further embodiment, the lipophilic moiety is selected from the group consisting of lipid, cholesterol, retinoic acid, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-bis-O(hexadecyl)glycerol, geranyloxyhexyanol, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine. In a further embodiment, the lipophilic moiety contains a saturated or unsaturated C4-C30 hydrocarbon chain, and an optional functional group selected from the group consisting of hydroxyl, amine, carboxylic acid, sulfonate, phosphate, thiol, azide, and alkyne. In a further embodiment, the lipophilic moiety contains a saturated or unsaturated C6-C18 hydrocarbon chain. In a further embodiment, the lipophilic moiety contains a saturated or unsaturated C16 hydrocarbon chain.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties, wherein the lipophilic moiety is conjugated via a carrier that replaces one or more nucleotide(s) in the internal position(s) or the double stranded region. In a further embodiment, the carrier is a cyclic group selected from the group consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl,

tetrahydrofuranyl, and decalinyl; or is an acyclic moiety based on a serinol backbone or a diethanolamine backbone.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand the antisense strand is conjugated to one or more lipophilic moieties, wherein the lipophilic moiety is conjugated to the double-stranded iRNA agent via a linker containing an ether, thioether, urea, carbonate, amine, amide, maleimide-thioether, disulfide, phosphodiester, sulfonamide linkage, a product of a click reaction, or carbamate.

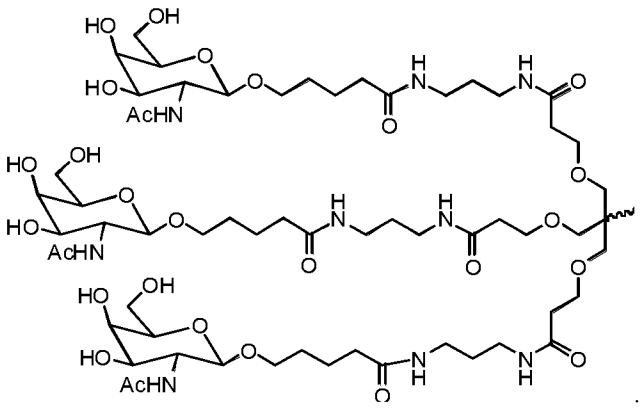
In a certain embodiment, provided is the double-stranded iRNA agent of any one of the preceding embodiments wherein at least one of the sense strand the antisense strand is conjugated to one or more lipophilic moieties, wherein the lipophilic moiety is conjugated to a nucleobase, sugar moiety, or internucleosidic linkage.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand the antisense strand is conjugated to one or more lipophilic moieties, wherein the lipophilic moiety is conjugated via a bio-cleavable linker selected from the group consisting of DNA, RNA, disulfide, amide, functionalized monosaccharides or oligosaccharides of galactosamine, glucosamine, glucose, galactose, mannose, and combinations thereof.

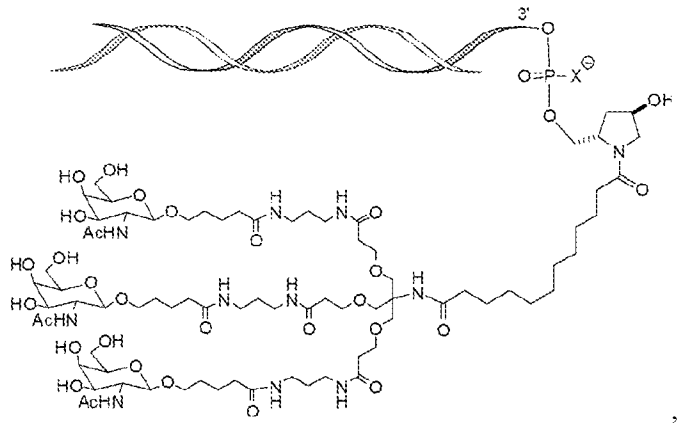
In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand the antisense strand is conjugated to one or more lipophilic moieties, wherein the 3' end of the sense strand is protected via an end cap which is a cyclic group having an amine, said cyclic group being selected from the group consisting of pyrrolidinyl, pyrazolinyl, pyrazolidinyl, imidazolinyl, imidazolidinyl, piperidinyl, piperazinyl, [1,3]dioxolanyl, oxazolidinyl, isoxazolidinyl, morpholinyl, thiazolidinyl, isothiazolidinyl, quinoxalinyl, pyridazinonyl, tetrahydrofuranyl, and decalinyl.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments wherein at least one of the sense strand the antisense strand is conjugated to one or more lipophilic moieties, further comprising a targeting ligand, *e.g.*, a ligand that targets an ocular tissue. In a further embodiment, the ligand is conjugated to the sense strand. In a further embodiment, the ligand is conjugated to the 3' end or the 5' end of the sense strand. In a further embodiment, the ligand is conjugated to the 3' end of the sense strand. In a further embodiment, the ocular tissue is an optic nerve, a trabecular meshwork, a juxtacanalicular tissue, a ganglion (*e.g.*, including a retinal ganglion), episcleral veins or a Schlemm's canal (*e.g.*, including an endothelial cell). In a further embodiment, the targeting ligand comprises N-acetylgalactosamine (GalNAc). In another further embodiment, the targeting ligand is one or more GalNAc conjugates or one or more or GalNAc derivatives. In a further embodiment, the one or more GalNAc conjugates or one or more GalNAc derivatives are attached through a monovalent linker, or a bivalent, trivalent, or tetravalent branched linker.

In a further embodiment wherein the targeting ligand is one or more GalNAc conjugates or one or more or GalNAc derivatives, the ligand is



In a further embodiment of the preceding embodiment, the dsRNA agent is conjugated to the ligand as shown in the following schematic



wherein X is O or S.

In a further embodiment of the preceding embodiment, the X is O.

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

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, further comprising:

a terminal, chiral modification occurring at the first and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration;

a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration; and
a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

Alternatively, in a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, further comprising:
a terminal, chiral modification occurring at the first, second and third internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration;
a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration; and
a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

Yet alternatively, in a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, further comprising:
a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration;
a terminal, chiral modification occurring at the third internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Rp configuration;
a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration; and
a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

Yet alternatively, in a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, further comprising:
a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 3' end of the antisense strand, having the linkage phosphorus atom in Sp configuration;
a terminal, chiral modification occurring at the first, and second internucleotide linkages at the 5' end of the antisense strand, having the linkage phosphorus atom in Rp configuration; and
a terminal, chiral modification occurring at the first internucleotide linkage at the 5' end of the sense strand, having the linkage phosphorus atom in either Rp or Sp configuration.

In a certain embodiment, provided is the dsRNA agent of any one of the preceding embodiments, further comprising a phosphate or phosphate mimic at the 5'-end of the antisense strand. In a further embodiment, the phosphate mimic is a 5'-vinyl phosphonate (VP). In one embodiment, the phosphate mimic is a 5'-cyclopropyl phosphonate (CP). In some embodiments, the 5'-end of the antisense strand of the double-stranded iRNA agent does not contain a 5'-vinyl phosphonate (VP).

In one embodiment, at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a glycol modified nucleotide (GNA), e.g., Ggn, Cgn, Tgn, or Agn, a nucleotide with a 2' phosphate, e.g., G2p, C2p, A2p or U2p, and, a vinyl-phosphonate nucleotide; and combinations thereof. In other embodiments, each of the duplexes of Tables 3, 5, and 7 may be particularly modified to provide another double-stranded iRNA agent of the present disclosure. In one example, the 3'-terminus of each sense duplex may be modified by removing the 3'-terminal L96 ligand and exchanging the two phosphodiester internucleotide linkages between the three 3'-terminal nucleotides with phosphorothioate internucleotide linkages. That is, the three 3'-terminal nucleotides (N) of a sense sequence of the formula:

$$5'\text{-}\ N_1\text{-}\ldots\ \text{-}N_{n-2}N_{n-1}N_nL96\ 3'$$

may be replaced with

$$5'\text{-}\ N_1\text{-}\ldots\ \text{-}N_{n-2}\underline{s}N_{n-1}\underline{s}N_n\ 3'.$$

That is, for example, AD-1561710, the sense sequence:

csusuggaAfgGfAfAfagcuaua**gguL96** (SEQ ID NO: 393)

may be replaced with

csusuggaAfgGfAfAfagcuaua**gsgsu** (SEQ ID NO: 1473)

while the antisense sequence remains unchanged to provide another double-stranded iRNA agent of the present disclosure.

(2) Cells

In a certain aspect, the present disclosure provides a cell containing the dsRNA agent of any one of the preceding embodiments.

In a certain embodiment, the present disclosure provides a human ocular cell, *e.g.*, (an optic nerve cell, a trabecular meshwork cell, a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel) comprising a reduced level of ANGPTL7 mRNA or a reduced level of ANGPTL7 protein as compared to an otherwise similar untreated cell, wherein optionally the level is reduced by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%. In a further embodiment, the human cell of the preceding embodiment was produced by a process comprising contacting a human cell with the dsRNA agent of any one of the preceding embodiments.

(3) Pharmaceutical Compositions

In a certain aspect, the present disclosure provides a pharmaceutical composition for inhibiting expression of ANGPTL7, comprising the dsRNA agent of any one of the preceding embodiments.

In a certain aspect, the present disclosure provides a pharmaceutical composition comprising the dsRNA agent of any one of the preceding embodiments and a lipid formulation.

(4) Methods of Inhibiting Expression of ANGPTL7 in a Cell

In a certain aspect, the present disclosure provides a method of inhibiting expression of ANGPTL7 in a cell, the method comprising:

(a) contacting the cell with the dsRNA agent of any one of the preceding embodiments, or a pharmaceutical composition of one of the preceding embodiments; and

(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of ANGPTL7, thereby inhibiting expression of ANGPTL7 in the cell.

In a certain aspect, the present disclosure provides a method of inhibiting expression of ANGPTL7 in a cell, the method comprising:

(a) contacting the cell with the dsRNA agent of any one of the preceding embodiments, or a pharmaceutical composition of one of the preceding embodiments; and

(b) maintaining the cell produced in step (a) for a time sufficient to reduce levels of ANGPTL7 mRNA, ANGPTL7 protein, or both of ANGPTL7 mRNA and protein, thereby inhibiting expression of ANGPTL7 in the cell.

In a certain embodiment, provided is the method of one of preceding embodiments, wherein the cell is within a subject. In a further embodiment, the subject is a human.

In a certain embodiment, provided is the method of any one of the preceding embodiments, wherein the level of ANGPTL7 mRNA is inhibited by at least 50%.

In a certain embodiment, provided is the method of any one of the preceding embodiments, wherein the level of ANGPTL7 protein is inhibited by at least 50%.

In a certain embodiment, provided is the method of one of the preceding embodiments wherein the cell is within a subject, wherein inhibiting expression of ANGPTL7 decreases an ANGPTL7 protein level in a biological sample (*e.g.,* an optic nerve sample) from the subject by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 95%. In a further embodiment, the subject has been diagnosed with an ANGPTL7-associated disorder, *e.g.,* glaucoma. In a specific embodiment, the ANGPTL 7-associated disorder is glaucoma or a glaucoma associated condition.

In a certain embodiment, provided is a method of inhibiting expression of ANGPTL7 in an ocular cell or tissue, the method comprising:

(a) contacting the cell or tissue with a dsRNA agent that binds ANGPTL7; and

(b) maintaining the cell or tissue produced in step (a) for a time sufficient to reduce levels of ANGPTL7 mRNA, ANGPTL7 protein, or both of ANGPTL7 mRNA and protein, thereby inhibiting

expression of ANGPTL7 in the cell or tissue. In a further embodiment, the ocular cell or tissue comprises an optic nerve cell, a trabecular meshwork cell, a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel.

(5) Methods of Treating a Subject

In a certain aspect, the present disclosure provides a method of treating a subject diagnosed with an ANGPTL7-associated disorder comprising administering to the subject a therapeutically effective amount of the dsRNA agent of any one of the preceding embodiments or a pharmaceutical composition of any one of the preceding embodiments, thereby treating the disorder. In a specific embodiment, the ANGPTL7-associated disorder is glaucoma or a glaucoma associated condition.

In a certain embodiment, provided is the method of treating a subject according to one of the preceding embodiments, wherein treating comprises amelioration of at least one sign or symptom of the disorder. In a further embodiment, at least one sign or symptom of glaucoma comprises a measure of one or more of intraocular pressure, vision loss, optic nerve damage, ocular inflammation, visual acuity, or presence, level, or activity of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein).

In a certain embodiment, provided is the method of treating a subject according to one of the preceding embodiments, where treating comprises prevention of progression of the disorder.

In a certain embodiment, provided is the method of treating a subject according to any one of the preceding embodiments wherein treating comprises amelioration of at least one sign or symptom of the disorder, or prevention of progression of the disorder, wherein the treating comprises one or more of (a) inhibiting or reducing intraocular pressure; (b) inhibiting or reducing the expression or activity of ANGPTL7; (c) increasing drainage of aqueous humor; (d) inhibiting or reducing optic nerve damage; or (e) inhibiting or reducing retinal ganglion cell death. medication to reduce intraocular pressure, laser treatment, surgery or trabeculectomy. In a further embodiment, the treating results in at least a 30% mean reduction from baseline of ANGPTL7 mRNA in an optic nerve cell, a trabecular meshwork cell, a Schlemm's canal cell (*e.g.*, including an endothelial cell), a juxtacanalicular tissue cell, a ciliary muscle cell, retinal pigment epithelium (RPE), a retinal cell, an astrocyte, a pericyte, a Müller cell, a ganglion cell (*e.g.*, including a retinal ganglion cell), an endothelial cell, a photoreceptor cell, a retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, a choroid vessel. In a further embodiment, the treating results in at least a 60% mean reduction from baseline of ANGPTL7 mRNA in the optic nerve cell, trabecular meshwork cell, Schlemm's canal cell (*e.g.*, including an endothelial cell), juxtacanalicular tissue cell, ciliary muscle cell, retinal pigment epithelium (RPE), retinal cell, astrocyte, pericyte, Müller cell, ganglion cell (*e.g.*, including retinal ganglion cell), endothelial cell,

photoreceptor cell, retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, choroid vessel. In a further embodiment, the treating results in at least a 90% mean reduction from baseline of ANGPTL7 mRNA in the optic nerve cell, trabecular meshwork cell, Schlemm's canal cell (*e.g.*, including an endothelial cell), juxtacanalicular tissue cell, ciliary muscle cell, retinal pigment epithelium (RPE), retinal cell, astrocyte, pericyte, Müller cell, ganglion cell (*e.g.*, including retinal ganglion cell), endothelial cell, photoreceptor cell, retinal blood vessel (*e.g.*, including endothelial cells and vascular smooth muscle cells), episcleral veins or choroid tissue, *e.g.*, choroid vessel.

In a certain embodiment, provided is the method of treating a subject according to any one of the preceding embodiments wherein treating comprises amelioration of at least one sign or symptom of the disorder, or prevention of progression of the disorder, wherein after treatment the subject experiences at least an 8-week duration of knockdown following a single dose of dsRNA as assessed by ANGPTL7 protein in the optic nerve. In a further embodiment, treating results in at least a 12-week duration of knockdown following a single dose of dsRNA as assessed by ANGPTL7 protein in the optic nerve. In a further embodiment, treating results in at least a 16-week duration of knockdown following a single dose of dsRNA as assessed by ANGPTL7 protein in the optic nerve.

(6) Methods of Delivery and Dosage

In a certain embodiment, the present disclosure provides a method of any of the preceding embodiments for inhibiting expression of ANGPTL7 in a cell in a subject or for treating a subject diagnosed with an ANGPTL 7-associated disease, wherein the subject is human.

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

In a specific embodiment of the preceding embodiment, the dsRNA agent is administered to the subject intraocularly, intravenously, or topically. In a further embodiment, wherein the intraocular administration comprises intravitreal administration (*e.g.*, intravitreal injection), transscleral administration (*e.g.*, transscleral injection), subconjunctival administration (*e.g.*, subconjunctival injection), retrobulbar administration (*e.g.*, retrobulbar injection), intracameral administration (*e.g.*, intracameral injection), or subretinal administration (*e.g.*, subretinal injection).

In a certain embodiment, provided is the method of any one of the preceding embodiments, further comprising measuring level of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein) in the subject. In a further embodiment, measuring the level of ANGPTL7 in the subject comprises measuring the level of ANGPTL7 gene, ANGPTL7 protein or ANGPTL7 mRNA in a biological sample from the subject (*e.g.,* an optic nerve sample).

In a certain embodiment, provided is the method of any one of the preceding embodiments, further comprising performing a blood test, an imaging test, a tonometry test or an optic nerve biopsy.

In a further embodiment, measuring level of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein) in the subject is performed prior to treatment with the dsRNA agent or

the pharmaceutical composition. In a further embodiment upon determination that a subject has a level of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein) that is greater than a reference level, the dsRNA agent or the pharmaceutical composition is administered to the subject. In a further embodiment, measuring level of ANGPTL7 (*e.g.,* ANGPTL7 gene, ANGPTL7 mRNA, or ANGPTL7 protein) in the subject is performed after treatment with the dsRNA agent or the pharmaceutical composition.

In a certain embodiment, provided is the method of any one of the preceding embodiments, further comprising administering to the subject an additional agent and/or therapy suitable for treatment or prevention of an ANGPTL7-associated disorder. In a further embodiment, the additional agent and/or therapy comprises one or more of a prostaglandin analog, a beta blocker, an alpha-adrenergic agonist, a carbonic anhydrase inhibitor, a ROCK inhibitor, a ROCK iRNA agent, an inhibitor of Rho GTPases, an anti-Rho GTPase agent, or an anti-ANGPTL7 agent.

EXAMPLES

Example 1: ANGPTL7 siRNA

Nucleic acid sequences provided herein are represented using standard nomenclature. *See* the abbreviations of Table 1.

Table 1. Abbreviations of nucleotide monomers used in nucleic acid sequence representation

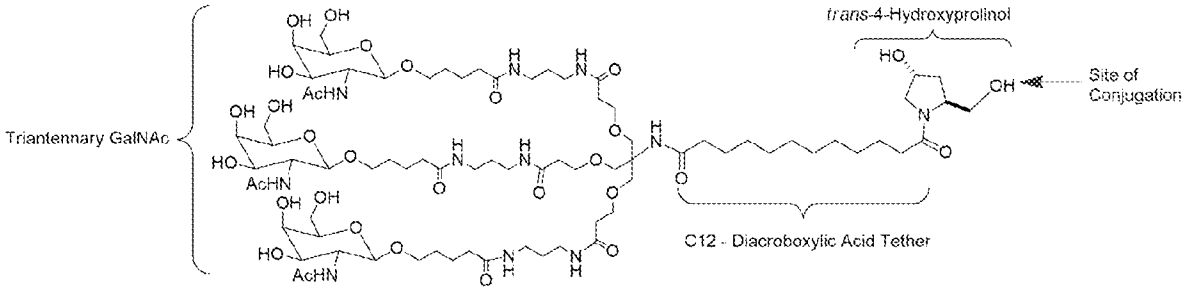
It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds; and it is understood that when the nucleotide contains a 2'-fluoro modification, then the fluoro replaces the hydroxy at that position in the parent nucleotide (i.e., it is a 2'-deoxy-2'-fluoronucleotide).

Abbreviation	Nucleotide(s)
A	Adenosine-3'-phosphate
Ab	beta-L-adenosine-3`-phosphate
Abs	beta-L-adenosine-3`-phosphorothioate
Af	2'-fluoroadenosine-3'-phosphate
Afs	2'-fluoroadenosine-3'-phosphorothioate
(Ahd)	2'-O-hexadecyl-adenosine-3'-phosphate
(Ahds)	2'-O-hexadecyl-adenosine-3'-phosphorothioate
As	adenosine-3'-phosphorothioate
(A2p)	adenosine-2`-phosphate
(A2ps)	adenosine-2`-phosphorothioate
C	cytidine-3'-phosphate
Cb	beta-L-cytidine-3'-phosphate
Cbs	beta-L-cytidine-3'-phosphorothioate
Cf	2'-fluorocytidine-3'-phosphate
Cfs	2'-fluorocytidine-3'-phosphorothioate
(Chd)	2'-O-hexadecyl-cytidine-3'-phosphate
(Chds)	2'-O-hexadecyl-cytidine-3'-phosphorothioate
Cs	cytidine-3'-phosphorothioate

(C2p)	cytidine-2`-phosphate
(C2ps)	cytidine-2`-phosphorothioate
G	guanosine-3'-phosphate
Gb	beta-L-guanosine-3`-phosphate
Gbs	beta-L-guanosine-3`-phosphorothioate
Gf	2'-fluoroguanosine-3'-phosphate
Gfs	2'-fluoroguanosine-3'-phosphorothioate
(Ghd)	2'-O-hexadecyl-guanosine-3'-phosphate
(Ghds)	2'-O-hexadecyl-guanosine-3'-phosphorothioate
Gs	guanosine-3'-phosphorothioate
(G2p)	guanosine-2`-phosphate
(G2ps)	guanosine-2`-phosphorothioate
T	5'-methyluridine-3'-phosphate
Tb	beta-L-thymidine-3'-phosphate
Tbs	beta-L-thymidine-3'-phosphorothioate
Tf	2'-fluoro-5-methyluridine-3'-phosphate
Tfs	2'-fluoro-5-methyluridine-3'-phosphorothioate
Tgn	thymidine-glycol nucleic acid (GNA) S-Isomer
Agn	adenosine- glycol nucleic acid (GNA) S-Isomer
Cgn	cytidine-glycol nucleic acid (GNA) S-Isomer
Ggn	guanosine-glycol nucleic acid (GNA) S-Isomer
Ts	5-methyluridine-3'-phosphorothioate
U	Uridine-3'-phosphate
Ub	beta-L-uridine-3`-phosphate
Ubs	beta-L-uridine-3`-phosphorothioate
Uf	2'-fluorouridine-3'-phosphate
Ufs	2'-fluorouridine -3'-phosphorothioate
(Uhd)	2'-O-hexadecyl-uridine-3'-phosphate
(Uhds)	2'-O-hexadecyl-uridine-3'-phosphorothioate
Us	uridine -3'-phosphorothioate
(U2p)	uridine-2`-phosphate
(U2ps)	uridine-2`-phosphorothioate
N	any nucleotide (G, A, C, T or U)
VP	Vinyl phosphonate
a	2'-O-methyladenosine-3'-phosphate
as	2'-O-methyladenosine-3'- phosphorothioate
c	2'-O-methylcytidine-3'-phosphate
cs	2'-O-methylcytidine-3'- phosphorothioate
g	2'-O-methylguanosine-3'-phosphate
gs	2'-O-methylguanosine-3'- phosphorothioate
t	2'-O-methyl-5-methyluridine-3'-phosphate
ts	2'-O-methyl-5-methyluridine-3'-phosphorothioate
u	2'-O-methyluridine-3'-phosphate
us	2'-O-methyluridine-3'-phosphorothioate
dA	2`-deoxyadenosine-3`-phosphate
dAs	2`-deoxyadenosine-3`-phosphorothioate
dC	2`-deoxycytidine-3`-phosphate
dCs	2`-deoxycytidine-3`-phosphorothioate
dG	2`-deoxyguanosine-3`-phosphate
dGs	2`-deoxyguanosine-3`-phosphorothioate
dT	2'-deoxythymidine
dTs	2`-deoxythymidine-3`-phosphorothioate
dU	2`-deoxyuridine
s	phosphorothioate linkage

L96[1]	N-[tris(GalNAc-alkyl)-amidodecanoyl)]-4-hydroxyprolinol Hyp-(GalNAc-alkyl)3
(Aeo)	2'-O-methoxyethyladenosine-3'-phosphate
(Aeos)	2'-O-methoxyethyladenosine-3'-phosphorothioate
(Geo)	2'-O-methoxyethylguanosine-3'-phosphate
(Geos)	2'-O-methoxyethylguanosine-3'- phosphorothioate
(Teo)	2'-O-methoxyethyl-5-methyluridine-3'-phosphate
(Teos)	2'-O-methoxyethyl-5-methyluridine-3'- phosphorothioate
(m5Ceo)	2'-O-methoxyethyl-5-methylcytidine-3'-phosphate
(m5Ceos)	2'-O-methoxyethyl-5-methylcytidine-3'- phosphorothioate

[1] The chemical structure of L96 is as follows:



Experimental Methods

Bioinformatics

Transcripts

siRNAs targeting the mouse ANGPTL7, "angiopoietin like 7" (NCBI GeneID: 654812) were generated. The mouse NM_001039554.3 REFSEQ mRNA has a length of 2062 bases. Pairs of oligos were generated using bioinformatic methods and ranked, and exemplary pairs of oligos are shown in Tables 2, 3, 4, and 5. Modified sequences are presented in Tables 3 and 5. Unmodified sequences are presented in Tables 2 and 4. The oligos in Tables 2, 3, 4, and 5 cross-react with rat ANGPTL7 and may cross-react with human and monkey ANGPTL7.

siRNAs targeting the human ANGPTL7, "angiopoietin like 7" (NCBI GeneID: 10218) were generated. The human NM_021146.4 REFSEQ mRNA has a length of 2224 bases. Pairs of oligos were generated using bioinformatic methods and ranked, and exemplary pairs of oligos are shown in Tables 6 and 7. Modified sequences are presented in Table 7. Unmodified sequences are presented in Table 6. The oligos in Tables 6 and 7 may cross-react with monkey, mouse, and rat ANGPTL7.

It is to be understood that, throughout the application, a duplex name without a decimal is equivalent to a duplex name with a decimal which merely references the batch number of the duplex. For example, AD-1094991 is equivalent to AD-1094991.1.

siRNA Synthesis

siRNAs were synthesized and annealed using routine methods known in the art.

Briefly, siRNA sequences were synthesized at 1 μmol scale on a Mermade 192 synthesizer (BioAutomation) using the solid support mediated phosphoramidite chemistry. The solid support was

controlled pore glass (500 A) loaded with custom GalNAc ligand or universal solid support (AM biochemical). Ancillary synthesis reagents, 2'-F and 2'-O-Methyl RNA and deoxy phosphoramidites were obtained from Thermo Fisher (Waltham, MA) and Hongene (China). 2'F 2'-O-Methyl, GNA (glycol nucleic acids), 5'phosphate and other modifications were introduced using the corresponding phosphoramidites. Synthesis of 3' GalNAc conjugated single strands was performed on a GalNAc modified CPG support. Custom CPG universal solid support was used for the synthesis of antisense single strands. Coupling time for all phosphoramidites (100 mM in acetonitrile) was 5 min employing 5-Ethylthio-1H-tetrazole (ETT) as activator (0.6 M in acetonitrile). Phosphorothioate linkages were generated using a 50 mM solution of 3-((Dimethylamino-methylidene) amino)-3H-1,2,4-dithiazole-3-thione (DDTT, obtained from Chemgenes (Wilmington, MA, USA)) in anhydrous acetonitrile/pyridine (1:1 v/v). Oxidation time was 3 minutes. All sequences were synthesized with final removal of the DMT group ("DMT off").

Upon completion of the solid phase synthesis, oligoribonucleotides were cleaved from the solid support and deprotected in sealed 96 deep well plates using 200 µL Aqueous Methylamine reagents at 60 °C for 20 minutes. For sequences containing 2' ribo residues (2'-OH) that are protected with a tert-butyl dimethyl silyl (TBDMS) group, a second step deprotection was performed using TEA.3HF (triethylamine trihydro fluoride) reagent. To the methylamine deprotection solution, 200µL of dimethyl sulfoxide (DMSO) and 300 µL TEA.3HF reagent was added and the solution was incubated for additional 20 min at 60 °C. At the end of cleavage and deprotection step, the synthesis plate was allowed to come to room temperature and was precipitated by addition of 1 mL of acetontile: ethanol mixture (9:1). The plates were cooled at -80 °C for 2 hrs, supernatant decanted carefully with the aid of a multi-channel pipette. The oligonucleotide pellet was re-suspended in 20 mM NaOAc buffer and were desalted using a 5 mL HiTrap size exclusion column (GE Healthcare) on an AKTA Purifier System equipped with an A905 autosampler and a Frac 950 fraction collector. Desalted samples were collected in 96-well plates. Samples from each sequence were analyzed by LC-MS to confirm the identity, UV (260 nm) for quantification and a selected set of samples by IEX chromatography to determine purity.

Annealing of single strands was performed on a Tecan liquid handling robot. Equimolar mixture of sense and antisense single strands were combined and annealed in 96 well plates. After combining the complementary single strands, the 96-well plate was sealed tightly and heated in an oven at 100 °C for 10 minutes and allowed to come slowly to room temperature over a period 2-3 hours. The concentration of each duplex was normalized to 10 µM in 1X PBS and then submitted for *in vitro* screening assays.

Table 2. Unmodified sense and antisense strand sequences of ANGPTL7 dsRNA agents

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3
AD-1094991	ACACUUCCUUGUGUCUAUAGA	13	1564-1584	UCUAUAGACACAAGGAAGUGUCG	35	1562-1584
AD-1093984	GUACCAGAAGAACUACCGAAA	14	548-568	UUUCGGUAGUUCUUCUGGUACAG	36	546-568
AD-1093985	UACCAGAAGAACUACCGAAUA	15	549-569	UAUUCGGUAGUUCUUCUGGUACA	37	547-569
AD-1094047	CUGUGACAUGGAAACUUCAGA	16	629-649	UCUGAAGUUUCCAUGUCACAGAA	38	627-649
AD-1093988	CAGAAGAACUACCGAAUCUCA	17	552-572	UGAGAUUCGGUAGUUCUUCUGGU	39	550-572
AD-1093989	AGAAGAACUACCGAAUCUCUA	18	553-573	UAGAGAUUCGGUAGUUCUUCUGG	40	551-573
AD-1094130	GACAGUAUAAGCAAGGGUUUA	19	712-732	UAAACCCUUGCUUAUACUGUCUC	41	710-732
AD-1093990	GAAGAACUACCGAAUCUCUGA	20	554-574	UCAGAGAUUCGGUAGUUCUUCUG	42	552-574
AD-1094048	UGUGACAUGGAAACUUCAGGA	21	630-650	UCCUGAAGUUUCCAUGUCACAGA	43	628-650
AD-1094108	GUCUCCUUCUACCAAGACUGA	22	690-710	UCAGUCUUGGUAGAAGGAGACAA	44	688-710
AD-1093887	ACUCUGAGAUGAACAACCAGA	23	451-471	UCUGGUUGUUCAUCUCAGAGUAC	45	449-471
AD-1094129	AGACAGUAUAAGCAAGGGUUA	24	711-731	UAACCCUUGCUUAUACUGUCUCC	46	709-731
AD-1094131	ACAGUAUAAGCAAGGGUUUGA	25	713-733	UCAAACCCUUGCUUAUACUGUCU	47	711-733
AD-1094262	UUGGGCAAUGAACUGAACAGA	26	864-884	UCUGUUCAGUUCAUUGCCCAACG	48	862-884
AD-1094471	GCCAACUAUUCCCUCAAACGA	27	1128-1148	UCGUUUGAGGGAAUAGUUGGCUC	49	1126-1148
AD-1093875	CCGAGAGCAAGUACUCUGAGA	28	439-459	UCUCAGAGUACUUGCUCUCGGCA	50	437-459
AD-1094304	CAUAACAACACCGUCUUCAGA	29	942-962	UCUGAAGACGGUGUUGUUAUGGU	51	940-962
AD-1093983	UGUACCAGAAGAACUACCGAA	30	547-567	UUCGGUAGUUCUUCUGGUACAGG	52	545-567
AD-1094050	UGACAUGGAAACUUCAGGAGA	31	632-652	UCUCCUGAAGUUUCCAUGUCACA	53	630-652
AD-1093670	CUGCAGAAGCCUCAUAAACGA	32	234-254	UCGUUUAUGAGGCUUCUGCAGCC	54	232-254
AD-1093672	GCAGAAGCCUCAUAAACGCAA	33	236-256	UUGCGUUUAUGAGGCUUCUGCAG	55	234-256
AD-1093873	UGCCGAGAGCAAGUACUCUGA	34	437-457	UCAGAGUACUUGCUCUCGGCAGU	56	435-457

Table 3. Modified sense and antisense strand sequences of ANGPTL7 dsRNA agents

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1094991	ascsacu(Uhd)CfcUfUfGfugucuauasgsa	57	VPusCfsuauAfgAfCfacaaGfgAfaguguscsg	79	CGACACUUCCUUGUGUCUAUAGU	101
AD-1093984	gsusacc(Ahd)GfaAfGfAfacuaccgasasa	58	VPusUfsucgGfuAfGfucucUfcUfgguacsasg	80	CUGUACCAGAAGAACUACCGAAU	102
AD-1093985	usascca(Ghd)AfaGfAfAfcuaccgaasusa	59	VPusAfsuucGfgUfAfguucUfuCfugguascsa	81	UGUACCAGAAGAACUACCGAAUC	103
AD-1094047	csusgug(Ahd)CfaUfGfGfaaacuucasgsa	60	VPusCfsugaAfgUfUfuccaUfgUfcacagsasa	82	UUCUGUGACAUGGAAACUUCAGG	104
AD-1093988	csasgaa(Ghd)AfaCfUfAfccgaaucuscsa	61	VPusGfsagaUfuCfGfguagUfuCfuucugsgsu	83	ACCAGAAGAACUACCGAAUCUCU	105
AD-1093989	asgsaag(Ahd)AfcUfAfCfcgaaucucsusa	62	VPusAfsgagAfuUfCfgguaGfuUfcuucusgsg	84	CCAGAAGAACUACCGAAUCUCUG	106
AD-1094130	gsascag(Uhd)AfuAfAfGfcaaggguususa	63	VPusAfsaacCfcUfUfgcuuAfuAfcugucsusc	85	GAGACAGUAUAAGCAAGGGUUUG	107
AD-1093990	gsasaga(Ahd)CfuAfCfCfgaaucucusgsa	64	VPusCfsagaGfaUfUfcgguAfgUfucuucsusg	86	CAGAAGAACUACCGAAUCUCUGG	108
AD-1094048	usgsuga(Chd)AfuGfGfAfacuucagsgsa	65	VPusCfscugAfaGfUfuuccAfuGfucacasgsa	87	UCUGUGACAUGGAAACUUCAGGA	109
AD-1094108	gsuscuc(Chd)UfuCfUfAfccaagacusgsa	66	VPusCfsaguCfuUfGfguagAfaGfgagacsasa	88	UUGUCUCCUUCUACCAAGACUGG	110
AD-1093887	ascsucu(Ghd)AfgAfUfGfaacaaccasgsa	67	VPusCfsuggUfuGfUfucauCfuCfagagusasc	89	GUACUCUGAGAUGAACAACCAGA	111
AD-1094129	asgsaca(Ghd)UfaUfAfAfgcaagggususa	68	VPusAfsaccCfuUfGfcuuaUfaCfugucuscsc	90	GGAGACAGUAUAAGCAAGGGUUU	112
AD-1094131	ascsagu(Ahd)UfaAfGfCfaaggguuusgsa	69	VPusCfsaaaCfcCfUfugcuUfaUfacuguscsu	91	AGACAGUAUAAGCAAGGGUUUGG	113
AD-1094262	ususggg(Chd)AfaUfGfAfacugaacasgsa	70	VPusCfsuguUfcAfGfucaUfuGfcccaascsg	92	CGUUGGGCAAUGAACUGAACAGC	114
AD-1094471	gscscaa(Chd)UfaUfUfCfccucaaacsgsa	71	VPusCfsguuUfgAfGfggaaUfaGfuuggcsusc	93	GAGCCAACUAUUCCCUCAAACGU	115
AD-1093875	cscsgag(Ahd)GfcAfAfGfuacucugasgsa	72	VPusCfsucaGfaGfUfacuuGfcUfcucggscsa	94	UGCCGAGAGCAAGUACUCUGAGA	116
AD-1094304	csasuaa(Chd)AfaCfAfCfcgucuucasgsa	73	VPusCfsugaAfgAfCfggugUfuGfuuaugsgsu	95	ACCAUAACAACACCGUCUUCAGC	117
AD-1093983	usgsuac(Chd)AfgAfAfGfaacuaccgsasa	74	VPusUfscggUfaGfUfucuuCfuGfguacasgsg	96	CCUGUACCAGAAGAACUACCGAA	118
AD-1094050	usgsaca(Uhd)GfgAfAfAfcuucaggasgsa	75	VPusCfsuccUfgAfAfguuuCfcAfugucascsa	97	UGUGACAUGGAAACUUCAGGAGG	119
AD-1093670	csusgca(Ghd)AfaGfCfCfucauaaacsgsa	76	VPusCfsguuUfaUfGfaggcUfuCfugcagscsc	98	GGCUGCAGAAGCCUCAUAAACGC	120
AD-1093672	gscsaga(Ahd)GfcCfUfCfauaaacgcsasa	77	VPusUfsgcgUfuUfAfugagGfcUfucugcsasg	99	CUGCAGAAGCCUCAUAAACGCAA	121
AD-1093873	usgsccg(Ahd)GfaGfCfAfaguacucusgsa	78	VPusCfsagaGfuAfCfugcUfcUfcggcasgsu	100	ACUGCCGAGAGCAAGUACUCUGA	122

Table 4. Unmodified sense and antisense strand sequences of ANGPTL7 dsRNA agents

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Region	Exon
AD-1561710	CUUGGAAGGAAAGCUAUAGGU	123	4-24	ACCUAUAGCUUUCCUUCCAAGCC	258	2-24	5'UTR	1
AD-1561724	UAUAGGCUACCCAUUCAGCUU	124	18-38	AAGCUGAAUGGGUAGCCUAUAGC	259	16-38	5'UTR	1
AD-1561733	GAGACUCAAGCUUUGAGAAAU	125	47-67	AUUUCUCAAAGCUUGAGUCUCUG	260	45-67	5'UTR	1
AD-1561754	GCUAGCAAAGAGCAAGGAAAU	126	68-88	AUUUCCUUGCUCUUUGCUAGCCU	261	66-88	5'UTR	1
AD-1561758	AAGAGAGAAAACAACAAAGUU	127	86-106	AACUUUGUUGUUUUCUCUCUUUC	262	84-106	5'UTR	1
AD-1561776	GUGGCGAGGCCCUCAGAGUGU	128	104-124	ACACUCUGAGGGCCUCGCCACUU	263	102-124	5'UTR	1
AD-1561789	CAGAGUGAAAGCGUAAGGUUU	129	117-137	AAACCUUACGCUUUCACUCUGAG	264	115-137	5'UTR	1
AD-1561800	CGUAAGGUUCAGUCAGCCUGU	130	128-148	ACAGGCUGACUGAACCUUACGCU	265	126-148	5'UTR	1
AD-1561820	CUGCAGCUUUGCAGACCUCAU	131	148-168	AUGAGGUCUGCAAAGCUGCAGCA	266	146-168	5'UTR	1
AD-1561836	CUCAGCUGGGCAUCUCCAGAU	132	164-184	AUCUGGAGAUGCCCAGCUGAGGU	267	162-184	5'UTR	1
AD-1561842	UGAAGGAAGAGCCUUCCUCAU	133	190-210	AUGAGGAAGGCUCUUCCUUCAGG	268	188-210	5'UTR	1
AD-1561854	CACCCAAACCCACAAAAGAUU	134	208-228	AAUCUUUUGUGGGUUUGGGUGAG	269	206-228	5'UTR-CDS	1
AD-1561883	GCCUCUCUCAGCUGUGACCUU	135	237-257	AAGGUCACAGCUGAGAGAGGCUU	270	235-257	CDS	1
AD-1561902	UGGCUCUGCAUUUUCAUCGUU	136	256-276	AACGAUGAAAAUGCAGAGCCAGG	271	254-276	CDS	1
AD-1561913	UUUCAUCGUGGCCUUUGUCAU	137	267-287	AUGACAAAGGCCACGAUGAAAAU	272	265-287	CDS	1
AD-1561946	CUGCAGAAGCUCUCUAAGCAU	138	301-321	AUGCUUAGAGAGCUUCUGCAGCC	273	299-321	CDS	1
AD-1561961	AAGCACAAGACACCAGCACAU	139	316-336	AUGUGCUGGUGUCUUGUGCUUAG	274	314-336	CDS	1
AD-1561973	CCAGCACAGCCACAGCUCAAU	140	328-348	AUUGAGCUGUGGCUGUGCUGGUG	275	326-348	CDS	1
AD-1561985	CAGCUCAAAGCGGCCAACUGU	141	340-360	ACAGUUGGCCGCUUUGAGCUGUG	276	338-360	CDS	1
AD-1561997	GCCAACUGCUGUGAGGAGGUU	142	352-372	AACCUCCUCACAGCAGUUGGCCG	277	350-372	CDS	1
AD-1562009	GAGGAGGUGAAGGAGCUCAAU	143	364-384	AUUGAGCUCCUUCACCUCCUCAC	278	362-384	CDS	1
AD-1562020	GGAGCUCAAGGCCCAAGUUGU	144	375-395	ACAACUUGGGCCUUGAGCUCCUU	279	373-395	CDS	1
AD-1562032	CCAAGUUGCCAACCUUAGCAU	145	387-407	AUGCUAAGGUUGGCAACUUGGGC	280	385-407	CDS	1
AD-1562045	CUUAGCAGCCUGCUGAGUGAU	146	400-420	AUCACUCAGCAGGCUGCUAAGGU	281	398-420	CDS	1
AD-1562056	GCUGAGUGAACUGAACAAGAU	147	411-431	AUCUUGUUCAGUUCACUCAGCAG	282	409-431	CDS	1

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Region	Exon
AD-1562067	UGAACAAGAAGCAGGAGAGGU	148	422-442	ACCUCUCCUGCUUCUUGUUCAGU	283	420-442	CDS	1
AD-1562087	GACUGGGUCAGCGUGGUCAUU	149	442-462	AAUGACCACGCUGACCCAGUCCC	284	440-462	CDS	1
AD-1562099	GUGGUCAUGCAGGUGAUGGAU	150	454-474	AUCCAUCACCUGCAUGACCACGC	285	452-474	CDS	1
AD-1562111	GUGAUGGAGCUGGAGAGCAAU	151	466-486	AUUGCUCUCCAGCUCCAUCACCU	286	464-486	CDS	1
AD-1562122	GGAGAGCAACAGCAAGCGCAU	152	477-497	AUGCGCUUGCUGUUGCUCUCCAG	287	475-497	CDS	1
AD-1562141	AUGGAGUCGCGGCUCACAGAU	153	496-516	AUCUGUGAGCCGCGACUCCAUGC	288	494-516	CDS	1
AD-1562153	CUCACAGAUGCUGAGAGCAAU	154	508-528	AUUGCUCUCAGCAUCUGUGAGCC	289	506-528	CDS	1
AD-1562167	GAGCAAGUACUCCGAGAUGAU	155	522-542	AUCAUCUCGGAGUACUUGCUCUC	290	520-542	CDS	1
AD-1562179	CGAGAUGAACAACCAAAUUGU	156	534-554	ACAAUUUGGUUGUUCAUCUCGGA	291	532-554	CDS	1
AD-1562190	ACCAAAUUGACAUCAUGCAGU	157	545-565	ACUGCAUGAUGUCAAUUUGGUUG	292	543-565	CDS	1
AD-1562207	CAGCUGCAGGCAGCACAGACU	158	562-582	AGUCUGUGCUGCCUGCAGCUGCA	293	560-582	CDS	1
AD-1562218	AGCACAGACGGUCACUCAGAU	159	573-593	AUCUGAGUGACCGUCUGUGCUGC	294	571-593	CDS	1
AD-1562229	UCACUCAGACCUCCGCAGAUU	160	584-604	AAUCUGCGGAGGUCUGAGUGACC	295	582-604	CDS	1-2
AD-1562242	CGCAGAUGCCAUCUACGACUU	161	597-617	AAGUCGUAGAUGGCAUCUGCGGA	296	595-617	CDS	1-2
AD-1562255	UACGACUGCUCUUCCCUCUAU	162	610-630	AUAGAGGGAAGAGCAGUCGUAGA	297	608-630	CDS	2
AD-1562267	UCCCUCUACCAGAAGAACUAU	163	622-642	AUAGUUCUUCUGGUAGAGGGAAG	298	620-642	CDS	2
AD-1562278	GAAGAACUACCGCAUCUCUGU	164	633-653	ACAGAGAUGCGGUAGUUCUUCUG	299	631-653	CDS	2
AD-1562292	UCUCUGGAGUGUAUAAGCUUU	165	647-667	AAAGCUUAUACACUCCAGAGAUG	300	645-667	CDS	2
AD-1562309	CUUCCUCCUGAUGACUUCCUU	166	664-684	AAGGAAGUCAUCAGGAGGAAGCU	301	662-684	CDS	2
AD-1562333	AGCCCUGAACUGGAGGUGUUU	167	688-708	AAACACCUCCAGUUCAGGGCUGC	302	686-708	CDS	2-3
AD-1562344	GGAGGUGUUCUGUGACAUGGU	168	699-719	ACCAUGUCACAGAACACCUCCAG	303	697-719	CDS	2-3
AD-1562355	GUGACAUGGAGACUUCAGGCU	169	710-730	AGCCUGAAGUCUCCAUGUCACAG	304	708-730	CDS	3
AD-1562369	UCAGGCGGAGGCUGGACCAUU	170	724-744	AAUGGUCCAGCCUCCGCCUGAAG	305	722-744	CDS	3
AD-1562383	GACCAUCAUCCAGAGACGAAU	171	738-758	AUUCGUCUCUGGAUGAUGGUCCA	306	736-758	CDS	3
AD-1562406	GUGGCCUUGUCUCCUUCUACU	172	761-781	AGUAGAAGGAGACAAGGCCACUU	307	759-781	CDS	3
AD-1562417	UCCUUCUACCGGGACUGGAAU	173	772-792	AUUCCAGUCCCGGUAGAAGGAGA	308	770-792	CDS	3

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Region	Exon
AD-1562428	GGACUGGAAGC AGUACAAGCU	174	783-803	AGCUUGUACUGC UUCCAGUCCCG	309	781-803	CDS	3
AD-1562449	GGGCUUUGGCA GCAUCCGUGU	175	804-824	ACACGGAUGCUG CCAAAGCCCUG	310	802-824	CDS	3
AD-1562454	AACGAACACAU CCACCGGCUU	176	841-861	AAGCCGGUGGAU GUGUUCGUUCC	311	839-861	CDS	3
AD-1562468	CCGGCUCUCCA GACAGCCAAU	177	855-875	AUUGGCUGUCUG GAGAGCCGGUG	312	853-875	CDS	3
AD-1562482	AGCCAACCCGG CUGCGUGUAU	178	869-889	AUACACGCAGCC GGGUUGGCUGU	313	867-889	CDS	3
AD-1562493	CUGCGUGUAGA GAUGGAGGAU	179	880-900	AUCCUCCAUCUC UACACGCAGCC	314	878-900	CDS	3-4
AD-1562508	GAGGACUGGGA GGGCAACCUU	180	895-915	AAGGUUGCCCUC CCAGUCCUCCA	315	893-915	CDS	3-4
AD-1562520	GGCAACCUGCG CUACGCUGAU	181	907-927	AUCAGCGUAGCG CAGGUUGCCCU	316	905-927	CDS	4
AD-1562532	UACGCUGAGUA UAGCCACUUU	182	919-939	AAAGUGGCUAUA CUCAGCGUAGC	317	917-939	CDS	4
AD-1562543	UAGCCACUUUG UUUUGGGCAU	183	930-950	AUGCCCAAAACA AAGUGGCUAUA	318	928-950	CDS	4
AD-1562555	UUUGGGCAAUG AACUCAACAU	184	942-962	AUGUUGAGUUCA UUGCCCAAAAC	319	940-962	CDS	4
AD-1562571	AACAGCUAUCG CCUCUUCCUU	185	958-978	AAGGAAGAGGCG AUAGCUGUUGA	320	956-978	CDS	4
AD-1562576	GAACUACACUG GCAAUGUGGU	186	981-1001	ACCACAUUGCCA GUGUAGUUCCC	321	979-1001	CDS	4
AD-1562588	CCUCCAGUAUC AUAACAACAU	187	1011-1031	AUGUUGUUAUGA UACUGGAGGGC	322	1009-1031	CDS	4
AD-1562609	AGCCUUCAGCA CCAAGGACAU	188	1032-1052	AUGUCCUUGGUG CUGAAGGCUGU	323	1030-1052	CDS	4
AD-1562622	AAGGACAAGGA CAAUGACAAU	189	1045-1065	AUUGUCAUUGUC CUUGUCCUUGG	324	1043-1065	CDS	4
AD-1562636	UGACAACUGCU UGGACAAGUU	190	1059-1079	AACUUGUCCAAG CAGUUGUCAUU	325	1057-1079	CDS	4
AD-1562647	UGGACAAGUGU GCACAGCUCU	191	1070-1090	AGAGCUGUGCAC ACUUGUCCAAG	326	1068-1090	CDS	4
AD-1562663	GCUCCGCAAAG GUGGCUACUU	192	1086-1106	AAGUAGCCACCU UUGCGGAGCUG	327	1084-1106	CDS	4-5
AD-1562675	UGGCUACUGGU ACAACUGCUU	193	1098-1118	AAGCAGUUGUAC CAGUAGCCACC	328	1096-1118	CDS	4-5
AD-1562695	GCACAGACUCC AACCUCAAUU	194	1118-1138	AAUUGAGGUUGG AGUCUGUGCAG	329	1116-1138	CDS	5
AD-1562706	AACCUCAAUGG AGUGUACUAU	195	1129-1149	AUAGUACACUCC AUUGAGGUUGG	330	1127-1149	CDS	5
AD-1562722	ACUACCGCCUG GGUGAGCACU	196	1145-1165	AGUGCUCACCCA GGCGGUAGUAC	331	1143-1165	CDS	5
AD-1562733	GGUGAGCACAA UAAGCACCUU	197	1156-1176	AAGGUGCUUAUU GUGCUCACCCA	332	1154-1176	CDS	5
AD-1562752	UGGAUGGCAUC ACCUGGUAUU	198	1175-1195	AAUACCAGGUGA UGCCAUCCAGG	333	1173-1195	CDS	5
AD-1562763	ACCUGGUAUGG CUGGCAUGGU	199	1186-1206	ACCAUGCCAGCC AUACCAGGUGA	334	1184-1206	CDS	5

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Region	Exon
AD-1562774	CUGGCAUGGAUCUACCUACUU	200	1197-1217	AAGUAGGUAGAUCCAUGCCAGCC	335	1195-1217	CDS	5
AD-1562786	UACCUACUCCCUCAAACGGGU	201	1209-1229	ACCCGUUUGAGGGAGUAGGUAGA	336	1207-1229	CDS	5
AD-1562801	ACGGGUGGAGAUGAAAAUCCU	202	1224-1244	AGGAUUUUCAUCUCCACCCGUUU	337	1222-1244	CDS	5
AD-1562822	CCCAGAAGACUUCAAGCCUUU	203	1245-1265	AAAGGCUUGAAGUCUUCUGGGCG	338	1243-1265	CDS	5
AD-1562833	UCAAGCCUUAAAAGGAGGCUU	204	1256-1276	AAGCCUCCUUUUAAGGCUUGAAG	339	1254-1276	CDS-3'UTR	5
AD-1562859	AGCACGGAUACAGAAACUGAU	205	1283-1303	AUCAGUUUCUGUAUCCGUGCUCC	340	1281-1303	3'UTR	5
AD-1562877	GAGACACGUGGAGACUGGAUU	206	1301-1321	AAUCCAGUCUCCACGUGUCUCAG	341	1299-1321	3'UTR	5
AD-1562888	AGACUGGAUGAGGGCAGAUGU	207	1312-1332	ACAUCUGCCCUCAUCCAGUCUCC	342	1310-1332	3'UTR	5
AD-1562900	GGCAGAUGAGGACAGGAAGAU	208	1324-1344	AUCUUCCUGUCCUCAUCUGCCCU	343	1322-1344	3'UTR	5
AD-1562912	CAGGAAGAGAGUGUUAGAAAU	209	1336-1356	AUUUCUAACACUCUCUUCCUGUC	344	1334-1356	3'UTR	5
AD-1562928	GAAAGGGUAGGACUGAGAAAU	210	1352-1372	AUUUCUCAGUCCUACCCUUUCUA	345	1350-1372	3'UTR	5
AD-1562939	ACUGAGAAACAGCCUAUAAUU	211	1363-1383	AAUUAUAGGCUGUUUCUCAGUCC	346	1361-1383	3'UTR	5
AD-1562958	UCUCCAAAGAAAGAAUAAGUU	212	1382-1402	AACUUAUUCUUUCUUUGGAGAUU	347	1380-1402	3'UTR	5
AD-1563023	UAAGUCUCCAAGGAGCACAAU	213	1397-1417	AUUGUGCUCCUUGGAGACUUAUU	348	1395-1417	3'UTR	5
AD-1563029	UCAUAUGUACCAAGGAUGUUU	214	1422-1442	AAACAUCCUUGGUACAUAUGAUU	349	1420-1442	3'UTR	5
AD-1563040	AAGGAUGUUACAGUAAACAGU	215	1433-1453	ACUGUUUACUGUAACAUCCUUGG	350	1431-1453	3'UTR	5
AD-1563056	ACAGGAUGAACUAUUUAAACU	216	1449-1469	AGUUUAAAUAGUUCAUCCUGUUU	351	1447-1469	3'UTR	5
AD-1563118	AUUUAAACCCACUGGGUCCUU	217	1461-1481	AAGGACCCAGUGGGUUUAAAUAG	352	1459-1481	3'UTR	5
AD-1563137	UGCCACAUCCUUCUCAAGGUU	218	1480-1500	AACCUUGAGAAGGAUGUGGCAGG	353	1478-1500	3'UTR	5
AD-1563148	UCUCAAGGUGGUAGACUGAGU	219	1491-1511	ACUCAGUCUACCACCUUGAGAAG	354	1489-1511	3'UTR	5
AD-1563155	UCUCUCUGCCCAAGAUCCCUU	220	1516-1536	AAGGGAUCUUGGGCAGAGAGACC	355	1514-1536	3'UTR	5
AD-1563220	UCCCUGACAUAGCAGUAGCUU	221	1531-1551	AAGCUACUGCUAUGUCAGGGAUC	356	1529-1551	3'UTR	5
AD-1563231	GCAGUAGCUUGUCUUUUCCAU	222	1542-1562	AUGGAAAAGACAAGCUACUGCUA	357	1540-1562	3'UTR	5
AD-1563242	UCUUUUCCACAUGAUUUGUCU	223	1553-1573	AGACAAAUCAUGUGGAAAAGACA	358	1551-1573	3'UTR	5
AD-1563255	AUUUGUCUGUGAAAGAAAAUU	224	1566-1586	AAUUUUCUUUCACAGACAAAUCA	359	1564-1586	3'UTR	5
AD-1563325	AGAUCGUUUUAUCUAUUUUCU	225	1593-1613	AGAAAAUAGAUAAAACGAUCUCA	360	1591-1613	3'UTR	5

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Region	Exon
AD-1563343	UCUACGGCUUAGGCUAUGUGU	226	1613-1633	ACACAUAGCCUAAGCCGUAGAGA	361	1611-1633	3'UTR	5
AD-1563410	GUGAGGGCAAAACACAAAUCU	227	1630-1650	AGAUUUGUGUUUUGCCCUCACAU	362	1628-1650	3'UTR	5
AD-1563421	ACACAAAUCCCUUUGCUAAAU	228	1641-1661	AUUUAGCAAAGGGAUUUGUGUUU	363	1639-1661	3'UTR	5
AD-1563440	ACCAUAUUAUUUUGAUUCUCU	229	1665-1685	AGAGAAUCAAAAUAAUAUGGUUC	364	1663-1685	3'UTR	5
AD-1563454	CUCAAAGGAUAGGCCUUUGAU	230	1682-1702	AUCAAAGGCCUAUCCUUUGAGAA	365	1680-1702	3'UTR	5
AD-1563516	GCCUUUGAGUGUUAGAGAAAU	231	1694-1714	AUUUCUCUAACACUCAAAGGCCU	366	1692-1714	3'UTR	5
AD-1563527	GAGAAAGGAGUGAAGGAGGCU	232	1708-1728	AGCCUCCUUCACUCCUUUCUCUA	367	1706-1728	3'UTR	5
AD-1563547	AGGUGGGAAAUGGUAUUUCUU	233	1728-1748	AAGAAAUACCAUUUCCCACCUGC	368	1726-1748	3'UTR	5
AD-1563621	CAGUGAAAUUAUCUUGAGUCU	234	1759-1779	AGACUCAAGAUAAUUUCACUGGA	369	1757-1779	3'UTR	5
AD-1563634	UUGAGUCUACACAUUAUUUUU	235	1772-1792	AAAAAUAAUGUGUAGACUCAAGA	370	1770-1792	3'UTR	5
AD-1563649	AAUUGUUCGGCUGGAACUGAU	236	1803-1823	AUCAGUUCCAGCCGAACAAUUUU	371	1801-1823	3'UTR	5
AD-1563716	UGACCCAGGCUGGACUUGCGU	237	1820-1840	ACGCAAGUCCAGCCUGGGUCAGU	372	1818-1840	3'UTR	5
AD-1563720	GAGGAAACUCCAGGGCACUGU	238	1842-1862	ACAGUGCCCUGGAGUUUCCUCCC	373	1840-1862	3'UTR	5
AD-1563734	GCACUGCAUCUGGCGAUCAGU	239	1856-1876	ACUGAUCGCCAGAUGCAGUGCCC	374	1854-1876	3'UTR	5
AD-1563746	GCGAUCAGACUCUGAGCACUU	240	1868-1888	AAGUGCUCAGAGUCUGAUCGCCA	375	1866-1888	3'UTR	5
AD-1563755	CGCCUUGGUCAUGUACAGCAU	241	1897-1917	AUGCUGUACAUGACCAAGGCGAG	376	1895-1917	3'UTR	5
AD-1563822	CAGCACUGAAAGGAAUGAAGU	242	1912-1932	ACUUCAUUCCUUUCAGUGCUGUA	377	1910-1932	3'UTR	5
AD-1563833	GGAAUGAAGCACCAGCAGGAU	243	1923-1943	AUCCUGCUGGUGCUUCAUUCCUU	378	1921-1943	3'UTR	5
AD-1563845	CAGCAGGAGGUGGACAGAGUU	244	1935-1955	AACUCUGUCCACCUCCUGCUGGU	379	1933-1955	3'UTR	5
AD-1563856	GGACAGAGUCUCUCAUGGAUU	245	1946-1966	AAUCCAUGAGAGACUCUGUCCAC	380	1944-1966	3'UTR	5
AD-1563917	CUCAUGGAUGCCGGCACAAAU	246	1957-1977	AUUUGUGCCGGCAUCCAUGAGAG	381	1955-1977	3'UTR	5
AD-1563930	GCACAAAACUGCCUUAAAAUU	247	1970-1990	AAUUUUAAGGCAGUUUUGUGCCG	382	1968-1990	3'UTR	5
AD-1563948	UAGUUAAUACAGGUAUAUCUU	248	1995-2015	AAGAUAUACCUGUAUUAACUAUG	383	1993-2015	3'UTR	5
AD-1564013	CUUUGUAAGAAACAAGCUCAU	249	2026-2046	AUGAGCUUGUUUCUUACAAAGUA	384	2024-2046	3'UTR	5
AD-1564034	GGAGCUUCCUUUUAAAUUUUU	250	2047-2067	AAAAAUUUAAAAGGAAGCUCCUU	385	2045-2067	3'UTR	5
AD-1564055	CUGUAGGAAAUGGUUGAAAAU	251	2069-2089	AUUUUCAACCAUUUCCUACAGAC	386	2067-2089	3'UTR	5

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_001039554.3	Region	Exon
AD-1564117	GUUGAAAACUGAAGGUAGAUU	252	2081-2101	AAUCUACCUUCAGUUUUCAACCA	387	2079-2101	3'UTR	5
AD-1564128	AAGGUAGAUGGUGUUAUAGUU	253	2092-2112	AACUAUAACACCAUCUACCUUCA	388	2090-2112	3'UTR	5
AD-1564149	GUAAAUAAGCAUCUCACUUUU	254	2126-2146	AAAAGUGAGAUGCUUAUUUACAG	389	2124-2146	3'UTR	5
AD-1564170	UGGUUUUGUUUUAAACAUUCU	255	2163-2183	AGAAUGUUUAAAACAAAACCACA	390	2161-2183	3'UTR	5
AD-1564181	AACAUUCAACGUUUCUUUUCU	256	2176-2196	AGAAAAGAAACGUUGAAUGUUUA	391	2174-2196	3'UTR	5
AD-1564195	CUUUUCCUUCUACAAUAAACU	257	2190-2210	AGUUUAUUGUAGAAGGAAAAGAA	392	2188-2210	3'UTR	5

Table 5. Modified sense and antisense strand sequences of ANGPTL7 dsRNA agents

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1561710	csusuggaAfgGfAfAfagcuauagguL96	393	asCfscuaUfaGfCfuuucCfuUfccaagscsc	528	GGCTTGGAAGGAAAGCTATAGGC	663
AD-1561724	usasuaggCfuAfCfCfcauucagcuuL96	394	asAfsgcuGfaAfUfggguAfgCfcuauasgsc	529	GCTATAGGCTACCCATTCAGCTC	664
AD-1561733	gsasgacuCfaAfGfCfuuugagaaauL96	395	asUfsuucUfcAfAfagcuUfgAfgucucsusg	530	CAGAGACTCAAGCTTTGAGAAAG	665
AD-1561754	gscsuagcAfaAfGfAfgcaaggaaauL96	396	asUfsuucCfuUfGfcucuUfuGfcuagcscsu	531	AGGCTAGCAAAGAGCAAGGAAAG	666
AD-1561758	asasgagaGfaAfAfAfcaacaaaguuL96	397	asAfscuuUfgUfUfguuuUfcUfcucuususc	532	GAAAGAGAGAAAACAACAAAGTG	667
AD-1561776	gsusggcgAfgGfCfCfcucagaguguL96	398	asCfsacuCfuGfAfgggcCfuCfgccacsusu	533	AAGTGGCGAGGCCCTCAGAGTGA	668
AD-1561789	csasgaguGfaAfAfGfcguaaggguuuL96	399	asAfsaccUfuAfCfgcuuUfcAfcucugsasg	534	CTCAGAGTGAAAGCGTAAGGTTC	669
AD-1561800	csgsuaagGfuUfCfAfgucagccuguL96	400	asCfsaggCfuGfAfcugaAfcCfuuacgscsu	535	AGCGTAAGGTTCAGTCAGCCTGC	670
AD-1561820	csusgcagCfuUfUfGfcagaccucauL96	401	asUfsgagGfuCfUfgcaaAfgCfugcagscsa	536	TGCTGCAGCTTTGCAGACCTCAG	671
AD-1561836	csuscagcUfgGfGfCfaucuccagauL96	402	asUfscugGfaGfAfugccCfaGfcugagsgsu	537	ACCTCAGCTGGGCATCTCCAGAC	672
AD-1561842	usgsaaggAfaGfAfGfccuuccucauL96	403	asUfsgagGfaAfGfgcucUfuCfcuucasgsg	538	CCTGAAGGAAGAGCCTTCCTCAC	673
AD-1561854	csascccaAfaCfCfCfcacaaaagauuL96	404	asAfsucuUfuUfGfuggguUfuUfgggugsasg	539	CTCACCCAAACCCACAAAAGATG	674
AD-1561883	gscscucuCfuCfAfGfcugugaccuuL96	405	asAfsgguCfaCfAfgcugAfgAfgaggcsusu	540	AAGCCTCTCTCAGCTGTGACCTG	675
AD-1561902	usgsgcucUfgCfAfUfuucaucguuL96	406	asAfscgaUfgAfAfaaugCfaGfagccasgsg	541	CCTGGCTCTGCATTTTCATCGTG	676
AD-1561913	ususucauCfgUfGfGfccuuugucauL96	407	asUfsgacAfaAfGfgccaCfgAfugaaasasu	542	ATTTTCATCGTGGCCTTTGTCAG	677
AD-1561946	csusgcagAfaGfCfUfcucuaagcauL96	408	asUfsgcuUfaGfAfgagcUfuCfugcagscsc	543	GGCTGCAGAAGCTCTCTAAGCAC	678

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1561961	asasgcacAfaGfAfCfaccagcacauL96	409	asUfsgugCfuGfGfugucUfuGfugcuusasg	544	CTAAGCACAAGACACCAGCACAG	679
AD-1561973	cscsagcaCfaGfCfCfacagcucaauL96	410	asUfsugaGfcUfGfuggcUfgUfgcuggsusg	545	CACCAGCACAGCCACAGCTCAAA	680
AD-1561985	csasgcucAfaAfGfCfggccaacuguL96	411	asCfsaguUfgGfCfcgcuUfuGfagcugsusg	546	CACAGCTCAAAGCGGCCAACTGC	681
AD-1561997	gscscaacUfgCfUfGfuggaggagguuL96	412	asAfsccuCfcUfCfacagCfaGfuuggcscsg	547	CGGCCAACTGCTGTGAGGAGGTG	682
AD-1562009	gsasggagGfuGfAfAfggagcucaauL96	413	asUfsugaGfcUfCfcuucAfcCfuccucsasc	548	GTGAGGAGGTGAAGGAGCTCAAG	683
AD-1562020	gsgsagcuCfaAfGfGfcccaaguuguL96	414	asCfsaacUfuGfGfgccuUfgAfgcuccsusu	549	AAGGAGCTCAAGGCCCAAGTTGC	684
AD-1562032	cscsaaguUfgCfCfAfaccuuagcauL96	415	asUfsgcuAfaGfGfuuggCfaAfcuuggsgsc	550	GCCCAAGTTGCCAACCTTAGCAG	685
AD-1562045	csusuagcAfgCfCfUfgcugagugauL96	416	asUfscacUfcAfGfcaggCfuGfcuaagsgsu	551	ACCTTAGCAGCCTGCTGAGTGAA	686
AD-1562056	gscsugagUfgAfAfCfugaacaagauL96	417	asUfscuuGfuUfCfaguuCfaCfucagcsasg	552	CTGCTGAGTGAACTGAACAAGAA	687
AD-1562067	usgsaacaAfgAfAfGfcaggagaggguL96	418	asCfscucUfcCfUfgcuuCfuUfguucasgsu	553	ACTGAACAAGAAGCAGGAGAGGG	688
AD-1562087	gsascuggGfuCfAfGfcguggucauuL96	419	asAfsugaCfcAfCfgcugAfcCfcagucscsc	554	GGGACTGGGTCAGCGTGGTCATG	689
AD-1562099	gsusggucAfuGfCfAfggugauggauL96	420	asUfsccaUfcAfCfcugcAfuGfaccacsgsc	555	GCGTGGTCATGCAGGTGATGGAG	690
AD-1562111	gsusgaugGfaGfCfUfggagagcaauL96	421	asUfsugcUfcUfCfcagcUfcCfaucacscsu	556	AGGTGATGGAGCTGGAGAGCAAC	691
AD-1562122	gsgsagagCfaAfCfAfgcaagcgcauL96	422	asUfsgcgCfuUfGfcuguUfgCfucuccsasg	557	CTGGAGAGCAACAGCAAGCGCAT	692
AD-1562141	asusggagUfcGfCfGfgcucacagauL96	423	asUfscugUfgAfGfccgcGfaCfuccausgsc	558	GCATGGAGTCGCGGCTCACAGAT	693
AD-1562153	csuscacaGfaUfGfCfugagagcaauL96	424	asUfsugcUfcUfCfagcaUfcUfgugagscsc	559	GGCTCACAGATGCTGAGAGCAAG	694
AD-1562167	gsasgcaaGfuAfCfUfccgagaugauL96	425	asUfscauCfuCfGfgaguAfcUfugcucsusc	560	GAGAGCAAGTACTCCGAGATGAA	695
AD-1562179	csgsagauGfaAfCfAfaccaaauuguL96	426	asCfsaauUfuGfGfuuguUfcAfucucgsgsa	561	TCCGAGATGAACAACCAAATTGA	696
AD-1562190	ascscaaaUfuGfAfCfaucaugcaguL96	427	asCfsugcAfuGfAfugucAfaUfuuggususg	562	CAACCAAATTGACATCATGCAGC	697
AD-1562207	csasgcugCfaGfGfCfagcacagacuL96	428	asGfsucuGfuGfCfugccUfgCfagcugscsa	563	TGCAGCTGCAGGCAGCACAGACG	698
AD-1562218	asgscacaGfaCfGfGfucacucagauL96	429	asUfscugAfgUfGfaccgUfcUfgugcusgsc	564	GCAGCACAGACGGTCACTCAGAC	699
AD-1562229	uscsacucAfgAfCfCfuccgcagauuL96	430	asAfsucuGfcGfGfagguCfuGfagugascsc	565	GGTCACTCAGACCTCCGCAGATG	700
AD-1562242	csgscagaUfgCfCfAfucuacgacuuL96	431	asAfsgucGfuAfGfauggCfaUfcugcgsgsa	566	TCCGCAGATGCCATCTACGACTG	701
AD-1562255	usascgacUfgCfUfCfuucccucuauL96	432	asUfsagaGfgGfAfagagCfaGfucguasgsa	567	TCTACGACTGCTCTTCCCTCTAC	702
AD-1562267	uscsccucUfaCfCfAfgaagaacuauL96	433	asUfsaguUfcUfUfcuggUfaGfagggasasg	568	CTTCCCTCTACCAGAAGAACTAC	703
AD-1562278	gsasagaaCfuAfCfCfgcaucucuguL96	434	asCfsagaGfaUfGfcgguAfgUfucuucsusg	569	CAGAAGAACTACCGCATCTCTGG	704

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1562292	uscsucugGfaGfUfGfuauaagcuuuL96	435	asAfsagcUfuAfUfacacUfcCfagagasusg	570	CATCTCTGGAGTGTATAAGCTTC	705
AD-1562309	csusuccuCfcUfGfAfugacuuccuuL96	436	asAfsggaAfgUfCfaucaGfgAfggaagscsu	571	AGCTTCCTCCTGATGACTTCCTG	706
AD-1562333	asgscccuGfaAfCfUfggagguguuuL96	437	asAfsacaCfcUfCfcaguUfcAfgggcusgsc	572	GCAGCCCTGAACTGGAGGTGTTC	707
AD-1562344	gsgsagguGfuUfCfUfgugacaugguL96	438	asCfscauGfuCfAfcagaAfcAfccuccsasg	573	CTGGAGGTGTTCTGTGACATGGA	708
AD-1562355	gsusgacaUfgGfAfGfacuucaggcuL96	439	asGfsccuGfaAfGfucucCfaUfgucacsasg	574	CTGTGACATGGAGACTTCAGGCG	709
AD-1562369	uscsaggcGfgAfGfGfcuggaccauuL96	440	asAfsuggUfcCfAfgccuCfcGfccugasasg	575	CTTCAGGCGGAGGCTGGACCATC	710
AD-1562383	gsasccauCfaUfCfCfagagacgaauL96	441	asUfsucgUfcUfCfuggaUfgAfuggucscsa	576	TGGACCATCATCCAGAGACGAAA	711
AD-1562406	gsusggccUfuGfUfCfuccuucuacuL96	442	asGfsuagAfaGfGfagacAfaGfgccacsusu	577	AAGTGGCCTTGTCTCCTTCTACC	712
AD-1562417	uscscuucUfaCfCfGfggacuggaauL96	443	asUfsuccAfgUfCfccggUfaGfaaggasgsa	578	TCTCCTTCTACCGGGACTGGAAG	713
AD-1562428	gsgsacugGfaAfGfCfaguacaagcuL96	444	asGfscuuGfuAfCfugcuUfcCfaguccscsg	579	CGGGACTGGAAGCAGTACAAGCA	714
AD-1562449	gsgsgcuuUfgGfCfAfgcauccguguL96	445	asCfsacgGfaUfGfcugcCfaAfagcccsusg	580	CAGGGCTTTGGCAGCATCCGTGG	715
AD-1562454	asascgaaCfaCfAfUfccaccggcuuL96	446	asAfsgccGfgUfGfgaugUfgUfucguuscsc	581	GGAACGAACACATCCACCGGCTC	716
AD-1562468	cscsggcuCfuCfCfAfgacagccaauL96	447	asUfsuggCfuGfUfcuggAfgAfgccggsusg	582	CACCGGCTCTCCAGACAGCCAAC	717
AD-1562482	asgsccaaCfcCfGfGfcugcguguauL96	448	asUfsacaCfgCfAfgccgGfgUfuggcusgsu	583	ACAGCCAACCCGGCTGCGTGTAG	718
AD-1562493	csusgcguGfuAfGfAfgauggaggauL96	449	asUfsccuCfcAfUfcucuAfcAfcgcagscsc	584	GGCTGCGTGTAGAGATGGAGGAC	719
AD-1562508	gsasggacUfgGfGfAfgggcaaccuuL96	450	asAfsgguUfgCfCfcuccCfaGfuccucscsa	585	TGGAGGACTGGGAGGGCAACCTG	720
AD-1562520	gsgscaacCfuGfCfGfcuacgcugauL96	451	asUfscagCfgUfAfgcgcAfgGfuugccscsu	586	AGGGCAACCTGCGCTACGCTGAG	721
AD-1562532	usascgcuGfaGfUfAfuagccacuuuL96	452	asAfsaguGfgCfUfauacUfcAfgcguasgsc	587	GCTACGCTGAGTATAGCCACTTT	722
AD-1562543	usasgccaCfuUfUfGfuuuugggcauL96	453	asUfsgccCfaAfAfacaaAfgUfggcuasusa	588	TATAGCCACTTTGTTTTGGGCAA	723
AD-1562555	ususugggCfaAfUfGfaacucaacauL96	454	asUfsguuGfaGfUfucauUfgCfccaaasasc	589	GTTTTGGGCAATGAACTCAACAG	724
AD-1562571	asascagcUfaUfCfGfccucuuccuuL96	455	asAfsggaAfgAfGfgcgaUfaGfcuguuusgsa	590	TCAACAGCTATCGCCTCTTCCTG	725
AD-1562576	gsasacuaCfaCfUfGfgcaauguggguL96	456	asCfscacAfuUfGfccagUfgUfaguucscsc	591	GGGAACTACACTGGCAATGTGGG	726
AD-1562588	cscsuccaGfuAfUfCfauaacaacauL96	457	asUfsguuGfuUfAfugauAfcUfggaggsgsc	592	GCCCTCCAGTATCATAACAACAC	727
AD-1562609	asgsccuuCfaGfCfAfccaaggacauL96	458	asUfsgucCfuUfGfgugcUfgAfaggcusgsu	593	ACAGCCTTCAGCACCAAGGACAA	728
AD-1562622	asasggacAfaGfGfAfcaaugacaauL96	459	asUfsuguCfaUfUfgucc UfuGfuccuusgsg	594	CCAAGGACAAGGACAATGACAAC	729
AD-1562636	usgsacaaCfuGfCfUfuggacaaguuL96	460	asAfscuuGfuCfCfaagcAfgUfugucasusu	595	AATGACAACTGCTTGGACAAGTG	730

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1562647	usgsgacaAfgUfGfUfgcacagcucuL96	461	asGfsagcUfgUfGfcacaCfuUfguccasasg	596	CTTGGACAAGTGTGCACAGCTCC	731
AD-1562663	gscsuccgCfaAfAfGfguggcuacuuL96	462	asAfsguaGfcCfAfccuuUfgCfggagcsusg	597	CAGCTCCGCAAAGGTGGCTACTG	732
AD-1562675	usgsgcuaCfuGfGfUfacaacugcuuL96	463	asAfsgcaGfuUfGfuaccAfgUfagccascsc	598	GGTGGCTACTGGTACAACTGCTG	733
AD-1562695	gscsacagAfcUfCfCfaaccucaauuL96	464	asAfsuugAfgGfUfuggaGfuCfugugcsasg	599	CTGCACAGACTCCAACCTCAATG	734
AD-1562706	asasccucAfaUfGfGfaguguacuauL96	465	asUfsaguAfcAfCfuccaUfuGfagguusgsg	600	CCAACCTCAATGGAGTGTACTAC	735
AD-1562722	ascsuaccGfcCfUfGfggugagcacuL96	466	asGfsugcUfcAfCfccagGfcGfguagusasc	601	GTACTACCGCCTGGGTGAGCACA	736
AD-1562733	gsgsugagCfaCfAfAfuaagcaccuuL96	467	asAfsgguGfcUfUfauugUfgCfucaccscsa	602	TGGGTGAGCACAATAAGCACCTG	737
AD-1562752	usgsgaugGfcAfUfCfaccugguauuL96	468	asAfsuacCfaGfGfugauGfcCfauccasgsg	603	CCTGGATGGCATCACCTGGTATG	738
AD-1562763	ascscuggUfaUfGfGfcuggcaugguL96	469	asCfscauGfcCfAfgccaUfaCfcaggusgsa	604	TCACCTGGTATGGCTGGCATGGA	739
AD-1562774	csusggcaUfgGfAfUfcuaccuacuuL96	470	asAfsguaGfgUfAfgaucCfaUfgccagscsc	605	GGCTGGCATGGATCTACCTACTC	740
AD-1562786	usasccuaCfuCfCfCfucaaacggguL96	471	asCfsccgUfuUfGfagggAfgUfagguasgsa	606	TCTACCTACTCCCTCAAACGGGT	741
AD-1562801	ascsggguGfgAfGfAfugaaaauccuL96	472	asGfsgauUfuUfCfaucuCfcAfcccgususu	607	AAACGGGTGGAGATGAAAATCCG	742
AD-1562822	cscscagaAfgAfCfUfucaagccuuuL96	473	asAfsaggCfuUfGfaaguCfuUfcugggscsg	608	CGCCCAGAAGACTTCAAGCCTTA	743
AD-1562833	uscsaagcCfuUfAfAfaaggaggcuuL96	474	asAfsgccUfcCfUfuuuaAfgGfcuugasasg	609	CTTCAAGCCTTAAAAGGAGGCTG	744
AD-1562859	asgscacgGfaUfAfCfagaaacugauL96	475	asUfscagUfuUfCfuguaUfcCfgugcuscsc	610	GGAGCACGGATACAGAAACTGAG	745
AD-1562877	gsasgacaCfgUfGfGfagacuggauuL96	476	asAfsuccAfgUfCfuccaCfgUfgucucsasg	611	CTGAGACACGTGGAGACTGGATG	746
AD-1562888	asgsacugGfaUfGfAfgggcagauguL96	477	asCfsaucUfgCfCfcucaUfcCfagucuscsc	612	GGAGACTGGATGAGGGCAGATGA	747
AD-1562900	gsgscagaUfgAfGfGfacaggaagauL96	478	asUfscuuCfcUfGfuccuCfaUfcugccscsu	613	AGGGCAGATGAGGACAGGAAGAG	748
AD-1562912	csasggaaGfaGfAfGfuguuagaaauL96	479	asUfsuucUfaAfCfacucUfcUfuccugsusc	614	GACAGGAAGAGAGTGTTAGAAAG	749
AD-1562928	gsasaaggGfuAfGfGfacugagaaauL96	480	asUfsuucUfcAfGfuccuAfcCfcuuucsusa	615	TAGAAAGGGTAGGACTGAGAAAC	750
AD-1562939	ascsugagAfaAfCfAfgccuauaauuL96	481	asAfsuuaUfaGfGfcuguUfuCfucaguscsc	616	GGACTGAGAAACAGCCTATAATC	751
AD-1562958	uscsuccaAfaGfAfAfagaauaaguuL96	482	asAfscuuAfuUfCfuuucUfuUfggagasusu	617	AATCTCCAAAGAAAGAATAAGTC	752
AD-1563023	usasagucUfcCfAfAfggagcacaauL96	483	asUfsuguGfcUfCfcuugGfaGfacuuasusu	618	AATAAGTCTCCAAGGAGCACAAA	753
AD-1563029	uscsauauGfuAfCfCfaaggauguuuL96	484	asAfsacaUfcCfUfugguAfcAfuaugasusu	619	AATCATATGTACCAAGGATGTTA	754
AD-1563040	asasggauGfuUfAfCfaguaaacaguL96	485	asCfsuguUfuAfCfuguaAfcAfuccuusgsg	620	CCAAGGATGTTACAGTAAACAGG	755
AD-1563056	ascsaggaUfgAfAfCfuauuuaaacuL96	486	asGfsuuuAfaAfUfaguuCfaUfccugususu	621	AAACAGGATGAACTATTTAAACC	756

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1563118	asususuaaAfcCfCfAfcuggguccuuL96	487	asAfsggaCfcCfAfgugggGfuUfuaaausasg	622	CTATTTAAACCCACTGGGTCCTG	757
AD-1563137	usgsccacAfuCfCfUfucucaagguuL96	488	asAfsccuUfgAfGfaaggAfuGfuggcasgsg	623	CCTGCCACATCCTTCTCAAGGTG	758
AD-1563148	uscsucaaGfgUfGfGfuagacugaguL96	489	asCfsucaGfuCfUfaccaCfcUfugagasasg	624	CTTCTCAAGGTGGTAGACTGAGT	759
AD-1563155	uscsucucUfgCfCfCfaagaucccuuL96	490	asAfsgggAfuCfUfugggCfaGfagagascsc	625	GGTCTCTCTGCCCAAGATCCCTG	760
AD-1563220	uscsccugAfcAfUfAfgcaguagcuuL96	491	asAfsgcuAfcUfGfcuauGfuCfagggasusc	626	GATCCCTGACATAGCAGTAGCTT	761
AD-1563231	gscsaguaGfcUfUfGfucuuuuccauL96	492	asUfsggaAfaAfGfacaaGfcUfacugcsusa	627	TAGCAGTAGCTTGTCTTTTCCAC	762
AD-1563242	uscsuuuuCfcAfCfAfugauuugucuL96	493	asGfsacaAfaUfCfauguGfgAfaaagascsa	628	TGTCTTTTCCACATGATTTGTCT	763
AD-1563255	asusuuguCfuGfUfGfaaagaaaauuL96	494	asAfsuuuUfcUfUfucacAfgAfcaaauscsa	629	TGATTTGTCTGTGAAAGAAAATA	764
AD-1563325	asgsaucgUfuUfUfAfucuauuuucuL96	495	asGfsaaaAfuAfGfauaaAfaCfgaucuscsa	630	TGAGATCGTTTTATCTATTTTCT	765
AD-1563343	uscsuacgGfcUfUfAfggcuauguguL96	496	asCfsacaUfaGfCfcuaaGfcCfguagasgsa	631	TCTCTACGGCTTAGGCTATGTGA	766
AD-1563410	gsusgaggGfcAfAfAfacacaaaucuL96	497	asGfsauuUfgUfGfuuuuGfcCfcucacsasu	632	ATGTGAGGGCAAAACACAAATCC	767
AD-1563421	ascsacaaAfuCfCfCfuuugcuaaauL96	498	asUfsuuaGfcAfAfagggAfuUfugugususu	633	AAACACAAATCCCTTTGCTAAAA	768
AD-1563440	ascscauaUfuAfUfUfuugauucucuL96	499	asGfsagaAfuCfAfaaauAfaUfauggususc	634	GAACCATATTATTTTGATTCTCA	769
AD-1563454	csuscaaaGfgAfUfAfggccuuugauL96	500	asUfscaaAfgGfCfcuauCfcUfuugagsasa	635	TTCTCAAAGGATAGGCCTTTGAG	770
AD-1563516	gscscuuuGfaGfUfGfuuagagaaauL96	501	asUfsuucUfcUfAfacacUfcAfaaggcscsu	636	AGGCCTTTGAGTGTTAGAGAAAG	771
AD-1563527	gsasgaaaGfgAfGfUfgaaggaggcuL96	502	asGfsccuCfcUfUfcacuCfcUfuucucsusa	637	TAGAGAAAGGAGTGAAGGAGGCA	772
AD-1563547	asgsguggGfaAfAfUfgguauuucuuL96	503	asAfsgaaAfuAfCfcauuUfcCfcaccusgsc	638	GCAGGTGGGAAATGGTATTTCTA	773
AD-1563621	csasgugaAfaUfUfAfucuugagucuL96	504	asGfsacuCfaAfGfauaaUfuUfcacugsgsa	639	TCCAGTGAAATTATCTTGAGTCT	774
AD-1563634	ususgaguCfuAfCfAfcauuauuuuuL96	505	asAfsaaaUfaAfUfguguAfgAfcucaasgsa	640	TCTTGAGTCTACACATTATTTTT	775
AD-1563649	asasuuguUfcGfGfCfuggaacugauL96	506	asUfscagUfuCfCfagccGfaAfcaauususu	641	AAAATTGTTCGGCTGGAACTGAC	776
AD-1563716	usgsacccAfgGfCfUfggacuugcguL96	507	asCfsgcaAfgUfCfcagcCfuGfggucasgsu	642	ACTGACCCAGGCTGGACTTGCGG	777
AD-1563720	gsasggaaAfcUfCfCfaggcacuguL96	508	asCfsaguGfcCfCfuggaGfuUfuccucscsc	643	GGGAGGAAACTCCAGGGCACTGC	778
AD-1563734	gscsacugCfaUfCfUfggcgaucaguL96	509	asCfsugaUfcGfCfcagaUfgCfagugcscsc	644	GGGCACTGCATCTGGCGATCAGA	779
AD-1563746	gscsgaucAfgAfCfUfcugagcacuuL96	510	asAfsgugCfuCfAfgaguCfuGfaucgcscsa	645	TGGCGATCAGACTCTGAGCACTG	780
AD-1563755	csgsccuuGfgUfCfAfuguacagcauL96	511	asUfsgcuGfuAfCfaugaCfcAfaggcgsasg	646	CTCGCCTTGGTCATGTACAGCAC	781
AD-1563822	csasgcacUfgAfAfAfggaaugaaguL96	512	asCfsuucAfuUfCfcuuuCfaGfugcugsusa	647	TACAGCACTGAAAGGAATGAAGC	782

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1563833	gsgsaaugAfaGfCfAfccagcaggauL96	513	asUfsccuGfcUfGfgugcUfuCfauuccsusu	648	AAGGAATGAAGCACCAGCAGGAG	783
AD-1563845	csasgcagGfaGfGfUfggacagaguuL96	514	asAfscucUfgUfCfcaccUfcCfugcugsgsu	649	ACCAGCAGGAGGTGGACAGAGTC	784
AD-1563856	gsgsacagAfgUfCfUfcucauggauuL96	515	asAfsuccAfuGfAfgagaCfuCfuguccsasc	650	GTGGACAGAGTCTCTCATGGATG	785
AD-1563917	csuscaugGfaUfGfCfcggcacaaauL96	516	asUfsuugUfgCfCfggcaUfcCfaugagsasg	651	CTCTCATGGATGCCGGCACAAAA	786
AD-1563930	gscsacaaAfaCfUfGfccuuaaaauuL96	517	asAfsuuuUfaAfGfgcagUfuUfugugcscsg	652	CGGCACAAAACTGCCTTAAAATA	787
AD-1563948	usasguuaAfuAfCfAfgguauaucuuL96	518	asAfsgauAfuAfCfcuguAfuUfaacuasusg	653	CATAGTTAATACAGGTATATCTA	788
AD-1564013	csusuuguAfaGfAfAfacaagcucauL96	519	asUfsgagCfuUfGfuuucUfuAfcaaagsusa	654	TACTTTGTAAGAAACAAGCTCAA	789
AD-1564034	gsgsagcuUfcCfUfUfuuaaauuuuuL96	520	asAfsaaaUfuUfAfaaagGfaAfgcuccsusu	655	AAGGAGCTTCCTTTTAAATTTTG	790
AD-1564055	csusguagGfaAfAfUfgguugaaaauL96	521	asUfsuuuCfaAfCfcauuUfcCfuacagsasc	656	GTCTGTAGGAAATGGTTGAAAAC	791
AD-1564117	gsusugaaAfaCfUfGfaagguagauuL96	522	asAfsucuAfcCfUfucagUfuUfucaacscsa	657	TGGTTGAAAACTGAAGGTAGATG	792
AD-1564128	asasgguaGfaUfGfGfguguuauaguuL96	523	asAfscuaUfaAfCfaccaUfcUfaccuuscsa	658	TGAAGGTAGATGGTGTTATAGTT	793
AD-1564149	gsusaaauAfaGfCfAfucucacuuuuL96	524	asAfsaagUfgAfGfaugcUfuAfuuuacsasg	659	CTGTAAATAAGCATCTCACTTTG	794
AD-1564170	usgsguuuUfgUfUfUfuaaacauucuL96	525	asGfsaauGfuUfUfaaaaCfaAfaaccascsa	660	TGTGGTTTTGTTTTAAACATTCA	795
AD-1564181	asascauuCfaAfCfGfuuucuuuucuL96	526	asGfsaaaAfgAfAfacguUfgAfauguususa	661	TAAACATTCAACGTTTCTTTTCC	796
AD-1564195	csusuuucCfuUfCfUfacaauaaacuL96	527	asGfsuuuAfuUfGfuagaAfgGfaaaagsasa	662	TTCTTTTCCTTCTACAATAAACA	797

Table 6. Unmodified sense and antisense strand sequences of ANGPTL7 dsRNA agents

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4
AD-1094381	UGGCUACUGGUACAACUGCUA	798	1098-1118	UAGCAGUUGUACCAGUAGCCACC	933	1096-1118
AD-1094401	GCACAGACUCCAACCUCAAUA	799	1118-1138	UAUUGAGGUUGGAGUCUGUGCAG	934	1116-1138
AD-1562960	CUUGGAAGGAAAGCUAUAGGA	800	4-24	UCCUAUAGCUUUCCUUCCAAGCC	935	2--24
AD-1562974	UAUAGGCUACCCAUUCAGCUA	801	18-38	UAGCUGAAUGGGUAGCCUAUAGC	936	16-38
AD-1562983	GAGACUCAAGCUUUGAGAAAA	802	47-67	UUUUCUCAAAGCUUGAGUCUCUG	937	45-67
AD-1563004	GCUAGCAAAGAGCAAGGAAAA	803	68-88	UUUUCCUUGCUCUUUGCUAGCCU	938	66-88
AD-1563008	AAGAGAGAAAACAACAAAGUA	804	86-106	UACUUUGUUGUUUUCUCUCUUUC	939	84-106

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4
AD-1563076	GUGGCGAGGCCCUCAGAGUGA	805	104-124	UCACUCUGAGGGCCUCGCCACUU	940	102-124
AD-1563089	CAGAGUGAAAGCGUAAGGUUA	806	117-137	UAACCUUACGCUUUCACUCUGAG	941	115-137
AD-1563100	CGUAAGGUUCAGUCAGCCUGA	807	128-148	UCAGGCUGACUGAACCUUACGCU	942	126-148
AD-1563170	CUGCAGCUUUGCAGACCUCAA	808	148-168	UUGAGGUCUGCAAAGCUGCAGCA	943	146-168
AD-1563186	CUCAGCUGGGCAUCUCCAGAA	809	164-184	UUCUGGAGAUGCCCAGCUGAGGU	944	162-184
AD-1563192	UGAAGGAAGAGCCUUCCUCAA	810	190-210	UUGAGGAAGGCUCUUCCUUCAGG	945	188-210
AD-1563204	CACCCAAACCCACAAAAGAUA	811	208-228	UAUCUUUUGUGGGUUUGGGUGAG	946	206-228
AD-1563283	GCCUCUCUCAGCUGUGACCUA	812	237-257	UAGGUCACAGCUGAGAGAGGCUU	947	235-257
AD-1563302	UGGCUCUGCAUUUUCAUCGUA	813	256-276	UACGAUGAAAAUGCAGAGCCAGG	948	254-276
AD-1563363	UUUCAUCGUGGCCUUUGUCAA	814	267-287	UUGACAAAGGCCACGAUGAAAAU	949	265-287
AD-1563396	CUGCAGAAGCUCUCUAAGCAA	815	301-321	UUGCUUAGAGAGCUUCUGCAGCC	950	299-321
AD-1563461	AAGCACAAGACACCAGCACAA	816	316-336	UUGUGCUGGUGUCUUGUGCUUAG	951	314-336
AD-1563473	CCAGCACAGCCACAGCUCAAA	817	328-348	UUUGAGCUGUGGCUGUGCUGGUG	952	326-348
AD-1563485	CAGCUCAAAGCGGCCAACUGA	818	340-360	UCAGUUGGCCGCUUUGAGCUGUG	953	338-360
AD-1563497	GCCAACUGCUGUGAGGAGGUA	819	352-372	UACCUCCUCACAGCAGUUGGCCG	954	350-372
AD-1563559	GAGGAGGUGAAGGAGCUCAAA	820	364-384	UUUGAGCUCCUUCACCUCCUCAC	955	362-384
AD-1563570	GGAGCUCAAGGCCCAAGUUGA	821	375-395	UCAACUUGGGCCUUGAGCUCCUU	956	373-395
AD-1563582	CCAAGUUGCCAACCUUAGCAA	822	387-407	UUGCUAAGGUUGGCAACUUGGGC	957	385-407
AD-1563595	CUUAGCAGCCUGCUGAGUGAA	823	400-420	UUCACUCAGCAGGCUGCUAAGGU	958	398-420
AD-1563606	GCUGAGUGAACUGAACAAGAA	824	411-431	UUCUUGUUCAGUUCACUCAGCAG	959	409-431
AD-1563609	GUGGUCAUGCAGGUGAUGGAA	825	454-474	UUCCAUCACCUGCAUGACCACGC	960	452-474
AD-1563669	UGAACAAGAAGCAGGAGAGGA	826	422-442	UCCUCUCCUGCUUCUUGUUCAGU	961	420-442
AD-1563689	GACUGGGUCAGCGUGGUCAUA	827	442-462	UAUGACCACGCUGACCCAGUCCC	962	440-462
AD-1563701	GUGAUGGAGCUGGAGAGCAAA	828	466-486	UUUGCUCUCCAGCUCCAUCACCU	963	464-486
AD-1563762	GGAGAGCAACAGCAAGCGCAA	829	477-497	UUGCGCUUGCUGUUGCUCUCCAG	964	475-497
AD-1563781	AUGGAGUCGCGGCUCACAGAA	830	496-516	UUCUGUGAGCCGCGACUCCAUGC	965	494-516

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4
AD-1563793	CUCACAGAUGCUGAGAGCAAA	831	508-528	UUUGCUCUCAGCAUCUGUGAGCC	966	506-528
AD-1563807	GAGCAAGUACUCCGAGAUGAA	832	522-542	UUCAUCUCGGAGUACUUGCUCUC	967	520-542
AD-1563871	CGAGAUGAACAACCAAAUUGA	833	534-554	UCAAUUUGGUUGUUCAUCUCGGA	968	532-554
AD-1563882	ACCAAAUUGACAUCAUGCAGA	834	545-565	UCUGCAUGAUGUCAAUUUGGUUG	969	543-565
AD-1563895	CAGCUGCAGGCAGCACAGACA	835	562-582	UGUCUGUGCUGCCUGCAGCUGCA	970	560-582
AD-1563906	AGCACAGACGGUCACUCAGAA	836	573-593	UUCUGAGUGACCGUCUGUGCUGC	971	571-593
AD-1563967	UCACUCAGACCUCCGCAGAUA	837	584-604	UAUCUGCGGAGGUCUGAGUGACC	972	582-604
AD-1563980	CGCAGAUGCCAUCUACGACUA	838	597-617	UAGUCGUAGAUGGCAUCUGCGGA	973	595-617
AD-1563993	UACGACUGCUCUUCCCUCUAA	839	610-630	UUAGAGGGAAGAGCAGUCGUAGA	974	608-630
AD-1564005	UCCCUCUACCAGAAGAACUAA	840	622-642	UUAGUUCUUCUGGUAGAGGGAAG	975	620-642
AD-1564066	GAAGAACUACCGCAUCUCUGA	841	633-653	UCAGAGAUGCGGUAGUUCUUCUG	976	631-653
AD-1564080	UCUCUGGAGUGUAUAAGCUUA	842	647-667	UAAGCUUAUACACUCCAGAGAUG	977	645-667
AD-1564097	CUUCCUCCUGAUGACUUCCUA	843	664-684	UAGGAAGUCAUCAGGAGGAAGCU	978	662-684
AD-1564215	AGCCCUGAACUGGAGGUGUUA	844	688-708	UAACACCUCCAGUUCAGGGCUGC	979	686-708
AD-1564226	GGAGGUGUUCUGUGACAUGGA	845	699-719	UCCAUGUCACAGAACACCUCCAG	980	697-719
AD-1564236	GUGACAUGGAGACUUCAGGCA	846	710-730	UGCCUGAAGUCUCCAUGUCACAG	981	708-730
AD-1564250	UCAGGCGGAGGCUGGACCAUA	847	724-744	UAUGGUCCAGCCUCCGCCUGAAG	982	722-744
AD-1564258	GUGGCCUUGUCUCCUUCUACA	848	761-781	UGUAGAAGGAGACAAGGCCACUU	983	759-781
AD-1564259	GACCAUCAUCCAGAGACGAAA	849	738-758	UUUCGUCUCUGGAUGAUGGUCCA	984	736-758
AD-1564290	UCCUUCUACCGGGACUGGAAA	850	772-792	UUUCCAGUCCCGGUAGAAGGAGA	985	770-792
AD-1564301	GGACUGGAAGCAGUACAAGCA	851	783-803	UGCUUGUACUGCUUCCAGUCCCG	986	781-803
AD-1564322	GGGCUUUGGCAGCAUCCGUGA	852	804-824	UCACGGAUGCUGCCAAAGCCCUG	987	802-824
AD-1564327	AACGAACACAUCCACCGGCUA	853	841-861	UAGCCGGUGGAUGUGUUCGUUCC	988	839-861
AD-1564341	CCGGCUCUCCAGACAGCCAAA	854	855-875	UUUGGCUGUCUGGAGAGCCGGUG	989	853-875
AD-1564355	AGCCAACCCGGCUGCGUGUAA	855	869-889	UUACACGCAGCCGGGUUGGCUGU	990	867-889
AD-1564366	CUGCGUGUAGAGAUGGAGGAA	856	880-900	UUCCUCCAUCUCUACACGCAGCC	991	878-900

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4
AD-1564381	GAGGACUGGGAGGGCAACCUA	857	895-915	UAGGUUGCCCUCCCAGUCCUCCA	992	893-915
AD-1564393	GGCAACCUGCGCUACGCUGAA	858	907-927	UUCAGCGUAGCGCAGGUUGCCCU	993	905-927
AD-1564405	UACGCUGAGUAUAGCCACUUA	859	919-939	UAAGUGGCUAUACUCAGCGUAGC	994	917-939
AD-1564416	UAGCCACUUUGUUUUGGGCAA	860	930-950	UUGCCCAAAACAAAGUGGCUAUA	995	928-950
AD-1564428	UUUGGGCAAUGAACUCAACAA	861	942-962	UUGUUGAGUUCAUUGCCCAAAAC	996	940-962
AD-1564444	AACAGCUAUCGCCUCUUCCUA	862	958-978	UAGGAAGAGGCGAUAGCUGUUGA	997	956-978
AD-1564449	GAACUACACUGGCAAUGUGGA	863	981-1001	UCCACAUUGCCAGUGUAGUUCCC	998	979-1001
AD-1564464	CCUCCAGUAUCAUAACAACAA	864	1011-1031	UUGUUGUUAUGAUACUGGAGGGC	999	1009-1031
AD-1564485	AGCCUUCAGCACCAAGGACAA	865	1032-1052	UUGUCCUUGGUGCUGAAGGCUGU	1000	1030-1052
AD-1564493	AAGGACAAGGACAAUGACAAA	866	1045-1065	UUUGUCAUUGUCCUUGUCCUUGG	1001	1043-1065
AD-1564507	UGACAACUGCUUGGACAAGUA	867	1059-1079	UACUUGUCCAAGCAGUUGUCAUU	1002	1057-1079
AD-1564519	UGGACAAGUGUGCACAGCUCA	868	1070-1090	UGAGCUGUGCACACUUGUCCAAG	1003	1068-1090
AD-1564535	GCUCCGCAAAGGUGGCUACUA	869	1086-1106	UAGUAGCCACCUUUGCGGAGCUG	1004	1084-1106
AD-1564550	AACCUCAAUGGAGUGUACUAA	870	1129-1149	UUAGUACACUCCAUUGAGGUUGG	1005	1127-1149
AD-1564566	ACUACCGCCUGGGUGAGCACA	871	1145-1165	UGUGCUCACCCAGGCGGUAGUAC	1006	1143-1165
AD-1564577	GGUGAGCACAAUAAGCACCUA	872	1156-1176	UAGGUGCUUAUUGUGCUCACCCA	1007	1154-1176
AD-1564596	UGGAUGGCAUCACCUGGUAUA	873	1175-1195	UAUACCAGGUGAUGCCAUCCAGG	1008	1173-1195
AD-1564607	ACCUGGUAUGGCUGGCAUGGA	874	1186-1206	UCCAUGCCAGCCAUACCAGGUGA	1009	1184-1206
AD-1564618	CUGGCAUGGAUCUACCUACUA	875	1197-1217	UAGUAGGUAGAUCCAUGCCAGCC	1010	1195-1217
AD-1564630	UACCUACUCCCUCAAACGGGA	876	1209-1229	UCCCGUUUGAGGGAGUAGGUAGA	1011	1207-1229
AD-1564645	ACGGGUGGAGAUGAAAAUCCA	877	1224-1244	UGGAUUUUCAUCUCCACCCGUUU	1012	1222-1244
AD-1564666	CCCAGAAGACUUCAAGCCUUA	878	1245-1265	UAAGGCUUGAAGUCUUCUGGGCG	1013	1243-1265
AD-1564677	UCAAGCCUUAAAAGGAGGCUA	879	1256-1276	UAGCCUCCUUUUAAGGCUUGAAG	1014	1254-1276
AD-1564703	AGCACGGAUACAGAAACUGAA	880	1283-1303	UUCAGUUUCUGUAUCCGUGCUCC	1015	1281-1303
AD-1564721	GAGACACGUGGAGACUGGAUA	881	1301-1321	UAUCCAGUCUCCACGUGUCUCAG	1016	1299-1321
AD-1564732	AGACUGGAUGAGGGCAGAUGA	882	1312-1332	UCAUCUGCCCUCAUCCAGUCUCC	1017	1310-1332

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4
AD-1564744	GGCAGAUGAGGACAGGAAGAA	883	1324-1344	UUCUUCCUGUCCUCAUCUGCCCU	1018	1322-1344
AD-1564756	CAGGAAGAGAGUGUUAGAAAA	884	1336-1356	UUUUCUAACACUCUCUUCCUGUC	1019	1334-1356
AD-1564772	GAAAGGGUAGGACUGAGAAAA	885	1352-1372	UUUUCUCAGUCCUACCCUUUCUA	1020	1350-1372
AD-1564783	ACUGAGAAACAGCCUAUAAUA	886	1363-1383	UAUUAUAGGCUGUUUCUCAGUCC	1021	1361-1383
AD-1564802	UCUCCAAAGAAAGAAUAAGUA	887	1382-1402	UACUUAUUCUUUCUUUGGAGAUU	1022	1380-1402
AD-1564817	UAAGUCUCCAAGGAGCACAAA	888	1397-1417	UUUGUGCUCCUUGGAGACUUAUU	1023	1395-1417
AD-1564823	UCAUAUGUACCAAGGAUGUUA	889	1422-1442	UAACAUCCUUGGUACAUAUGAUU	1024	1420-1442
AD-1564834	AAGGAUGUUACAGUAAACAGA	890	1433-1453	UCUGUUUACUGUAACAUCCUUGG	1025	1431-1453
AD-1564850	ACAGGAUGAACUAUUUAAACA	891	1449-1469	UGUUUAAAUAGUUCAUCCUGUUU	1026	1447-1469
AD-1564862	AUUUAAACCCACUGGGUCCUA	892	1461-1481	UAGGACCCAGUGGGUUUAAAUAG	1027	1459-1481
AD-1564881	UGCCACAUCCUUCUCAAGGUA	893	1480-1500	UACCUUGAGAAGGAUGUGGCAGG	1028	1478-1500
AD-1564892	UCUCAAGGUGGUAGACUGAGA	894	1491-1511	UCUCAGUCUACCACCUUGAGAAG	1029	1489-1511
AD-1564899	UCUCUCUGCCCAAGAUCCCUA	895	1516-1536	UAGGGAUCUUGGGCAGAGAGACC	1030	1514-1536
AD-1564914	UCCCUGACAUAGCAGUAGCUA	896	1531-1551	UAGCUACUGCUAUGUCAGGGAUC	1031	1529-1551
AD-1564925	GCAGUAGCUUGUCUUUUCCAA	897	1542-1562	UUGGAAAAGACAAGCUACUGCUA	1032	1540-1562
AD-1564936	UCUUUUCCACAUGAUUUGUCA	898	1553-1573	UGACAAAUCAUGUGGAAAAGACA	1033	1551-1573
AD-1564949	AUUUGUCUGUGAAAGAAAAUA	899	1566-1586	UAUUUUCUUUCACAGACAAAUCA	1034	1564-1586
AD-1564969	AGAUCGUUUUAUCUAUUUUCA	900	1593-1613	UGAAAAUAGAUAAAACGAUCUCA	1035	1591-1613
AD-1564987	UCUACGGCUUAGGCUAUGUGA	901	1613-1633	UCACAUAGCCUAAGCCGUAGAGA	1036	1611-1633
AD-1565004	GUGAGGGCAAAACACAAAUCA	902	1630-1650	UGAUUUGUGUUUUGCCCUCACAU	1037	1628-1650
AD-1565015	ACACAAAUCCCUUUGCUAAAA	903	1641-1661	UUUUAGCAAAGGGAUUUGUGUUU	1038	1639-1661
AD-1565034	ACCAUAUUAUUUUGAUUCUCA	904	1665-1685	UGAGAAUCAAAAUAAUAUGGUUC	1039	1663-1685
AD-1565048	CUCAAAGGAUAGGCCUUUGAA	905	1682-1702	UUCAAAGGCCUAUCCUUUGAGAA	1040	1680-1702
AD-1565060	GCCUUUGAGUGUUAGAGAAAA	906	1694-1714	UUUUCUCUAACACUCAAAGGCCU	1041	1692-1714
AD-1565071	GAGAAAGGAGUGAAGGAGGCA	907	1708-1728	UGCCUCCUUCACUCCUUUCUCUA	1042	1706-1728
AD-1565091	AGGUGGGAAAUGGUAUUUCUA	908	1728-1748	UAGAAAUACCAUUUCCCACCUGC	1043	1726-1748

Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4	Antisense Sequence 5' to 3'	SEQ ID NO:	Range in NM_021146.4
AD-1565113	CAGUGAAAUUAUCUUGAGUCA	909	1759-1779	UGACUCAAGAUAAUUUCACUGGA	1044	1757-1779
AD-1565126	UUGAGUCUACACAUUAUUUUA	910	1772-1792	UAAAAUAAUGUGUAGACUCAAGA	1045	1770-1792
AD-1565141	AAUUGUUCGGCUGGAACUGAA	911	1803-1823	UUCAGUUCCAGCCGAACAAUUUU	1046	1801-1823
AD-1565158	UGACCCAGGCUGGACUUGCGA	912	1820-1840	UCGCAAGUCCAGCCUGGGUCAGU	1047	1818-1840
AD-1565162	GAGGAAACUCCAGGGCACUGA	913	1842-1862	UCAGUGCCCUGGAGUUUCCUCCC	1048	1840-1862
AD-1565176	GCACUGCAUCUGGCGAUCAGA	914	1856-1876	UCUGAUCGCCAGAUGCAGUGCCC	1049	1854-1876
AD-1565188	GCGAUCAGACUCUGAGCACUA	915	1868-1888	UAGUGCUCAGAGUCUGAUCGCCA	1050	1866-1888
AD-1565197	CGCCUUGGUCAUGUACAGCAA	916	1897-1917	UUGCUGUACAUGACCAAGGCGAG	1051	1895-1917
AD-1565212	CAGCACUGAAAGGAAUGAAGA	917	1912-1932	UCUUCAUUCCUUUCAGUGCUGUA	1052	1910-1932
AD-1565223	GGAAUGAAGCACCAGCAGGAA	918	1923-1943	UUCCUGCUGGUGCUUCAUUCCUU	1053	1921-1943
AD-1565235	CAGCAGGAGGUGGACAGAGUA	919	1935-1955	UACUCUGUCCACCUCCUGCUGGU	1054	1933-1955
AD-1565246	GGACAGAGUCUCUCAUGGAUA	920	1946-1966	UAUCCAUGAGAGACUCUGUCCAC	1055	1944-1966
AD-1565257	CUCAUGGAUGCCGGCACAAAA	921	1957-1977	UUUUGUGCCGGCAUCCAUGAGAG	1056	1955-1977
AD-1565270	GCACAAAACUGCCUUAAAAUA	922	1970-1990	UAUUUUAAGGCAGUUUUGUGCCG	1057	1968-1990
AD-1565288	UAGUUAAUACAGGUAUAUCUA	923	1995-2015	UAGAUAUACCUGUAUUAACUAUG	1058	1993-2015
AD-1565303	CUUUGUAAGAAACAAGCUCAA	924	2026-2046	UUGAGCUUGUUUCUUACAAAGUA	1059	2024-2046
AD-1565324	GGAGCUUCCUUUUAAAUUUUA	925	2047-2067	UAAAAUUUAAAAGGAAGCUCCUU	1060	2045-2067
AD-1565345	CUGUAGGAAAUGGUUGAAAAA	926	2069-2089	UUUUUCAACCAUUUCCUACAGAC	1061	2067-2089
AD-1565357	GUUGAAAACUGAAGGUAGAUA	927	2081-2101	UAUCUACCUUCAGUUUUCAACCA	1062	2079-2101
AD-1565368	AAGGUAGAUGGUGUUAUAGUA	928	2092-2112	UACUAUAACACCAUCUACCUUCA	1063	2090-2112
AD-1565389	GUAAAUAAGCAUCUCACUUUA	929	2126-2146	UAAAGUGAGAUGCUUAUUUACAG	1064	2124-2146
AD-1565407	UGGUUUUGUUUUAAACAUUCA	930	2163-2183	UGAAUGUUUAAAACAAAACCACA	1065	2161-2183
AD-1565418	AACAUUCAACGUUUCUUUUCA	931	2176-2196	UGAAAAGAAACGUUGAAUGUUUA	1066	2174-2196
AD-1565432	CUUUUCCUUCUACAAUAAACA	932	2190-2210	UGUUUAUUGUAGAAGGAAAAGAA	1067	2188-2210

Table 7. Modified sense and antisense strand sequences of ANGPTL7 dsRNA agents

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1094381	usgsgcu(Ahd)CfuGfGfUfacaacugcsusa	1068	VPusAfsgcaGfuUfGfuaccAfgUfagccascsc	1203	GGUGGCUACUGGUACAACUGCUG	1338
AD-1094401	gscsaca(Ghd)AfcUfCfCfaaccucaasusa	1069	VPusAfsuugAfgGfUfuggaGfuCfugugcsasg	1204	CUGCACAGACUCCAACCUCAAUG	1339
AD-1562960	csusugg(Ahd)AfgGfAfAfagcuauagsgsa	1070	VPusCfscuaUfaGfCfuuucCfuUfccaagscsc	1205	GGCUUGGAAGGAAAGCUAUAGGC	1340
AD-1562974	usasuag(Ghd)CfuAfCfCfcauucagcsusa	1071	VPusAfsgcuGfaAfUfggguAfgCfcuauasgsc	1206	GCUAUAGGCUACCCAUUCAGCUC	1341
AD-1562983	gsasgac(Uhd)CfaAfGfCfuuugagaasasa	1072	VPusUfsuucUfcAfAfagcuUfgAfgucucsusg	1207	CAGAGACUCAAGCUUUGAGAAAG	1342
AD-1563004	gscsuag(Chd)AfaAfGfAfgcaaggaasasa	1073	VPusUfsuucCfuUfGfcucuUfuGfcuagcscsu	1208	AGGCUAGCAAAGAGCAAGGAAAG	1343
AD-1563008	asasgag(Ahd)GfaAfAfAfcaacaaagsusa	1074	VPusAfscuuUfgUfUfguuuUfcUfcucuususc	1209	GAAAGAGAGAAAACAACAAAGUG	1344
AD-1563076	gsusggc(Ghd)AfgGfCfCfcucagagusgsa	1075	VPusCfsacuCfuGfAfgggcCfuCfgccacsusu	1210	AAGUGGCGAGGCCCUCAGAGUGA	1345
AD-1563089	csasgag(Uhd)GfaAfAfGfcguaaggususa	1076	VPusAfsaccUfuAfCfgcuuUfcAfcucugsasg	1211	CUCAGAGUGAAAGCGUAAGGUUC	1346
AD-1563100	csgsuaa(Ghd)GfuUfCfAfgucagccusgsa	1077	VPusCfsaggCfuGfAfcugaAfcCfuuacgscsu	1212	AGCGUAAGGUUCAGUCAGCCUGC	1347
AD-1563170	csusgca(Ghd)CfuUfUfGfcagaccucsasa	1078	VPusUfsgagGfuCfUfgcaaAfgCfugcagscsa	1213	UGCUGCAGCUUUGCAGACCUCAG	1348
AD-1563186	csuscag(Chd)UfgGfGfCfaucuccagsasa	1079	VPusUfscugGfaGfAfugccCfaGfcugagsgsu	1214	ACCUCAGCUGGGCAUCUCCAGAC	1349
AD-1563192	usgsaag(Ghd)AfaGfAfGfccuuccucsasa	1080	VPusUfsgagGfaAfGfgcucUfuCfcuucasgsg	1215	CCUGAAGGAAGAGCCUUCCUCAC	1350
AD-1563204	csasccc(Ahd)AfaCfCfCfacaaaagasusa	1081	VPusAfsucuUfuUfGfuggguUfuUfggggugsasg	1216	CUCACCCAAACCCACAAAAGAUG	1351
AD-1563283	gscscuc(Uhd)CfuCfAfGfcugugaccsusa	1082	VPusAfsgguCfaCfAfgcugAfgAfgaggcsusu	1217	AAGCCUCUCUCAGCUGUGACCUG	1352
AD-1563302	usgsgcu(Chd)UfgCfAfUfuuucaucgsusa	1083	VPusAfscgaUfgAfAfaaugCfaGfagccasgsg	1218	CCUGGCUCUGCAUUUUCAUCGUG	1353
AD-1563363	ususuca(Uhd)CfgUfGfGfccuuugucsasa	1084	VPusUfsgacAfaAfGfgccaCfgAfugaaasasu	1219	AUUUUCAUCGUGGCCUUUGUCAG	1354
AD-1563396	csusgca(Ghd)AfaGfCfUfcucuaagcsasa	1085	VPusUfsgcuUfaGfAfgagcUfuCfugcagscsc	1220	GGCUGCAGAAGCUCUCUAAGCAC	1355
AD-1563461	asasgca(Chd)AfaGfAfCffaccagcacsasa	1086	VPusUfsgugCfuGfGfugucUfuGfugcuusasg	1221	CUAAGCACAAGACACCAGCACAG	1356
AD-1563473	cscsagc(Ahd)CfaGfCfCffacagcucasasa	1087	VPusUfsugaGfcUfGfuggcUfgUfgcuggsusg	1222	CACCAGCACAGCCACAGCUCAAA	1357
AD-1563485	csasgcu(Chd)AfaAfGfCffggccaacusgsa	1088	VPusCfsaguUfgGfCfcgcuUfuGfagcugsusg	1223	CACAGCUCAAAGCGGCCAACUGC	1358
AD-1563497	gscscaa(Chd)UfgCfUfGffugaggaggsusa	1089	VPusAfsccuCfcUfCfacagCfaGfuuggcscsg	1224	CGGCCAACUGCUGUGAGGAGGUG	1359
AD-1563559	gsasgga(Ghd)GfuGfAfAfggagcucasasa	1090	VPusUfsugaGfcUfCfcucucAfcCfuccucsasc	1225	GUGAGGAGGUGAAGGAGCUCAAG	1360
AD-1563570	gsgsagc(Uhd)CfaAfGfGfcccaaguusgsa	1091	VPusCfsaacUfuGfGfgccuUfgAfgcuccsusu	1226	AAGGAGCUCAAGGCCCAAGUUGC	1361
AD-1563582	cscsaag(Uhd)UfgCfCfAfaccuuagcsasa	1092	VPusUfsgcuAfaGfGfuuggCfaAfcuuggsgsc	1227	GCCCAAGUUGCCAACCUUAGCAG	1362

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1563595	csusuag(Chd)AfgCfCfUfgcugagugsasa	1093	VPusUfscacUfcAfGfcaggCfuGfcuaagsgsu	1228	ACCUUAGCAGCCUGCUGAGUGAA	1363
AD-1563606	gscsuga(Ghd)UfgAfAfCfugaacaagsasa	1094	VPusUfscuuGfuUfCfaguuCfaCfucagcsasg	1229	CUGCUGAGUGAACUGAACAAGAA	1364
AD-1563609	gsusggu(Chd)AfuGfCfAfggugauggsasa	1095	VPusUfsccaUfcAfCfcugcAfuGfaccacsgsc	1230	GCGUGGUCAUGCAGGUGAUGGAG	1365
AD-1563669	usgsaac(Ahd)AfgAfAfGfcaggagagsgsa	1096	VPusCfscucUfcCfUfgcuuCfuUfguucasgsu	1231	ACUGAACAAGAAGCAGGAGAGGG	1366
AD-1563689	gsascug(Ghd)GfuCfAfGfcguggucasusa	1097	VPusAfsugaCfcAfCfgcugAfcCfcagucscsc	1232	GGGACUGGGUCAGCGUGGUCAUG	1367
AD-1563701	gsusgau(Ghd)GfaGfCfUfggagagcasasa	1098	VPusUfsugcUfcUfCfcagcUfcCfaucacscsu	1233	AGGUGAUGGAGCUGGAGAGCAAC	1368
AD-1563762	gsgsaga(Ghd)CfaAfCfAfgcaagcgcsasa	1099	VPusUfsgcgCfuUfGfcuguUfgCfucuccsasg	1234	CUGGAGAGCAACAGCAAGCGCAU	1369
AD-1563781	asusgga(Ghd)UfcGfCfGfgcucacagsasa	1100	VPusUfscugUfgAfGfccgcGfaCfuccausgsc	1235	GCAUGGAGUCGCGGCUCACAGAU	1370
AD-1563793	csuscac(Ahd)GfaUfGfCfugagagcasasa	1101	VPusUfsugcUfcUfCfagcaUfcUfgugagscsc	1236	GGCUCACAGAUGCUGAGAGCAAG	1371
AD-1563807	gsasgca(Ahd)GfuAfCfUfccgagaugsasa	1102	VPusUfscauCfuCfGfgaguAfcUfugcucsusc	1237	GAGAGCAAGUACUCCGAGAUGAA	1372
AD-1563871	csgsaga(Uhd)GfaAfCfAfaccaaauusgsa	1103	VPusCfsaauUfuGfGfuuguUfcAfucucgsgsa	1238	UCCGAGAUGAACAACCAAAUUGA	1373
AD-1563882	ascscaa(Ahd)UfuGfAfCfaucaugcasgsa	1104	VPusCfsugcAfuGfAfugucAfaUfuuggususg	1239	CAACCAAAUUGACAUCAUGCAGC	1374
AD-1563895	csasgcu(Ghd)CfaGfGfCfagcacagascsa	1105	VPusGfsucuGfuGfCfugccUfgCfagcugscsa	1240	UGCAGCUGCAGGCAGCACAGACG	1375
AD-1563906	asgscac(Ahd)GfaCfGfGfucacucagsasa	1106	VPusUfscugAfgUfGfaccgUfcUfgugcusgsc	1241	GCAGCACAGACGGUCACUCAGAC	1376
AD-1563967	uscsacu(Chd)AfgAfCfCfuccgcagasusa	1107	VPusAfsucuGfcGfGfagguCfuGfagugascsc	1242	GGUCACUCAGACCUCCGCAGAUG	1377
AD-1563980	csgscag(Ahd)UfgCfCfAfucuacgacsusa	1108	VPusAfsgucGfuAfGfauggCfaUfcugcgsgsa	1243	UCCGCAGAUGCCAUCUACGACUG	1378
AD-1563993	usascga(Chd)UfgCfUfCfuucccucusasa	1109	VPusUfsagaGfgGfAfagagCfaGfucguasgsa	1244	UCUACGACUGCUCUUCCCUCUAC	1379
AD-1564005	uscsccu(Chd)UfaCfCfAfgaagaacusasa	1110	VPusUfsaguUfcUfUfcuggUfaGfagggasasg	1245	CUUCCCUCUACCAGAAGAACUAC	1380
AD-1564066	gsasaga(Ahd)CfuAfCfCfgcaucucusgsa	1111	VPusCfsagaGfaUfGfcgguAfgUfucuucsusg	1246	CAGAAGAACUACCGCAUCUCUGG	1381
AD-1564080	uscsucu(Ghd)GfaGfUfGfuauaagcususa	1112	VPusAfsagcUfuAfUfacacUfcCfagagasusg	1247	CAUCUCUGGAGUGUAUAAGCUUC	1382
AD-1564097	csusucc(Uhd)CfcUfGfAfugacuuccsusa	1113	VPusAfsggaAfgUfCfaucaGfgAfggaagscsu	1248	AGCUUCCUCCUGAUGACUUCCUG	1383
AD-1564215	asgsccc(Uhd)GfaAfCfUfggaggugususa	1114	VPusAfsacaCfcUfCfcaguUfcAfgggcusgsc	1249	GCAGCCCUGAACUGGAGGUGUUC	1384
AD-1564226	gsgsagg(Uhd)GfuUfCfUfgugacaugsgsa	1115	VPusCfscauGfuCfAfcagaAfcAfccuccsasg	1250	CUGGAGGUGUUCUGUGACAUGGA	1385
AD-1564236	gsusgac(Ahd)UfgGfAfGfacuucaggscsa	1116	VPusGfsccuGfaAfGfucucCfaUfgucacsasg	1251	CUGUGACAUGGAGACUUCAGGCG	1386
AD-1564250	uscsagg(Chd)GfgAfGfGfcuggaccasusa	1117	VPusAfsuggUfcCfAfgccuCfcGfccugasasg	1252	CUUCAGGCGGAGGCUGGACCAUC	1387
AD-1564258	gsusggc(Chd)UfuGfUfCfuccuucuascsa	1118	VPusGfsuagAfaGfGfagacAfaGfgccacsusu	1253	AAGUGGCCUUGUCUCCUUCUACC	1388

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1564259	gsascca(Uhd)CfaUfCfCfagagacgasasa	1119	VPusUfsucgUfcUfCfuggaUfgAfuggucscsa	1254	UGGACCAUCAUCCAGAGACGAAA	1389
AD-1564290	uscscuu(Chd)UfaCfCfGfggacuggasasa	1120	VPusUfsuccAfgUfCfccggUfaGfaaggasgsa	1255	UCUCCUUCUACCGGGACUGGAAG	1390
AD-1564301	gsgsacu(Ghd)GfaAfGfCfaguacaagscsa	1121	VPusGfscuuGfuAfCfugcuUfcCfaguccscsg	1256	CGGGACUGGAAGCAGUACAAGCA	1391
AD-1564322	gsgsgcu(Uhd)UfgGfCfAfgcauccgusgsa	1122	VPusCfsacgGfaUfGfcugcCfaAfagcccsusg	1257	CAGGGCUUUGGCAGCAUCCGUGG	1392
AD-1564327	asascga(Ahd)CfaCfAfUfccaccggcsusa	1123	VPusAfsgccGfgUfGfgaugUfgUfucguuscsc	1258	GGAACGAACACAUCCACCGGCUC	1393
AD-1564341	cscsggc(Uhd)CfuCfCfAfgacagccasasa	1124	VPusUfsuggCfuGfUfcuggAfgAfgccggsusg	1259	CACCGGCUCUCCAGACAGCCAAC	1394
AD-1564355	asgscca(Ahd)CfcCfGfGfcugcgugusasa	1125	VPusUfsacaCfgCfAfgccgGfgUfuggcusgsu	1260	ACAGCCAACCCGGCUGCGUGUAG	1395
AD-1564366	csusgcg(Uhd)GfuAfGfAfgauggaggsasa	1126	VPusUfsccuCfcAfUfcucuAfcAfcgcagscsc	1261	GGCUGCGUGUAGAGAUGGAGGAC	1396
AD-1564381	gsasgga(Chd)UfgGfGfAfgggcaaccsusa	1127	VPusAfsgguUfgCfCfcuccCfaGfuccucscsa	1262	UGGAGGACUGGGAGGGCAACCUG	1397
AD-1564393	gsgscaa(Chd)CfuGfCfGfcuacgcugsasa	1128	VPusUfscagCfgUfAfgcgcAfgGfuugccscsu	1263	AGGGCAACCUGCGCUACGCUGAG	1398
AD-1564405	usascgc(Uhd)GfaGfUfAfuagccacususa	1129	VPusAfsaguGfgCfUfauacUfcAfgcguasgsc	1264	GCUACGCUGAGUAUAGCCACUUU	1399
AD-1564416	usasgcc(Ahd)CfuUfUfGfuuuugggcsasa	1130	VPusUfsgccCfaAfAfacaaAfgUfggcuasusa	1265	UAUAGCCACUUUGUUUUGGGCAA	1400
AD-1564428	ususugg(Ghd)CfaAfUfGfaacucaacsasa	1131	VPusUfsguuGfaGfUfucauUfgCfccaaasasc	1266	GUUUUGGGCAAUGAACUCAACAG	1401
AD-1564444	asascag(Chd)UfaUfCfGfccucuuccsusa	1132	VPusAfsggaAfgAfGfgcgaUfaGfcuguusgsa	1267	UCAACAGCUAUCGCCUCUUCCUG	1402
AD-1564449	gsasacu(Ahd)CfaCfUfGfgcaaugugsgsa	1133	VPusCfscacAfuUfGfccagUfgUfaguucscsc	1268	GGGAACUACACUGGCAAUGUGGG	1403
AD-1564464	cscsucc(Ahd)GfuAfUfCfauaacaacsasa	1134	VPusUfsguuGfuUfAfugauAfcUfggaggsgsc	1269	GCCCUCCAGUAUCAUAACAACAC	1404
AD-1564485	asgsccu(Uhd)CfaGfCfAfccaaggacsasa	1135	VPusUfsgucCfuUfGfgugcUfgAfaggcusgsu	1270	ACAGCCUUCAGCACCAAGGACAA	1405
AD-1564493	asasgga(Chd)AfaGfGfAfcaaugacasasa	1136	VPusUfsuguCfaUfUfgucccUfuGfuccuusgsg	1271	CCAAGGACAAGGACAAUGACAAC	1406
AD-1564507	usgsaca(Ahd)CfuGfCfUfuggacaagsusa	1137	VPusAfscuuGfuCfCfaagcAfgUfugucasusu	1272	AAUGACAACUGCUUGGACAAGUG	1407
AD-1564519	usgsgac(Ahd)AfgUfGfUfgcacagcuscsa	1138	VPusGfsagcUfgUfGfcacaCfuUfguccasasg	1273	CUUGGACAAGUGUGCACAGCUCC	1408
AD-1564535	gscsucc(Ghd)CfaAfAfGfguggcuacsusa	1139	VPusAfsguaGfcCfAfccuuUfgCfggagcsusg	1274	CAGCUCCGCAAAGGUGGCUACUG	1409
AD-1564550	asasccu(Chd)AfaUfGfGffaguguacusasa	1140	VPusUfsaguAfcAfCfuccaUfuGfagguusgsg	1275	CCAACCUCAAUGGAGUGUACUAC	1410
AD-1564566	ascsuac(Chd)GfcCfUfGffggugagcascsa	1141	VPusGfsugcUfcAfCfccagGfcGfguagusasc	1276	GUACUACCGCCUGGGUGAGCACA	1411
AD-1564577	gsgsuga(Ghd)CfaCfAfAffuaagcaccsusa	1142	VPusAfsgguGfcUfUfauugUfgCfucaccscsa	1277	UGGGUGAGCACAAUAAGCACCUG	1412
AD-1564596	usgsgau(Ghd)GfcAfUfCfaccugguasusa	1143	VPusAfsuacCfaGfGfgauGfcCfauccasgsg	1278	CCUGGAUGGCAUCACCUGGUAUG	1413
AD-1564607	ascscug(Ghd)UfaUfGfGfcuggcaugsgsa	1144	VPusCfscauGfcCfAfgccaUfaCfcaggusgsa	1279	UCACCUGGUAUGGCUGGCAUGGA	1414

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1564618	csusggc(Ahd)UfgGfAfUfcuaccuacsusa	1145	VPusAfsguaGfgUfAfgaucCfaUfgccagscsc	1280	GGCUGGCAUGGAUCUACCUACUC	1415
AD-1564630	usasccu(Ahd)CfuCfCfCfucaaacggsgsa	1146	VPusCfsccgUfuUfGfaggAfgUfagguasgsa	1281	UCUACCUACUCCCUCAAACGGGU	1416
AD-1564645	ascsggg(Uhd)GfgAfGfAfugaaaaucscsa	1147	VPusGfsgauUfuUfCfaucuCfcAfcccgususu	1282	AAACGGGUGGAGAUGAAAAUCCG	1417
AD-1564666	cscscag(Ahd)AfgAfCfUfucaagccususa	1148	VPusAfsaggCfuUfGfaaguCfuUfcugggscsg	1283	CGCCCAGAAGACUUCAAGCCUUA	1418
AD-1564677	uscsaag(Chd)CfuUfAfAfaaggaggcsusa	1149	VPusAfsgccUfcCfUfuuuaAfgGfcuugasasg	1284	CUUCAAGCCUUAAAAGGAGGCUG	1419
AD-1564703	asgscac(Ghd)GfaUfAfCfagaaacugsasa	1150	VPusUfscagUfuUfCfuguaUfcCfgugcuscsc	1285	GGAGCACGGAUACAGAAACUGAG	1420
AD-1564721	gsasgac(Ahd)CfgUfGfGfagacuggasusa	1151	VPusAfsuccAfgUfCfuccaCfgUfgucucsasg	1286	CUGAGACACGUGGAGACUGGAUG	1421
AD-1564732	asgsacu(Ghd)GfaUfGfAfgggcagausgsa	1152	VPusCfsaucUfgCfCfcucaUfcCfagucuscsc	1287	GGAGACUGGAUGAGGGCAGAUGA	1422
AD-1564744	gsgscag(Ahd)UfgAfGfGfacaggaagsasa	1153	VPusUfscuuCfcUfGfuccuCfaUfcugccscsu	1288	AGGGCAGAUGAGGACAGGAAGAG	1423
AD-1564756	csasgga(Ahd)GfaGfAfGfuguuagaasasa	1154	VPusUfsuucUfaAfCfacucUfcUfuccugsusc	1289	GACAGGAAGAGAGUGUUAGAAAG	1424
AD-1564772	gsasaag(Ghd)GfuAfGfGfgacugagaasasa	1155	VPusUfsuucUfcAfGfuccuAfcCfcuuucsusa	1290	UAGAAAGGGUAGGACUGAGAAAC	1425
AD-1564783	ascsuga(Ghd)AfaAfCfAfgccuauaasusa	1156	VPusAfsuuaUfaGfGfcuguUfuCfucaguscsc	1291	GGACUGAGAAACAGCCUAUAAUC	1426
AD-1564802	uscsucc(Ahd)AfaGfAfAfagaauaagsusa	1157	VPusAfscuuAfuUfCfuuucUfuUfggagasusu	1292	AAUCUCCAAAGAAAGAAUAAGUC	1427
AD-1564817	usasagu(Chd)UfcCfAfAfggagcacasasa	1158	VPusUfsuguGfcUfCfcugGfaGfacuuasusu	1293	AAUAAGUCUCCAAGGAGCACAAA	1428
AD-1564823	uscsaua(Uhd)GfuAfCfCfaaggaugususa	1159	VPusAfsacaUfcCfUfuguAfcAfuaugasusu	1294	AAUCAUAUGUACCAAGGAUGUUA	1429
AD-1564834	asasgga(Uhd)GfuUfAfCfaguaaacasgsa	1160	VPusCfsuguUfuAfCfuguaAfcAfuccuusgsg	1295	CCAAGGAUGUUACAGUAAACAGG	1430
AD-1564850	ascsagg(Ahd)UfgAfAfCfuauuuaaascsa	1161	VPusGfsuuuAfaAfUfaguuCfaUfccugususu	1296	AAACAGGAUGAACUAUUUAAACC	1431
AD-1564862	asususua(Ahd)AfcCfCfAfcugggucusa	1162	VPusAfsggaCfcCfAfgugGfuUfuaaausasg	1297	CUAUUUAAACCCACUGGGUCCUG	1432
AD-1564881	usgscca(Chd)AfuCfCfUfucucaaggsusa	1163	VPusAfsccuUfgAfGfaaggAfuGfuggcasgsg	1298	CCUGCCACAUCCUUCUCAAGGUG	1433
AD-1564892	uscsuca(Ahd)GfgUfGfGfGfuagacugasgsa	1164	VPusCfsucaGfuCfUfaccaCfcUfugagasasg	1299	CUUCUCAAGGUGGUAGACUGAGU	1434
AD-1564899	uscsucu(Chd)UfgCfCfCfaagaucccsusa	1165	VPusAfsgggAfuCfUfuggCfaGfagagascsc	1300	GGUCUCUCUGCCCAAGAUCCCUG	1435
AD-1564914	uscsccu(Ghd)AfcAfUfAfgcaguagcsusa	1166	VPusAfsgcuAfcUfGfcuauGfuCfagggasusc	1301	GAUCCCUGACAUAGCAGUAGCUU	1436
AD-1564925	gscsagu(Ahd)GfcUfUfGfucuuuuccsasa	1167	VPusUfsggaAfaAfGfacaaGfcUfacugcsusa	1302	UAGCAGUAGCUUGUCUUUUCCAC	1437
AD-1564936	uscsuuu(Uhd)CfcAfCfAfufugauuuguscsa	1168	VPusGfsacaAfaUfCfauguGfgAfaaagascsa	1303	UGUCUUUUCCACAUGAUUUGUCU	1438
AD-1564949	asususg(Uhd)CfuGfUfGfaaagaaaasusa	1169	VPusAfsuuuUfcUfUfucacAfgAfcaaauscsa	1304	UGAUUUGUCUGUGAAAGAAAAUA	1439
AD-1564969	asgsauc(Ghd)UfuUfUfAfucuauuuuscsa	1170	VPusGfsaaaAfuAfGfauaaAfaCfgaucuscsa	1305	UGAGAUCGUUUUAUCUAUUUUCU	1440

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1564987	uscsuac(Ghd)GfcUfUfAfggcuaugusgsa	1171	VPusCfsacaUfaGfCfcuaaGfcCfguagasgsa	1306	UCUCUACGGCUUAGGCUAUGUGA	1441
AD-1565004	gsusgag(Ghd)GfcAfAfAfacacaaauscsa	1172	VPusGfsauuUfgUfGfuuuuGfcCfcucacsasu	1307	AUGUGAGGGCAAAACACAAAUCC	1442
AD-1565015	ascsaca(Ahd)AfuCfCfCfuuugcuaasasa	1173	VPusUfsuuaGfcAfAfaggaggAfuUfugugususu	1308	AAACACAAAUCCCUUUGCUAAAA	1443
AD-1565034	ascscau(Ahd)UfuAfUfUfuugauucuscsa	1174	VPusGfsagaAfuCfAfaaauAfaUfauggususc	1309	GAACCAUAUUAUUUUGAUUCUCA	1444
AD-1565048	csuscaa(Ahd)GfgAfUfAfggccuuugsasa	1175	VPusUfscaaAfgGfCfcuauCfcUfuugagsasa	1310	UUCUCAAAGGAUAGGCCUUUGAG	1445
AD-1565060	gscscuu(Uhd)GfaGfUfGfuuagagaasasa	1176	VPusUfsuucUfcUfAfacacUfcAfaaggcscsu	1311	AGGCCUUUGAGUGUUAGAGAAAG	1446
AD-1565071	gsasgaa(Ahd)GfgAfGfUfgaaggaggscsa	1177	VPusGfsccuCfcUfUfcacuCfcUfuucucsusa	1312	UAGAGAAAGGAGUGAAGGAGGCA	1447
AD-1565091	asgsgug(Ghd)GfaAfAfUfgguauuucsusa	1178	VPusAfsgaaAfuAfCfcauuUfcCfcaccusgsc	1313	GCAGGUGGGAAAUGGUAUUUCUA	1448
AD-1565113	csasgug(Ahd)AfaUfUfAfucuugaguscsa	1179	VPusGfsacuCfaAfGfauaaUfuUfcacugsgsa	1314	UCCAGUGAAAUUAUCUUGAGUCU	1449
AD-1565126	ususgag(Uhd)CfuAfCfAfcauuauuususa	1180	VPusAfsaaaUfaAfUfguguAfgAfcucaasgsa	1315	UCUUGAGUCUACACAUUAUUUUU	1450
AD-1565141	asasuug(Uhd)UfcGfGfCfuggaacugsasa	1181	VPusUfscagUfuCfCfagccGfaAfcaauususu	1316	AAAAUUGUUCGGCUGGAACUGAC	1451
AD-1565158	usgsacc(Chd)AfgGfCfUfggacuugcsgsa	1182	VPusCfsgcaAfgUfCfcagcCfuGfggucasgsu	1317	ACUGACCCAGGCUGGACUUGCGG	1452
AD-1565162	gsasgga(Ahd)AfcUfCfCfcfagggcacusgsa	1183	VPusCfsaguGfcCfCfuggaGfuUfuccucscsc	1318	GGGAGGAAACUCCAGGGCACUGC	1453
AD-1565176	gscsacu(Ghd)CfaUfCfUfuggcgaucasgsa	1184	VPusCfsugaUfcGfCfcagaUfgCfagugcscsc	1319	GGGCACUGCAUCUGGCGAUCAGA	1454
AD-1565188	gscsgau(Chd)AfgAfCfUfufcugagcacsusa	1185	VPusAfsgugCfuCfAfgaguCfuGfaucgcscsa	1320	UGGCGAUCAGACUCUGAGCACUG	1455
AD-1565197	csgsccu(Uhd)GfgUfCfAfufuguacagcsasa	1186	VPusUfsgcuGfuAfCfaugaCfcAfaggcgsasg	1321	CUCGCCUUGGUCAUGUACAGCAC	1456
AD-1565212	csasgca(Chd)UfgAfAfAfufggaaugaasgsa	1187	VPusCfsuucAfuUfCfcuuuCfaGfugcugsusa	1322	UACAGCACUGAAAGGAAUGAAGC	1457
AD-1565223	gsgsaau(Ghd)AfaGfCfAfufccagcaggsasa	1188	VPusUfsccuGfcUfGfgugcUfuCfauuccsusu	1323	AAGGAAUGAAGCACCAGCAGGAG	1458
AD-1565235	csasgca(Ghd)GfaGfGfUfufggacagagsusa	1189	VPusAfscucUfgUfCfcaccUfcCfugcugsgsu	1324	ACCAGCAGGAGGUGGACAGAGUC	1459
AD-1565246	gsgsaca(Ghd)AfgUfCfUfufcucauggasusa	1190	VPusAfsuccAfuGfAfgagaCfuCfuguccsasc	1325	GUGGACAGAGUCUCUCAUGGAUG	1460
AD-1565257	csuscau(Ghd)GfaUfGfCfufcggcacaasasa	1191	VPusUfsuugUfgCfCfggcaUfcCfaugagsasg	1326	CUCUCAUGGAUGCCGGCACAAAA	1461
AD-1565270	gscsaca(Ahd)AfaCfUfGfufccuuaaaasusa	1192	VPusAfsuuuUfaAfGfgcagUfuUfugugcscsg	1327	CGGCACAAAACUGCCUUAAAAUA	1462
AD-1565288	usasguu(Ahd)AfuAfCfAfufgguauaucsusa	1193	VPusAfsgauAfuAfCfcuguAfuUfaacuasusg	1328	CAUAGUUAAUACAGGUAUAUCUA	1463
AD-1565303	csusuug(Uhd)AfaGfAfAfufacaagcucsasa	1194	VPusUfsgagCfuUfGfuuucUfuAfcaaagsusa	1329	UACUUUGUAAGAAACAAGCUCAA	1464
AD-1565324	gsgsagc(Uhd)UfcCfUfUfufuuaaauuususa	1195	VPusAfsaaaUfuUfAfaaagGfaAfgcuccsusu	1330	AAGGAGCUUCCUUUUAAAUUUUG	1465
AD-1565345	csusgua(Ghd)GfaAfAfAfufgguugaaasasa	1196	VPusUfsuuuCfaAfCfcauuUfcCfuacagsasc	1331	GUCUGUAGGAAAUGGUUGAAAAC	1466

Duplex ID	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:	mRNA Target Sequence 5' to 3'	SEQ ID NO:
AD-1565357	gsusuga(Ahd)AfaCfUfGfaagguagasusa	1197	VPusAfsucuAfcCfUfucagUfuUfucaacscsa	1332	UGGUUGAAAACUGAAGGUAGAUG	1467
AD-1565368	asasggu(Ahd)GfaUfGfGfuguuauagsusa	1198	VPusAfscuaUfaAfCfaccaUfcUfaccuuscsa	1333	UGAAGGUAGAUGGUGUUAUAGUU	1468
AD-1565389	gsusaaa(Uhd)AfaGfCfAfucucacuususa	1199	VPusAfsaagUfgAfGfaugcUfuAfuuuacsasg	1334	CUGUAAAUAAGCAUCUCACUUUG	1469
AD-1565407	usgsguu(Uhd)UfgUfUfUfuaaacauuscsa	1200	VPusGfsaauGfuUfUfaaaaCfaAfaaccascsa	1335	UGUGGUUUUGUUUUAAACAUUCA	1470
AD-1565418	asascau(Uhd)CfaAfCfGfuuucuuuuscsa	1201	VPusGfsaaaAfgAfAfacguUfgAfauguususa	1336	UAAACAUUCAACGUUUCUUUUCC	1471
AD-1565432	csusuuu(Chd)CfuUfCfUfacaauaaascsa	1202	VPusGfsuuuAfuUfGfuagaAfgGfaaaagsasa	1337	UUCUUUUCCUUCUACAAUAAACA	1472

Example 2: *In vitro* screening of mouse ANGPTL7 siRNA in COS-7 Cells

Experimental Methods

Cloning of vector containing ANGPTL7 mRNA sequence and dual-luciferase reporter

The entire sequence of mouse NM_001039554.3 REFSEQ mRNA was cloned into the dual-luciferase reporter construct (psiCHECK™-2, Promega) at the XhoI/NotI sites. In cells transfected with this construct, a reduction in *Renilla* luciferase activity would indicate an effect of RNAi. Firefly luciferase is used for normalization of *Renilla* luciferase expression.

Cell culture and transfections

The ANGPTL7/reporter vector stock was diluted into 5 ng/μL in Opti-MEM® (Thermo Fisher). The vector solution (5 ng/μL) was added 5 μL per well to individual wells in a 384-well plate. Five μL per well of each siRNA duplex (in 10x final concentration) was then added to the vector solution. Dose experiments were performed at 50 nM, 10 nM, 1 nM, and 0.1 nM final siRNA duplex concentration.

Five μL of Opti-MEM plus 0.1 μL of Lipofectamine® 2000 (Thermo Fisher) per well was added to the vector/siRNA mixture. The mixture was incubated at room temperature for 15 minutes. Thirty-five μL of DMEM without antibiotic containing ~3 x 10^3 trypsinized COS-7 cells (ATCC, Manassas, VA) per well was then added to the vector/siRNA/Lipofectamine mixture. The cells were incubated for 48 hours prior to dual-luciferase reading.

Dual-luciferace reading

Dual-luciferase reading was performed using Dual-Glo® Luciferase Assay System (Cat #E2980, Promega) as follows. The medium was removed from each well. Dual-Glo® Luciferase Reagent was prepared by adding 1 bottle of Dual-Glo® Luciferase Buffer to 1 vial of lyophilized Dual-Glo® Luciferase Substrate. Mixture of 20 μL of Dual-Glo® Luciferase Reagent plus 20 μL of DMEM per well was prepared and was added to each well. The plates were incubated for 30 minutes on a shaker. Firefly luciferase activity was measured with a luminometer.

Following the firefly luciferase reading, mixture of 20 µL of Dual-Glo® Stop & Glo® Buffer plus 0.2 µL of Dual-Glo® Stop & Glo® Substrate per well was prepared and was added to each well. The wells were incubated for approximately 10 minutes. *Renilla* luciferase activity was measured with the luminometer. Each siRNA duplex was tested at least two times. Normalized *Renilla* luciferase activity for each well was compared to that of cells transfected with a non-targeting control siRNA.

Results

The results of the dose screen of exemplary mouse ANGPTL7 siRNAs in COS-7 cells are shown in Table 8. The experiments were performed at 50 nM, 10 nM, 1 nM, and 0.1 nM final duplex concentrations and the data are expressed as percent message remaining relative to non-targeting control.

Table 8. Mouse ANGPTL7 siRNA dose screen in COS-7 cells

	50 nM Dose		10 nM Dose		1 nM Dose		0.1 nM Dose	
Duplex	Avg % ANGPTL7 mRNA Remaining	SD	Avg % ANGPTL7 mRNA Remaining	SD	Avg % ANGPTL7 mRNA Remaining	SD	Avg % ANGPTL7 mRNA Remaining	SD
AD-1094991	26.3	9.3	42.0	9.9	58.4	16.4	90.5	28.5
AD-1093984	19.5	1.7	36.8	2.1	55.0	15.5	94.4	3.0
AD-1093985	33.2	1.5	52.2	15.2	71.0	6.9	113.0	11.8
AD-1094047	68.7	18.0	71.3	9.0	88.7	3.4	111.9	6.9
AD-1093988	57.4	19.2	70.6	6.5	71.5	2.8	113.0	16.1
AD-1093989	67.1	2.3	71.4	12.8	72.0	4.2	97.7	13.3
AD-1094130	45.7	13.0	66.3	11.6	63.7	1.1	123.3	13.8
AD-1093990	48.9	0.6	90.1	12.1	98.1	18.8	116.6	20.6
AD-1094048	56.7	24.4	78.9	32.9	79.5	25.9	109.5	10.5
AD-1094108	101.3	39.5	88.4	6.6	107.3	2.6	104.1	15.8
AD-1093887	31.7	6.4	52.4	13.5	79.7	0.5	100.8	12.1
AD-1094129	22.2	1.7	49.9	17.5	86.7	12.5	109.3	3.0
AD-1094131	46.7	9.6	62.4	1.8	81.5	3.9	105.0	7.4
AD-1094262	18.5	6.5	33.5	3.1	61.2	12.4	100.8	6.4
AD-1094471	50.8	10.2	66.3	7.6	100.2	6.2	101.8	17.4

	50 nM Dose		10 nM Dose		1 nM Dose		0.1 nM Dose	
Duplex	Avg % ANGPTL7 mRNA Remaining	SD	Avg % ANGPTL7 mRNA Remaining	SD	Avg % ANGPTL7 mRNA Remaining	SD	Avg % ANGPTL7 mRNA Remaining	SD
AD-1093875	27.5	1.4	63.6	16.9	76.1	20.8	93.7	26.7
AD-1094304	65.4	21.8	69.1	12.7	89.5	14.6	90.1	19.1
AD-1093983	105.9	9.2	130.8	5.1	129.6	22.0	72.0	15.9
AD-1094050	63.6	1.5	70.6	5.8	101.4	12.4	109.5	28.3
AD-1093670	30.4	3.6	44.0	5.3	62.6	1.5	98.6	25.8
AD-1093672	23.3	4.2	32.9	1.6	55.4	4.9	80.3	30.5
AD-1093873	47.3	10.4	64.6	8.1	80.8	12.0	108.0	7.9

It is expressly contemplated that nucleotides 1562-1584, 546-568, 709-731, 862-884, and/or 232-256 of NM_001039554.3 comprise hotspot regions, which are targeted by AD-1094991, AD-1093984, AD-1094129, AD-1094262, AD-1093670, and AD-1093672, respectively.

Example 3: *In vitro* screening of human ANGPTL7 siRNA in Hepa1-6 Cells

Experimental Methods

Cloning of vector containing ANGPTL7 mRNA sequence and dual-luciferase reporter

The entire sequence of human NM_021146.4 REFSEQ mRNA was cloned into the dual-luciferase reporter construct (Dual-Glo® V163 plasmid). In cells transfected with this construct, a reduction in *Renilla* luciferase activity would indicate an effect of RNAi. Firefly luciferase is used for normalization of *Renilla* luciferase expression.

Cell culture and transfections

The ANGPTL7/reporter plasmid (1000 ng/μL) was added 100 ng per well to individual wells in a 96-well plate. siRNA duplex mix (1000 nM) was then added to the plasmid solution to provide a 10 nM final siRNA duplex concentration.

Lipofectamine® 2000 (Thermo Fisher) was added 0.5 μL to the plasmid/siRNA mixture. Medium containing ~2 x 10^4 trypsinized Hepa1-6 cells (ATCC, Manassas, VA) per well was then added to the vector/siRNA/Lipofectamine mixture. The cells were incubated for 24 hours prior to dual-luciferase reading. Each siRNA duplex was tested at a final concentration of 10 nM in quadruplicates.

Dual-luciferace reading

Dual-luciferase reading was performed using Dual-Glo® Luciferase Assay System (Cat #E2980, Promega) as described in Example 2. Firefly and *Renilla* luciferase activity was measured

with a luminometer. *Renilla* luciferase activity for each well, normalized with firefly luciferase activity was compared to that of cells transfected with a non-targeting control siRNA.

Results

The results of the single dose screen of exemplary human ANGPTL7 siRNAs in Hepa1-6 cells are shown in Table 9. The experiments were performed at a 10 nM final duplex concentrations and the data are expressed as percent message remaining relative to non-targeting control.

Table 9. Human ANGPTL7 single dose screen in Hepa1-6 cells

	10 nM Dose			10 nM Dose	
Duplex	Avg % ANGPTL7 mRNA Remaining	SD	Duplex	Avg % ANGPTL7 mRNA Remaining	SD
AD-1565432	78.262	6.213	AD-1564485	81.951	3.188
AD-1565418	49.025	3.596	AD-1094381	35.977	3.164
AD-1565407	71.915	9.209	AD-1564464	62.104	11.408
AD-1565389	38.097	4.593	AD-1564449	66.834	4.628
AD-1565368	43.507	3.097	AD-1564444	74.922	4.315
AD-1565357	35.603	7.278	AD-1564428	39.901	4.136
AD-1565345	38.180	4.662	AD-1564416	53.171	5.312
AD-1565324	41.226	6.926	AD-1564405	41.891	6.046
AD-1565303	33.543	6.025	AD-1564393	68.992	4.431
AD-1565288	33.627	5.531	AD-1564381	100.410	10.360
AD-1565270	56.666	6.868	AD-1564366	90.955	5.378
AD-1565257	54.931	5.560	AD-1564355	83.084	4.767
AD-1565246	45.488	5.686	AD-1564341	110.104	7.283
AD-1565235	77.815	5.795	AD-1564327	108.591	4.895
AD-1565223	47.443	2.974	AD-1564322	69.007	6.266
AD-1565212	25.017	3.081	AD-1564301	57.777	3.300
AD-1565197	54.629	4.805	AD-1564290	105.594	9.828
AD-1565188	41.980	1.908	AD-1564258	58.303	3.692
AD-1565176	65.568	6.823	AD-1564259	67.150	7.050
AD-1565162	68.606	6.106	AD-1564250	120.257	9.477
AD-1565158	80.588	7.062	AD-1564236	68.178	6.357
AD-1565141	44.190	6.210	AD-1564226	74.987	9.117
AD-1565126	37.444	1.786	AD-1564215	78.267	8.455
AD-1565113	38.424	7.178	AD-1564097	57.729	4.148
AD-1565091	39.804	3.007	AD-1564080	47.136	2.655
AD-1565071	61.300	5.101	AD-1564066	66.027	6.764
AD-1565060	49.942	8.176	AD-1564005	54.238	6.303
AD-1565048	125.855	6.631	AD-1563993	56.326	4.221
AD-1565034	44.208	11.337	AD-1563980	67.304	3.156
AD-1565015	33.867	1.835	AD-1563967	59.236	3.564

Duplex	10 nM Dose		Duplex	10 nM Dose	
	Avg % ANGPTL7 mRNA Remaining	SD		Avg % ANGPTL7 mRNA Remaining	SD
AD-1565004	31.857	3.111	AD-1563906	73.340	6.167
AD-1564987	72.328	5.326	AD-1563895	89.000	4.205
AD-1564969	34.727	4.045	AD-1563882	63.287	7.137
AD-1564949	56.677	6.123	AD-1563871	59.144	2.732
AD-1564936	26.314	4.734	AD-1563807	106.580	7.692
AD-1564925	48.862	5.116	AD-1563793	67.845	3.377
AD-1564914	63.316	9.608	AD-1563781	121.814	8.215
AD-1564899	44.223	3.267	AD-1563762	88.435	6.529
AD-1564892	47.388	5.690	AD-1563701	77.867	6.759
AD-1564881	81.058	5.467	AD-1563609	80.691	3.551
AD-1564862	138.970	12.524	AD-1563689	84.502	7.960
AD-1564850	42.802	5.653	AD-1563669	124.653	3.558
AD-1564834	53.690	8.630	AD-1563606	53.634	4.267
AD-1564823	40.823	5.696	AD-1563595	88.246	2.940
AD-1564817	54.600	4.575	AD-1563582	49.419	3.176
AD-1564802	31.756	4.367	AD-1563570	80.569	5.316
AD-1564783	48.118	4.929	AD-1563559	68.371	1.247
AD-1564772	55.754	3.537	AD-1563497	70.420	2.837
AD-1564756	47.268	3.500	AD-1563485	98.025	5.223
AD-1564744	87.030	7.571	AD-1563473	71.700	1.377
AD-1564732	81.680	3.923	AD-1563461	90.837	7.303
AD-1564721	61.682	7.257	AD-1563396	40.064	4.604
AD-1564703	44.234	4.873	AD-1563363	75.967	5.761
AD-1564677	92.632	10.818	AD-1563302	51.785	1.820
AD-1564666	40.220	6.062	AD-1563283	61.723	4.662
AD-1564645	55.915	5.782	AD-1563204	61.598	4.739
AD-1564630	49.498	3.318	AD-1563192	121.849	3.411
AD-1564618	39.865	2.056	AD-1563186	77.984	7.519
AD-1564607	77.130	3.152	AD-1563170	59.095	1.955
AD-1564596	63.657	3.775	AD-1563100	74.988	5.641
AD-1564577	60.396	3.105	AD-1563089	48.804	1.953
AD-1564566	110.738	10.777	AD-1563076	69.592	4.399
AD-1564550	50.289	2.293	AD-1563008	43.754	7.168
AD-1564535	48.990	2.354	AD-1563004	42.665	3.349
AD-1564519	54.077	3.988	AD-1562983	49.454	5.361
AD-1564507	95.204	10.438	AD-1562974	44.184	4.758
AD-1564493	63.333	5.595	AD-1562960	58.828	2.296
AD-1094401	59.877	11.693			

It is expressly contemplated that nucleotides 1993-2146, 1910-1932, 1726-1823, 1628-1685, 1591-1613, 1551-1573, 1420-1442, 1380-1402, 1243-1265, 1195-1217, 1096-1118, 940-962, and/or 299-321 of NM_021146.4 comprise hotspot regions, which are targeted by AD-1565389, AD-1565368, AD-1565357, AD-1565345, AD-1565324, AD-1565303, AD-1565288, AD-1565212, AD-1565141, AD-1565126, AD-1565113, AD-1565091, AD-1565034, AD-1565015, AD-1565004, AD-1564969, AD-1094381, AD-1564428, AD-1564936, AD-1564823, AD-1564802, AD-1564666, AD-1564618, and AD-1563396, respectively.

Example 4: *In vitro* screening of ANGPTL7 siRNA in RPE-J cells

Experimental Methods

Cell culture and transfections

RPE-J cells (ATCC) are grown to near confluence at 37°C in an atmosphere of 5% CO_2 in Dulbecco's modified Eagle's Minimum Essential Medium (Gibco) supplemented with 10% FBS (ATCC) before being released from the plate by trypsinization. RPE-J cell, transfection is carried out by adding 14.8 µL of Opti-MEM plus 0.2 µL of Lipofectamine RNAiMax per well (Invitrogen, Carlsbad CA. cat # 13778-150) to 5 µL of each siRNA duplex to an individual well in a 96-well plate. The mixture is then incubated at room temperature for 15 minutes. Eighty µL of complete growth media without antibiotic containing ~2 x 10^4 RPE-J cells or PMH is then added to the siRNA mixture. Cells are incubated for 24 hours prior to RNA purification. Dose experiments are performed at 50 nM, 10 nM, 1 nM and 0.1 nM final duplex concentration.

Total RNA isolation using DYNABEADS mRNA Isolation Kit

RNA is isolated using an automated protocol on a BioTek-EL406 platform using DYNABEADs (Invitrogen, cat#61012). Briefly, 70 µl of Lysis/Binding Buffer and 10 µl of lysis buffer containing 3 µl of magnetic beads are added to the plate with cells. Plates are incubated on an electromagnetic shaker for 10 minutes at room temperature and then magnetic beads are captured and the supernatant is removed. Bead-bound RNA is then washed 2 times with 150 µl Wash Buffer A and once with Wash Buffer B. Beads are then washed with 150 µl Elution Buffer, re-captured and supernatant removed.

cDNA synthesis using ABI High capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA, Cat #4368813)

Ten µl of a master mix containing 1 µl 10x Buffer, 0.4 µl 25x dNTPs, 1 µl 10x Random primers, 0.5 µl Reverse Transcriptase, 0.5 µl RNase inhibitor and 6.6 µl of H_2O per reaction is added to RNA isolated above. Plates are sealed, mixed, and incubated on an electromagnetic shaker for 10 minutes at room temperature, followed by 2 h 37°C.

Real time PCR

Two µl of cDNA and 5µl Lightcycler 480 probe master mix (Roche Cat # 04887301001) are added to either 0.5 µl of rat GAPDH TaqMan probe (Rn01775763_g1, Thermo Fisher) or 0.5 µl of mouse ANGPTL7 probe (Mm01256626_m1, Thermo Fisher) per well in a 384 well plates (Roche cat

04887301001). Real time PCR is done in a LightCycler480 Real Time PCR system (Roche). Each duplex is tested at least two times and data are normalized to cells transfected with a non-targeting control siRNA. To calculate relative fold change, real time data are analyzed using the ΔΔCt method and normalized to assays performed with cells transfected with a non-targeting control siRNA.

Example 5: ANGPTL7 knockout inhibits DEX-Ac-induced ocular hypertension in mice

Weekly periocular conjunctival fornix (CF) injections of dexamethasone-21-acetate (DEX-Ac) in both eyes significantly elevated intraocular pressure (IOP) in ANGPTL7 WT mice as compared to vehicle-administered control WT mice. As shown in FIG. 1, IOP measurements of DEX-Ac-treated WT mice ("WT-DEX-Ac", n=18) produced IOP elevation from week 1 to 6 relative to vehicle-treated WT mice ("WT-Vehicle", n=6); **** $p < 0.0001$, ** $p < 0.01$. In contrast, weekly periocular CF injections of DEX-Ac in both eyes in ANGPTL7 knockout (KO) mice did not elevate IOP as compared to vehicle-administered ANGPTL7 KO mice. As shown in FIG. 1, IOP measurements of DEX-Ac-treated ANGPTL7 KO mice ("KO-DEX-Ac", n=20) produced no IOP elevation from week 1 to week 6 relative to vehicle-treated ANGPTL7 KO mice ("KO-Vehicle", n=12).

Example 6: *In vivo* evaluation of ANGPTL7 siRNA in wild-type mice

The dsRNA agents designed and assayed in Examples 1-4 were assessed for their ability to reduce the level of ANGPTL7 RNAs and/or reduce intraocular pressure (IOP) *in vivo* in wild-type mice.

Experimental Methods

Six different siRNAs targeting ANGPTL7 (siRNA #1-6; see Table 10) were tested in C57BL/6J wild-type mice and IOP was monitored over time. C57BL/6J mice were each intravitreally injected with 15 μg of an siRNA or PBS control. Animals in the naïve group received no injection. Six weeks later, animals were sacrificed, eyes were collected, and limbal rings were carefully micro-dissected. qPCR was performed on limbal rings dissected from mouse eyes enriched for the travecular meshwork (TM) for ANGPTL7 expression. The data were expressed as percent message remaining relative to the baseline value, and presented as mean ± standard error of the mean (SEM).

Table 10. Sense and antisense strand sequences of ANGPTL7 dsRNA agents used in *in vivo* study

siRNA#	Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:
1	AD-1094262	UUGGGCAAUGAACUGAACAGA	26	UCUGUUCAGUUCAUUGCCCAACG	48
2	AD-1093984	GUACCAGAAGAACUACCGAAA	14	UUUCGGUAGUUCUUCUGGUACAG	36
3	AD-1094129	AGACAGUAUAAGCAAGGGUUA	24	UAACCCUUGCUUAUACUGUCUCC	46
4	AD-1093672	GCAGAAGCCUCAUAAACGCAA	33	UUGCGUUUAUGAGGCUUCUGCAG	55

siRNA#	Duplex Name	Sense Sequence 5' to 3'	SEQ ID NO:	Antisense Sequence 5' to 3'	SEQ ID NO:
5	AD-1094991	ACACUUCCUUGUGU CUAUAGA	13	UCUAUAGACACAAGG AAGUGUCG	35
6	AD-1093670	CUGCAGAAGCCUCA UAAACGA	32	UCGUUUAUGAGGCUU CUGCAGCC	54

Results

The results of the *in vivo* evaluation are shown in FIGs. 2 and 3. As shown in FIG. 2, IOP was significantly lowered 2 weeks post-injection in mice treated with two of the six siRNAs (siRNA #3 and #5, n = 6-8/group) compared to the PBS-treated (n = 6) or naïve (no injection, n = 5) groups; * $p < 0.05$. Naïve and PBS-treated animals maintained their IOPs at baseline for the duration of the study (weeks 0-6). In contrast, in mice treated with siRNA#3 and #5, IOP was lowered by 2-4 mmHg starting at week 2 compared to PBS-treated or naïve mice, and remained lowered through the end of the study (i.e., 6 weeks); ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, ## $p < 0.01$, ### $p < 0.001$, #### $p < 0.0001$. siRNAs #3 and #5 represent AD-1094129 and AD-1094991, respectively.

As shown in FIG. 3, in qPCR of the limbal ring tissue harvested at the end of the study (i.e., 6 weeks after the siRNA administration), the highest level of knockdown (> 50%) of ANGPTL7 mRNA was observed with siRNAs #3 and #5 compared to PBS-treated or naïve mice. Such mRNA knockdown effect is consistent with the lowering of IOP observed in mice injected with one of these two siRNAs. The results suggest that inhibition of ANGPTL7 expression also lowers IOP, and demonstrate the ability of the exemplary dsRNA agents to reduce the ANGPTL7 expression and also lower IOP *in vivo*.

Example 7. *In vivo* knock down of ANGPTL7 by siRNA inhibits steroid-induced intraocular pressure elevation in in wild type mice

dsRNA agents targeting ANGPTL7 (siRNA #1-#6) were further assessed for their ability to reduce steroid induced IOP *in vivo* in wild-type mice. siRNAs #3 and #5 represent AD-1094129 and AD-1094991, respectively (see Table 10).

Mice were divided into following groups as shown in FIG. 4: (a) Vehicle (n=4), (b) Vehicle + PBS (n=6), (c) DEX-Ac (n=12), (d) DEX-Ac + siRNA#3 (n=14), and (e) DEX-Ac + siRNA#5 (n=14). Starting on day 1, each group of mice received weekly periocular CF injection of DEX-Ac suspension or vehicle to both eyes, and the intraocular pressure (IOP) was monitored over time. At Day 22, siRNA targeting ANGPTL7 (#3 and #5) or PBS were intravitreally (IVT) injected into mice in groups (d) (DEX-Ac + siRNA#3), (e) (DEX-Ac +siRNA#5), and (b) (Vehicle + PBS), respectively, and IOP measurements were continued to be recorded.

Weekly periocular CF injections of DEX-Ac suspension to both eyes caused DEX-induced ocular hypertension (OHT) with sustained and significantly elevated IOP in WT mice. IOP elevation was rapid and significantly higher in DEX-Ac-treated mice compared with vehicle-treated mice

starting 6-days post-injection; **** $p < 0.001$, *** $p < 0.001$, #### $p < 0.0001$, ### $p < 0.001$, ++++ $p < 0.0001$, ++ $p < 0.01$. DEX-Ac treated mice in group (c) developed DEX-induced OHT with sustained and significantly elevated IOP throughout the study. Following the siRNA administration on day 22, in groups (d) and (e), IOPs were significantly reduced and returned to baseline IOP within one week after the siRNA administration as compared with DEX-Ac treated and siRNA-untreated group (c). In the siRNA-treated mice in groups (d) and (e), the IOP levels remained at baseline and significantly lower than those in DEX-Ac treated and siRNA treated group (c) mice for the remainder of the study (i.e., through day 70) even though mice in groups (d) and (e) continued to receive weekly DEX-Ac treatment; #### $p < 0.0001$, ### $p < 0.001$, ++++ $p < 0.0001$, +++ $p < 0.001$.

ANGPTL7 Sequences

SEQ ID NO: 1

>NM_001039554.3 Mus musculus angiopoietin-like 7 (Angptl7), mRNA

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SEQ ID NO: 2

>Reverse complement of SEQ ID NO:1

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SEQ ID NO: 3
>NM_021146.4 Homo sapiens angiopoietin like 7 (ANGPTL7), mRNA
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SEQ ID NO: 5

>XM_005544804.2 PREDICTED: Macaca fascicularis angiopoietin like 7 (ANGPTL7), mRNA

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SEQ ID NO: 6
Reverse complement of SEQ ID NO: 5

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SEQ ID NO: 7
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SEQ ID NO: 8
Reverse complement of SEQ ID NO: 7
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TCCTGGCATCCTGAGTTCAAATCCCAGCAACCACATGGTGGCTCACAACCATCTATAAAGGAATC

We claim:

1. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of angiopoietin like 7 (ANGPTL7) in a cell, wherein the dsRNA agent comprises a sense strand and an antisense strand, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of any one of SEQ ID NOs: 1 or 3, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of any one of SEQ ID NOs: 2 or 4.

2. A double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of ANGPTL7, wherein the dsRNA agent comprises a sense strand and an antisense strand forming a double stranded region, wherein the antisense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from one of the antisense sequences listed in any one of Tables 2-7, and wherein the sense strand comprises a nucleotide sequence comprising at least 15 contiguous nucleotides, with 0, 1, 2, or 3 mismatches, from a sense sequence listed in any one of Tables 2-7 that corresponds to the antisense sequence.

3. The dsRNA agent of claim 1 or 2, wherein at least one of the sense strand and the antisense strand is conjugated to one or more lipophilic moieties.

4. The dsRNA agent of claim 3, wherein the lipophilic moiety is conjugated via a linker or carrier.

5. The dsRNA agent of claim 3 or 4, wherein one or more lipophilic moieties are conjugated to one or more internal positions on at least one strand.

6. The dsRNA agent of claim 5, wherein the one or more lipophilic moieties are conjugated to the one or more internal positions on at least one strand via a linker or carrier.

7. The dsRNA agent of any one of claims 3-6, wherein the lipophilic moiety is an aliphatic, alicyclic, or polyalicyclic compound.

8. The dsRNA agent of claim 7, wherein the lipophilic moiety contains a saturated or unsaturated C16 hydrocarbon chain.

9. The dsRNA agent of any one of claims 3-8, wherein the lipophilic moiety is conjugated via a carrier that replaces the one or more nucleotide(s) in the internal position(s) or the double stranded region.

10. The dsRNA agent of any one of claims 3-8, wherein the lipophilic moiety is conjugated to the double-stranded iRNA agent via a linker containing an ether, a thioether, a urea, a carbonate, an amine, an amide, a maleimide-thioether, a disulfide, a phosphodiester, a sulfonamide linkage, a product of a click reaction, or a carbamate.

11. The double-stranded iRNA agent of any one of claims 3-9, wherein the lipophilic moiety is conjugated to a nucleobase, sugar moiety, or internucleosidic linkage.

12. The dsRNA agent of any of one of claims 1-11, wherein the dsRNA agent comprises at least one modified nucleotide.

13. The dsRNA agent of claim 12, wherein no more than five of the sense strand nucleotides and not more than five of the nucleotides of the antisense strand are unmodified nucleotides.

14. The dsRNA agent of claim 12, wherein all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand are modified nucleotides.

15. The dsRNA agent of any one of claims 12-14, wherein at least one of the modified nucleotides is selected from the group consisting of a deoxy-nucleotide, a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-O-allyl-modified nucleotide, 2'-C-alkyl-modified nucleotide, a 2'-methoxyethyl modified nucleotide, a 2'-O-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a tetrahydropyran modified nucleotide, a 1,5-anhydrohexitol modified nucleotide, a cyclohexenyl modified nucleotide, a nucleotide comprising a phosphorothioate group, a nucleotide comprising a methylphosphonate group, a nucleotide comprising a 5'-phosphate, a nucleotide comprising a 5'-phosphate mimic, a glycol modified nucleotide, and a 2-O-(N-methylacetamide) modified nucleotide; and combinations thereof.

16. The dsRNA agent of any one of claims 1-15, wherein the sense strand, the antisense strand, or each of the sense strand and antisense strand comprises a 3' overhang of at least 2 nucleotides.

17. The dsRNA agent of any one of claims 1-16, wherein the double stranded region is 15-30 nucleotide pairs in length.

18. The dsRNA agent of claim 17, wherein the double stranded region is 17-23 nucleotide pairs in length.

19. The dsRNA agent of any one of claims 1-18, wherein the sense strand and the antisense strand each has 19-30 nucleotides.

20. The dsRNA agent of any one of claims 1-19, wherein the agent comprises at least one phosphorothioate or methylphosphonate internucleotide linkage.

21. The dsRNA agent of any one of claims 3-20, further comprising a targeting ligand.

22. The dsRNA agent of claim 21, wherein the targeting ligand targets an ocular tissue.

23. The dsRNA agent of claim 22, wherein the ocular tissue is an optic nerve, a trabecular meshwork, a juxtacanalicular tissue, a ganglion (*e.g.*, including a retinal ganglion), episcleral veins or a Schlemm's canal (*e.g.*, including an endothelial cell).

24. The dsRNA agent of any one of claims 1-23, further comprising a phosphate or phosphate mimic at the 5'-end of the antisense strand.

25. The dsRNA agent of claim 24, wherein the phosphate mimic is a 5'-vinyl phosphonate (VP).

26. The dsRNA of any one of claims 1-25, wherein the dsRNA agent targets a hotspot region of an mRNA encoding ANGPTL7.

27. The dsRNA agent of claim 26, wherein the hotspot region comprises nucleotides 1562-1584, 546-568, 709-731, 862-884, and/or 232-256 of SEQ ID NO: 1, or nucleotides 1993-2146, 1910-1932, 1726-1823, 1628-1685, 1591-1613, 1551-1573, 1420-1442, 1380-1402, 1243-1265, 1195-1217, 1096-1118, 940-962, and/or 299-321 of SEQ ID NO: 3.

28. The dsRNA agent of claim 27, wherein the dsRNA agent is selected from the group consisting of AD-1094991, AD-1093984, AD-1094129, AD-1094262, AD-1093670, AD-1093672, AD-1565389, AD-1565368, AD-1565357, AD-1565345, AD-1565324, AD-1565303, AD-1565288, AD-1565212, AD-1565141, AD-1565126, AD-1565113, AD-1565091, AD-1565034, AD-1565015,

AD-1565004, AD-1564969, AD-1094381, AD-1564428, AD-1564936, AD-1564823, AD-1564802, AD-1564666, AD-1564618, and AD-1563396.

29. A dsRNA agent that targets a hotspot region of an angiopoietin-like 7 (ANGPTL7) mRNA.

30. A cell containing the dsRNA agent of any one of claims 1-29.

31. A pharmaceutical composition for inhibiting expression of an ANGPTL7, comprising the dsRNA agent of any one of claims 1-29.

32. A method of inhibiting expression of ANGPTL7 in a cell, the method comprising:

(a) contacting the cell with the dsRNA agent of any one of claims 1-29, or the pharmaceutical composition of claim 31; and

(b) maintaining the cell produced in step (a) for a time sufficient to reduce levels of ANGPTL7 mRNA, ANGPTL7 protein, or both of ANGPTL7 mRNA and protein, thereby inhibiting expression of ANGPTL7 in the cell.

33. The method of claim 32, wherein the cell is within a subject.

34. The method of claim 33, wherein the subject is a human.

35. The method of claim 34, wherein the subject has been diagnosed with an ANGPTL7-associated disorder.

36. A method of treating a subject diagnosed with an ANGPTL7-associated disorder comprising administering to the subject a therapeutically effective amount of the dsRNA agent of any one of claims 1-25 or a pharmaceutical composition of claim 27, thereby treating the disorder.

37. The method of claim 36, wherein the ANGPTL7-associated disorder is glaucoma.

38. The method of claim 37, wherein the glaucoma is primary open-angle glaucoma.

39. The method of any one of claims 36-38, wherein the treating comprises amelioration of at least one sign or symptom of the disorder.

40. The method of any one of claims 36-39, wherein the treating comprises one or more of (a) inhibiting or reducing intraocular pressure; (b) inhibiting or reducing the expression or activity of

ANGPTL7; (c) increasing drainage of aqueous humor; (d) inhibiting or reducing optic nerve damage; or (e) inhibiting or reducing retinal ganglion cell death. medication to reduce intraocular pressure, laser treatment, surgery or trabeculectomy.

41. The method of any one of claims 33-40, wherein the dsRNA agent is administered to the subject intraocularly, intravenously, or topically.

42. The method of claim 41, wherein the intraocular administration comprises intravitreal administration (*e.g.*, intravitreal injection), transscleral administration (*e.g.*, transscleral injection), subconjunctival administration (*e.g.*, subconjunctival injection), retrobulbar administration (*e.g.*, retrobulbar injection), intracameral administration (*e.g.*, intracameral injection), or subretinal administration (*e.g.*, subretinal injection).

43. The method of any one of claims 33-42, further comprising administering to the subject an additional agent or therapy comprising one or more of a prostaglandin analog, a beta blocker, an alpha-adrenergic agonist, a carbonic anhydrase inhibitor, a ROCK inhibitor, a ROCK iRNA agent, an inhibitor of a Rho GTPase, an anti-Rho GTPase agent, or an anti-ANGPTL7 agent suitable for treatment or prevention of an ANGPTL7-associated disorder.

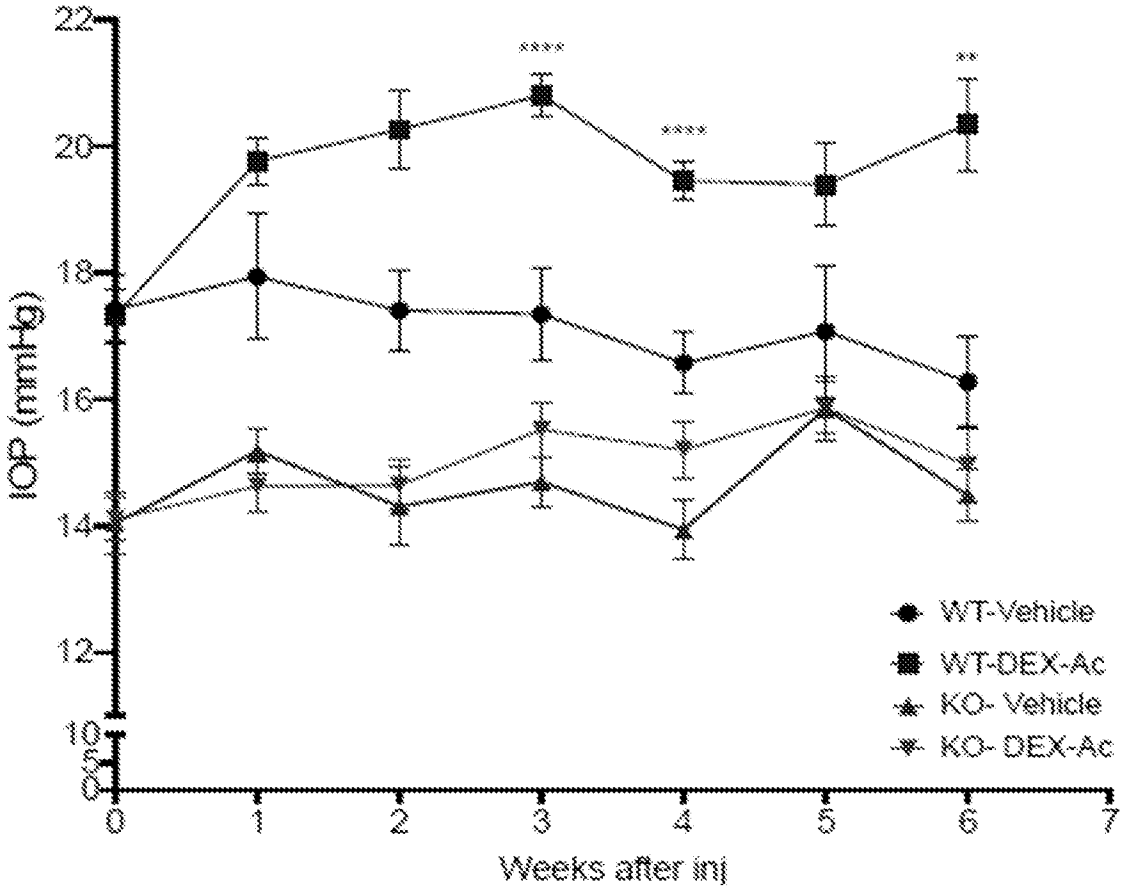

IOP (mmHg)
Weeks after inj
WT-Vehicle
WT-DEX-Ac
KO- Vehicle
KO- DEX-Ac
****
****
**

FIG. 1

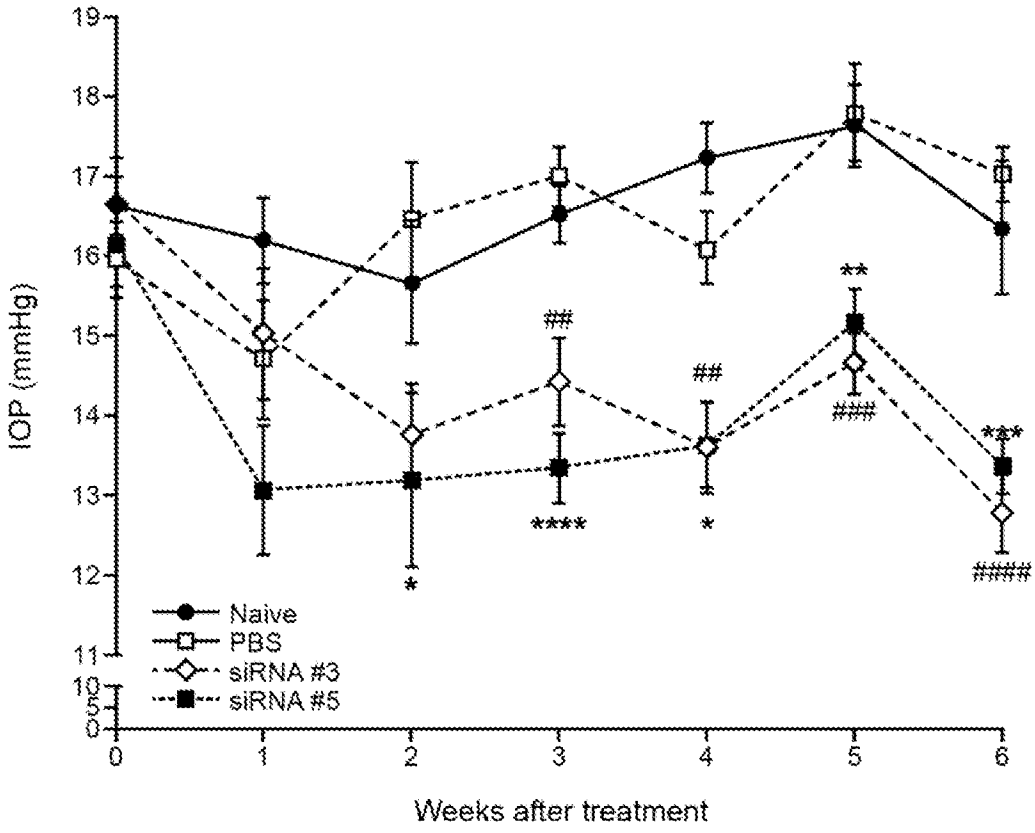


FIG. 2

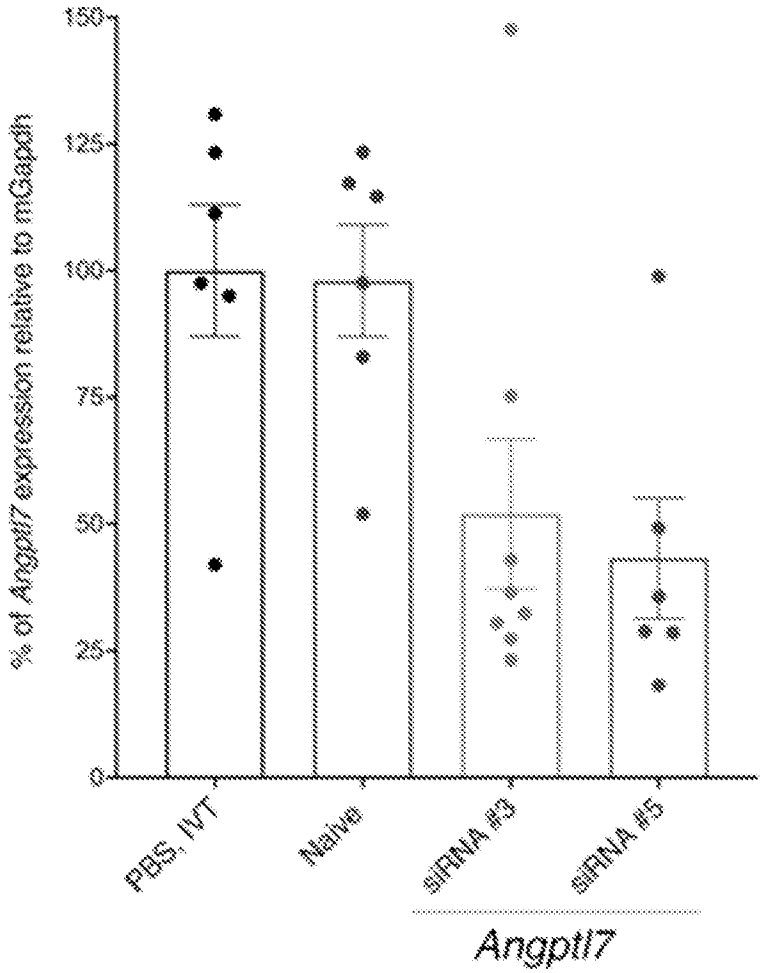

% of Angptl7 expression relative to mGapdh
150
125
100
75
50
25
0
PBS, IVT
Naive
siRNA #3
siRNA #5
Angptl7

FIG. 3

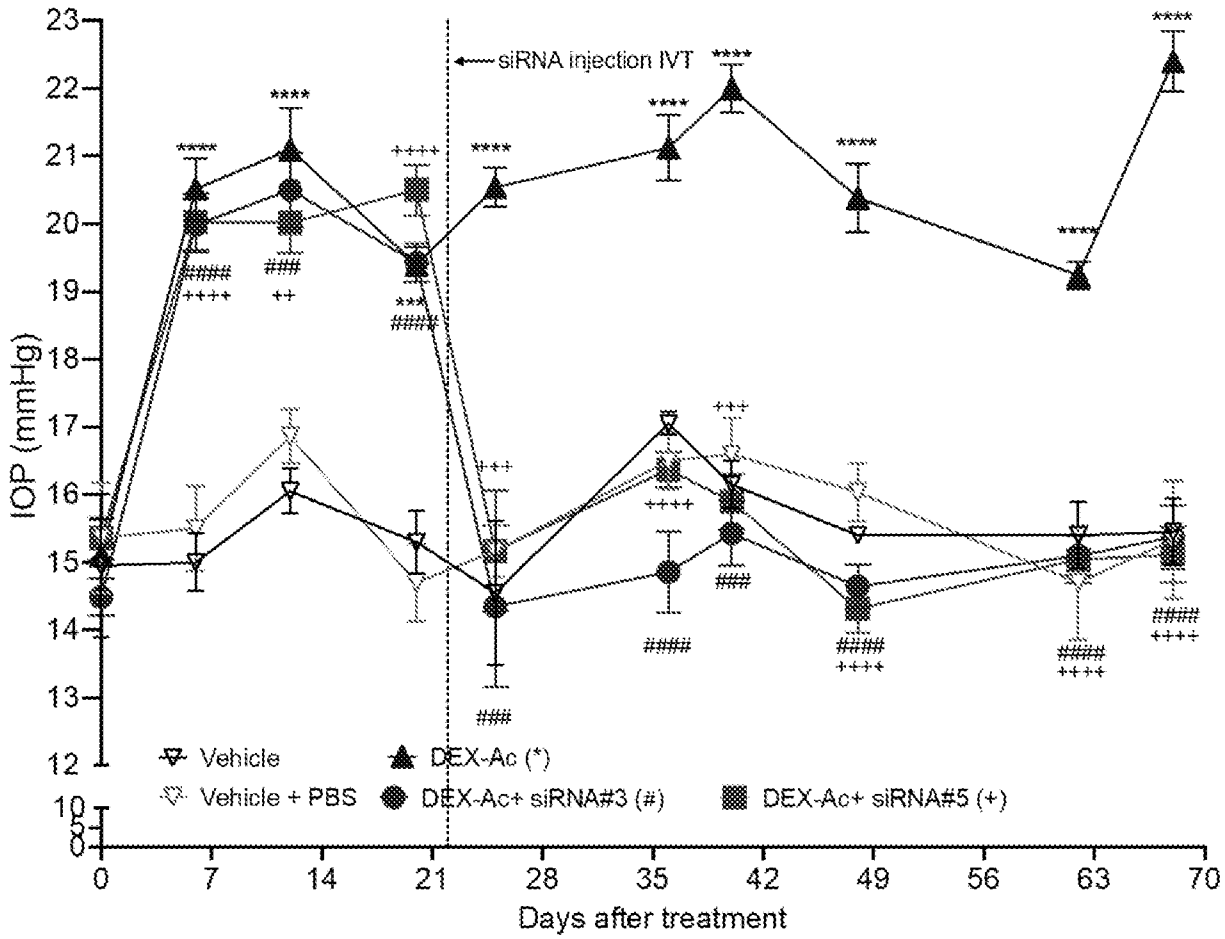

siRNA injection IVT
IOP (mmHg)
Days after treatment
Vehicle
Vehicle + PBS
DEX-Ac (*)
DEX-Ac+ siRNA#3 (#)
DEX-Ac+ siRNA#5 (+)

FIG. 4

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 22/77447

A. CLASSIFICATION OF SUBJECT MATTER
IPC - INV. A61K 31/713, A61K 48/00 (2022.01)
ADD. C12N 15/113, A61P 27/06 (2022.01)
CPC - INV. A61K 31/713, C12N 15/1136
ADD. C12N 2310/14, C12N 2310/11, C12N 2320/11
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 ---- Y ---- A	US 2020/0399640 A1 (EMPIRICO INC.) 24 December 2020 (24.12.2020) Claim 1; Claim 15; para [0008]; para [0044]; para [0075]; para [0090]; para [0270]; para [0276]; para [0284]	29 ----- 1, (3-4)/1 ---------- 2, (3-4)/2
Y ---- A	US 2013/0165338 A1 (SCHMIDT-OTT et al.) 27 June 2013 (27.06.2013) Abstract; Table 1; SEQ ID NO:15	1, (3-4)/1 ---------- 2, (3-4)/2

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

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"D" document cited by the applicant in the international application
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"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
3 December 2022 (03.12.2022)	FEB 09 2023
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 22/77447

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. [X] forming part of the international application as fi led.

   b. [ ] furnished subsequent to the international fi ling date for the purposes of international search (Rule 13ter.1(a)),

      [ ] accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.

2. [ ] With regard to any nucleotide and/or amino acid sequence disclosed in the international application, this report has been established to the extent that a meaningful search could be carried out without a WIPO Standard ST.26 compliant sequence listing.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 22/77447

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.: 5-28, 30-43
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.:
1-4, 29, limited to dsRNA agent comprising SEQ ID NOs:13 and 35

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.

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 1-4, 29, directed to a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of angiopoietin like 7 (ANGPTL7) in a cell. The dsRNA agent will be searched to the extent that the dsRNA agent encompasses wherein the dsRNA agent comprises a sense strand and an antisense strand, wherein the sense strand comprises at least 15 contiguous nucleotides with 0 mismatches from the nucleotide sequence of SEQ ID NO: 1 and comprises SEQ ID NO:13, and the antisense strand comprises at least 15 contiguous nucleotides with 0 mismatches from the nucleotide sequence of SEQ ID NO: 2 and comprises SEQ ID NO:35 (note, these are the first claimed sequences for the inventive dsRNA agent). The first named invention was determined based on the first claimed dsRNA sequences (claims 1-2, Table 2) for the inventive dsRNA agent embodiment. This first named invention has been selected based on the guidance set forth in section 10.54 of the PCT International Search and Preliminary Examination Guidelines. It is believed that claims 1-4, 29 encompass this first named invention, and thus these claims will be searched without fee to the extent that the dsRNA agent. Additional dsRNA agent(s) comprising additional sequence(s) will be searched upon the payment of additional fees. Applicants must specify the claims that encompass any additionally elected dsRNA agent(s) comprising additional sequence(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 a dsRNA agent comprising a sense strand of SEQ ID NO: 14 and an antisense strand sequence of SEQ ID NO:36 (claims 1-4, 29).

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 Groups I+ each include the special technical feature of a unique nucleic acid sequence. Each nucleic acid sequence has a unique target sequence for hybridization, and is considered a distinct technical feature.

Common technical features

No technical features are shared between the dsRNA agent sequences in each of Group I+ inventions and, accordingly, these inventions lack unity a priori.

Additionally, even if Group I+ inventions were considered to share the technical features of including:
a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of angiopoietin like 7 (ANGPTL7) in a cell, wherein the dsRNA agent comprises a sense strand and an antisense strand, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of a target sequence, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of a target sequence,
these shared technical features are previously disclosed by US 2020/0399640 A1 to Empirico Inc., (hereinafter 'Empirico').

----please see continuation on next sheet ----------

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

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Empirico teaches a double stranded ribonucleic acid (dsRNA) agent for inhibiting expression of angiopoietin like 7 (ANGPTL7) in a cell, wherein the dsRNA agent comprises a sense strand and an antisense strand, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of a target sequence, and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of a target sequence (Claim 1 - 'A composition comprising an oligonucleotide that targets Angiopoietin like 7 (ANGPTL7) and when administered to a cell decreases expression of ANGPTL7, wherein the oligonucleotide comprises a small interfering RNA (siRNA) comprising a sense strand and an antisense strand, wherein the sense strand comprises an oligonucleotide sequence of SEQ ID NOs: 1424, 1541, 2091 in which at least one internucleoside linkage is modified and at least one base is modified, or an oligonucleotide sequence comprising 1 or 2 nucleoside, substitutions, additions, or deletions of SEQ ID NOs: 1424, 1541, or 2091 in which at least one internucleoside linkage is modified and at least one base is modified, and wherein the antisense strand comprises an oligonucleotide sequence of SEQ ID NOs: 3630, 3747, or 4297 in which at least one internucleoside linkage is modified and at least one base is modified, or an oligonucleotide sequence comprising 1 or 2 nucleoside, substitutions, additions, or deletions of SEQ ID NOs: 3630, 3747, or 4297 in which at least one internucleoside linkage is modified and at least one base is modified.'; Claim 15 - 'A composition comprising an oligonucleotide that targets Angiopoietin like 7 (ANGPTL7) and when administered to a subject in an effective amount decreases intraocular pressure, wherein the oligonucleotide comprises a small interfering RNA (siRNA) comprising a sense strand and an antisense strand, the antisense strand being complementary to a portion of a nucleic acid having the nucleoside sequence of SEQ ID NO: 11085, and each strand having 14 to 30 nucleotides, and wherein the oligonucleotide comprises a lipid attached at a 3' or 5' terminus of the oligonucleotide.'; para [0044] - 'In some embodiments, the siRNA binds with a human ANGPTL7 mRNA with no more than 2 mismatches in the antisense strand.'; para [0090] - 'The sequence of an oligomeric compound need not be 100% complementary to that of its target nucleic acid to be specifically hybridizable. Moreover, an oligonucleotide may hybridize over one or more segments such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure, mismatch or hairpin structure). In some embodiments, oligomeric compounds disclosed herein comprise at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 99% sequence complementarity to a target region within the target nucleic acid sequence to which they are targeted.').

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 5-28, 30-43 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).