Compositions And Methods For Inhibition Of HAO1 (Hydroxyacid Oxidase 1 (Glycolate Oxidase)) Gene Expression

Cross Reference to Related Applications

This application claims the benefit of U.S. Provisional Application No. 62/062,751, filed October 10, 2014, and U.S. Provisional Application No. 62/147,976, filed April 15, 2015, and U.S. Provisional Application No. 62/214,602, filed September 4, 2015, each of which is hereby incorporated in its entirety by reference.

Sequence Listing

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on October 8, 2015, is named 30864PCT_CRF_sequencelisting. txt and is 735,705 bytes in size.

Background of the Invention

Primary Hyperoxaluria Type 1 (PH1) is an autosomal recessive disorder of glyoxylate metabolism. Hepatic glyoxylate detoxification is impaired due to mutation of the AGXT gene, which encodes the liver peroxisomal alanine-glyoxylate aminotransferase (AGT) enzyme. AGT1 is the final enzyme in the metabolic breakdown of hydroxyproline. Loss of AGT function to convert the intermediate metabolite glyoxylate to glycine causes accumulation and reduction of glyoxylate to glycolate which is oxidized to oxalate by the enzyme glycolate oxidase (GO), also known as hydroxyacid oxidase (HAO1).

Regulation of glyoxylate, the key precursor of oxalate, occurs at multiple cellular sites including the mitochondria, peroxisome and the cytosol. Excess oxalate in PH1 patients is unable to be fully excreted by the kidneys leading to the formation and deposition of calcium oxalate crystals in the kidneys and urinary tract. Renal damage is caused by a combination of tubular toxicity from oxalate, nephrocalcinosis and renal obstruction by stones. Greater than 30% of patients advance to end stage renal disease (ESRD).

The HAO1 gene encodes the enzyme Hydroxyacid Oxidase 1, also known as Glycolate Oxidase ("GO"). The HAO1 protein is expressed primarily in the liver and is a 2-hydroxyacid oxidase most active on glycolate.

In a mouse model of PH1, where the AGT1 gene is deleted, urine oxalate levels are reduced when the HAO1 gene is deleted.

PH1, AGXT, and HAO1 are described in the following: Angel L. Pey, Armando Albert, and Eduardo Salido, "Protein Homeostasis Defects of Alanine-Glyoxylate Aminotransferase: New Therapeutic Strategies in Primary Hyperoxaluria Type I," BioMed Research International, vol. 2013, Article ID 687658, 15 pages, 2013. doi:10.1155/2013/687658; Cochat and Rumsby (2013) NEJM 369:7; Salido et al (2006) PNAS 103:18249; Baker et al (2004) American Journal of Physiology - Heart and Circulatory Physiology Published 1 October 2004Vol. 287no. 4, H1771-H1779DOI: 10.1152/ajpheart.00234.2004.

Summary

In one aspect, the present invention refers to a double stranded RNAi agent capable of inhibiting expression of HAO1 in a cell, wherein said double stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:1 SEQ ID NO:2, SEQ ID NO:5, or SEQ ID NO:6 and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:3 SEQ ID NO:4, SEQ ID NO:7, or SEQ ID NO:8; wherein substantially all of the nucleotides of said sense strand and substantially all of the nucleotides of said antisense strand are modified nucleotides, wherein at least one of said modified nucleotides is selected from the group consisting of 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 abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a nucleotide comprising a 5'-phosphorothioate group, a nucleotide comprising a 5' phosphate or 5' phosphate mimic, and a terminal nucleotide linked to a cholesteryl derivative or a dodecanoic acid bisdecylamide group, and wherein said sense strand is conjugated to a ligand attached at the 3'-terminus.

In another aspect, the present invention refers to a double stranded RNAi agent capable of inhibiting expression of HAO1 in a cell, wherein said double stranded RNAi agent comprises a sense strand and an antisense strand forming a double stranded region, wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of from any one of the nucleotide sequences of SEQ ID NO:1 SEQ ID NO:2, SEQ ID NO:5, or SEQ ID NO:6 and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3

nucleotides from any one of the nucleotide sequences of SEQ ID NO:3 SEQ ID NO:4, SEQ ID NO:7, or SEQ ID NO:8, wherein substantially all of the nucleotides of said sense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification, wherein said sense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus, wherein substantially all of the nucleotides of said antisense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification, wherein said antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and wherein said sense strand is conjugated to one or more GalNAc derivatives attached through a branched bivalent or trivalent linker at the 3'-terminus.

In yet another aspect, the present invention refers to an RNAi agent selected from the group of RNAi agents listed in Table 1 or 2.

In yet another aspect, the present invention refers to the use of a double stranded RNAi agent in the manufacture of a medicament for treating a subject having Primary Hyperoxaluria 1 (PH1), wherein said double stranded RNAi agent comprises a sense strand and an antisense strand forming a double stranded region, wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of from any one of the nucleotide sequences of SEQ ID NO:1 SEQ ID NO:2, SEQ ID NO:5, or SEQ ID NO:6 and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:3 SEQ ID NO:4, SEQ ID NO:7, or SEQ ID NO:8, wherein substantially all of the nucleotides of said antisense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoromodification, wherein said antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, wherein substantially all of the nucleotides of said sense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoromodification, wherein said sense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and, wherein said sense strand is conjugated to one or more GalNAc derivatives attached through a branched bivalent or trivalent linker at the 3'-terminus.

The present disclosure provides compositions comprising RNAi agents, *e.g.*, double-stranded iRNA agents, targeting HAO1. The present disclosure also provides methods using the compositions of the invention for inhibiting HAO1 expression and for treating HAO1 associated disorders, *e.g.*, PH1.

Brief Description of the Drawings

Figure 1 shows the nucleotide sequence of *Homo sapiens* HAO1 mRNA (SEQ ID NO:1).

Figure 2 shows the nucleotide sequence of *Mus musculus* HAO1 mRNA (SEQ ID NO:2).

Figure 3A is a graph with the results of in vitro screening of GO (HAO) GalNac-siRNA conjugates in primary cynomologous monkey hepatocytes.

Figure 3B is a graph with the dose response curve of a GO (HAO) GalNac-siRNA conjugate in primary cynomologous monkey hepatocytes.

Figure 4A is a graph with the results of in vivo evaluation of GO (HAO) GalNac-siRNA conjugates in C57B6 mice after a single dose.

Figure 4B is a graph with the results of in vivo evaluation of GO (HAO) GalNac-siRNA conjugates in C57B6 mice after a repeat dose.

Figure 5A is a graph showing urinary oxalate levels in AGXT knock out (KO) mice after treatment with GO (HAO) GalNac-siRNA conjugates.

Figure 5B is a graph showing urinary glycolate levels in AGXT KO mice after treatment with GO (HAO) GalNac-siRNA conjugates.

Figure 6A is a graph showing AGXT mRNA levels in a rat model of PH1 72 hours after a single dose of an AGXT siRNA.

Figure 6B is a graph showing urinary oxalate levels in a rat model of PH1 72 hours after treatment with a GO (HAO) GalNac-siRNA conjugate.

Figure 6C is a graph showing urinary oxalate levels in a rat model of PH1 followed for 49 days with continued weekly dosing on days 14 and 21 of both AF-011-63102 and AD-62994 and 24 hour urine collections as shown.

Figure 6D is a graph showing duration of HAO1 knockdown in rats. Shown are mRNA levels either one week or four weeks after the last of 4 doses (corresponding to days 28 and 49 in Figure 6C) and expressed relative to levels seen in rats treated with PBS

Figure 7 shows the reverse complement of the nucleotide sequence of *Homo sapiens* HAO1 mRNA (SEQ ID NO:3).

Figure 8 shows the reverse complement of the nucleotide sequence of *Mus musculus* HAO1 mRNA (SEQ ID NO:4).

Figure 9 shows the nucleotide sequence of *Macaca fascicularis* HAO1 mRNA (SEQ ID NO:5).

Figure 10 shows the nucleotide sequence of *Rattus norvegicus* HAO1 mRNA (SEQ ID NO:6).

Figure 11 shows the reverse complement of the nucleotide sequence of *Macaca fascicularis* HAO1 mRNA (SEQ ID NO:7).

Figure 12 shows the reverse complement of the nucleotide sequence of *Rattus norvegicus* HAO1 mRNA (SEQ ID NO:8).

Figure 13 shows in vivo screening of GO GalNAc conjugates.

Figure 14 is a graph showing an in vivo evaluation of GO-GalNAc conjugates in mice.

Figure 15 is a graph showing a dose-response evaluation of GO-GalNAc conjugates in mice.

Figure 16 is a graph showing a dose-response evaluation of GO-GalNAc conjugates in mice.

Figure 17 is a graph showing a dose response evaluation in mice.

Figure 18 is two graphs showing the relationship of mRNA knockdown to serum glycolate levels in mice.

Figure 19 is two graphs showing relationship of mRNA knockdown to serum glycolate levels in rats.

Figure 20 is a graph showing dose dependent inhibition of HAO1 mRNA by ALN-65585 in primary cyno hepatocytes.

Figure 21 is two graphs showing HAO1 mRNA and serum glycolate levels following single does treatment with ALN-GO1 in mice.

Figure 22 is a graph showing duration of HAO1 mRNA silencing following single dose treatment with ALN-GO1 in mice.

Figure 23 is a graph showing HAO1 mRNA and serum glycolate levels following single dose treatment with ALN-GO1 in rats.

Figure 24 is two graphs showing urinary oxalate and glycolate levels in a mouse model of primary hyperoxaluria type I after a single dose of ALN-GO1.

Figure 25A is a graph showing HAO1 mRNA levels in a rat model of primary hyperoxaluria type I after a single dose of ALN-GO1.

Figure 25B is a graph showing urinary oxalate levels in a rat model of primary hyperoxaluria type Iafter a single dose of ALN-GO1.

Figure 26 is two graphs showing HAO1 mRNA and urinary oxalate levels in a rat model of primary hyperoxaluria type I after repeat dosing of ALN-GO1.

Figure 27 is two graphs showing HAO1 mRNA and serum glycolate levels after repeat dosing in non-human primates.

Detailed Description of the Invention

The present invention provides compositions comprising RNAi agents, *e.g.*, double-stranded RNAi agents, targeting HAO1. The present invention also provides methods using the compositions of the invention for inhibiting HAO1 expression and for treating HAO1 associated disorders.

I. Definitions

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

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

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

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

As used herein, "HAO1" refers to the gene encoding the enzyme hydroxyacid oxidase 1. Other gene names include GO, GOX, GOX1, and HAOX1. The protein is also known as glycolate oxidase and (S)-2-hydroxy-acid oxidase. The GenBank accession number of the human HAO1 mRNA is NM_017545.2; cynomolgous monkey (*Macaca fascicularis)* HAO1 mRNA is XM_005568381.1; Mouse (*Mus musculus)* HAO1 mRNA is NM_010403.2; Rat (*Rattus norvegicus)* HAO1 mRNA is XM_006235096.1.

The term"HAO1," as used herein, also refers to naturally occurring DNA sequence variations of the HAO1 gene, such as a single nucleotide polymorphism (SNP) in the HAO1 gene. Exemplary SNPs may be found in the NCBI dbSNP Short Genetic Variations database available at www.ncbi.nlm.nih.gov/projects/SNP.

As used herein, "target sequence" refers to a contiguous portion of the nucleotide sequence of an mRNA molecule formed during the transcription of a HAO1 gene, including mRNA that is a product of RNA processing of a primary transcription product.

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

"G," "C," "A" and "U" each generally stand for a nucleotide that contains guanine, cytosine, adenine, and uracil as a base, respectively. "T" and "dT" are used interchangeably herein and refer to a deoxyribonucleotide wherein the nucleobase is thymine, e.g., deoxyribothymine, 2'-deoxythymidine or thymidine. However, it will be understood that the

term "ribonucleotide" or "nucleotide" or "deoxyribonucleotide" 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 the invention by a nucleotide containing, for example, inosine. Sequences comprising such replacement moieties are embodiments of the invention.

The terms "iRNA", "RNAi agent," "iRNA agent,", "RNA interference agent" as used interchangeably herein, refer to an agent that contains RNA as that term is defined herein, and which mediates the targeted cleavage of an RNA transcript *via* an RNA-induced silencing complex (RISC) pathway. iRNA directs the sequence-specific degradation of mRNA through a process as RNA interference (RNAi). The iRNA modulates, *e.g.*, inhibits, the expression of HAO1 in a cell, *e.g.*, a cell within a subject, such as a mammalian subject.

In one embodiment, an RNAi agent of the invention includes a single stranded RNA that interacts with a target RNA sequence, *e.g.*, a HAO1 target mRNA sequence, to direct the cleavage of the target RNA. Without wishing to be bound by theory, it is believed that long double stranded RNA introduced into cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp *et al.* (2001) *Genes Dev.* 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, *et al.*, (2001) *Nature* 409:363). The siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, *et al.*, (2001) *Cell* 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce silencing (Elbashir, *et al.*, (2001) *Genes Dev.* 15:188). Thus, in one aspect the invention relates to a single stranded RNA (siRNA) generated within a cell and which promotes the formation of a RISC complex to effect silencing of the target gene, *i.e.*, a HAO1 gene. Accordingly, the term "siRNA" is also used herein to refer to an RNAi as described above.

In another embodiment, the RNAi agent may be a single-stranded siRNA that is introduced into a cell or organism to inhibit a target mRNA. Single-stranded RNAi agents bind to the RISC endonuclease Argonaute 2, which then cleaves the target mRNA. The

single-stranded siRNAs are generally 15-30 nucleotides and are chemically modified. The design and testing of single-stranded 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 may be used as a single-stranded siRNA as described herein or as chemically modified by the methods described in Lima *et al.*, (2012) *Cell* 150;:883-894.

In yet another embodiment, the present invention provides single-stranded antisense oligonucleotide molecules targeting HAO1. A "single-stranded antisense oligonucleotide molecule" is complementary to a sequence within the target mRNA (*i.e.*, HAO1). Single-stranded antisense oligonucleotide molecules can inhibit translation in a stoichiometric manner by base pairing to the mRNA and physically obstructing the translation machinery, see Dias, N. *et al.*, (2002) *Mol Cancer Ther* 1:347-355. Alternatively, the single-stranded antisense oligonucleotide molecules inhibit a target mRNA by hydridizing to the target and cleaving the target through an RNaseH cleavage event. The single-stranded antisense oligonucleotide molecule may be about 10 to about 30 nucleotides in length and have a sequence that is complementary to a target sequence. For example, the single-stranded antisense oligonucleotide molecule may comprise a sequence that is at least about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from any one of the antisense nucleotide sequences described herein, *e.g.*, the sequences provided in any one of Tables 1 or 2, or bind any of the target sites described herein. The single-stranded antisense oligonucleotide molecules may comprise modified RNA, DNA, or a combination thereof.

In another embodiment, an "iRNA" for use in the compositions, uses, and methods of the invention is a double-stranded RNA and is referred to herein as a "double stranded RNAi agent," "double-stranded RNA (dsRNA) molecule," "dsRNA agent," or "dsRNA". The term "dsRNA", refers to a complex of ribonucleic acid molecules, having a duplex structure comprising two anti-parallel and substantially complementary nucleic acid strands, referred to as having "sense" and "antisense" orientations with respect to a target RNA, *i.e.*, a HAO1 gene. In some embodiments of the invention, a double-stranded RNA (dsRNA) triggers the degradation of a target RNA, *e.g.*, an mRNA, through a post-transcriptional gene-silencing mechanism referred to herein as RNA interference or RNAi.

In general, the majority of nucleotides of each strand of a dsRNA molecule are ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, *e.g.*, a deoxyribonucleotide and/or a modified nucleotide. In

addition, as used in this specification, an "RNAi agent" may include ribonucleotides with chemical modifications; an RNAi agent may include substantial modifications at multiple nucleotides. Such modifications may include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a siRNA type molecule, are encompassed by "RNAi agent" for the purposes of this specification and claims.

The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting RNA chain is referred to as a "hairpin loop." Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting structure is referred to as a "linker." The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the dsRNA minus any overhangs that are present in the duplex. In addition to the duplex structure, an RNAi agent may comprise one or more nucleotide overhangs.

In one embodiment, an RNAi agent of the invention is a dsRNA of 24-30 nucleotides that interacts with a target RNA sequence, e.g., a HAO1 target mRNA sequence, to direct the cleavage of the target RNA. Without wishing to be bound by theory, long double stranded RNA introduced into cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp et al. (2001) Genes Dev. 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, et al., (2001) Nature 409:363). The siRNAs are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, et al., (2001) Cell 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce silencing (Elbashir, et al., (2001) Genes Dev. 15:188).

As used herein, a "nucleotide overhang" refers to the unpaired nucleotide or nucleotides that protrude from the duplex structure of an RNAi agent when a 3'-end of one strand of the RNAi agent extends beyond the 5'-end of the other strand, or vice versa. "Blunt" or "blunt end" means that there are no unpaired nucleotides at that end of the double

stranded RNAi agent, i.e., no nucleotide overhang. A "blunt ended" RNAi agent is a dsRNA that is double-stranded over its entire length, i.e., no nucleotide overhang at either end of the molecule. The RNAi agents of the invention include RNAi agents with nucleotide overhangs at one end (*i.e.*, agents with one overhang and one blunt end) or with nucleotide overhangs at both ends.

The term "antisense strand" refers to the strand of a double stranded RNAi agent which includes a region that is substantially complementary to a target sequence (*e.g.*, a human HAO1 mRNA). As used herein, the term "region complementary to part of an mRNA encoding HAO1" refers to a region on the antisense strand that is substantially complementary to part of a HAO1 mRNA sequence. Where the region of complementarity is not fully complementary to the target sequence, the mismatches are most tolerated in the terminal regions and, if present, are generally in a terminal region or regions, *e.g.*, within 6, 5, 4, 3, or 2 nucleotides of the 5' and/or 3' terminus.

The term "sense strand," as used herein, refers to the strand of a dsRNA that includes a region that is substantially complementary to a region of the antisense strand.

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

As used herein, and unless otherwise indicated, the term "complementary," when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. 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. For example, a

complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, *e.g.*, RNAi. 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.

Sequences can be "fully complementary" with respect to each when there is base-pairing of the nucleotides of the first nucleotide sequence with the nucleotides of the second nucleotide sequence over the entire length of the first and second nucleotide sequences. 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 4, 3 or 2 mismatched base pairs upon hybridization, while retaining the ability to hybridize under the conditions most relevant to their ultimate application. 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 not limited to, G:U Wobble or Hoogstein 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 a dsRNA 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 HAO1) including a 5' UTR, an open reading frame (ORF), or a 3' UTR. For example, a polynucleotide is

complementary to at least a part of a HAO1 mRNA if the sequence is substantially complementary to a non-interrupted portion of an mRNA encoding HAO1.

The term "inhibiting," as used herein, is used interchangeably with "reducing," "silencing," "downregulating," "suppressing" and other similar terms, and includes any level of inhibition.

The phrase "inhibiting expression of a HAO1," as used herein, includes inhibition of expression of any HAO1 gene (such as, *e.g.*, a mouse HAO1 gene, a rat HAO1 gene, a monkey HAO1 gene, or a human HAO1 gene) as well as variants, (*e.g.*, naturally occurring variants), or mutants of a HAO1 gene. Thus, the HAO1 gene may be a wild-type HAO1 gene, a mutant HAO1 gene, or a transgenic HAO1 gene in the context of a genetically manipulated cell, group of cells, or organism.

"Inhibiting expression of a HAO1 gene" includes any level of inhibition of a HAO1 gene, *e.g.*, at least partial suppression of the expression of a HAO1 gene, such as an inhibition of at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%,at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%.

The expression of a HAO1 gene may be assessed based on the level of any variable associated with HAO1 gene expression, *e.g.*, HAO1 mRNA level or HAO1 protein level, in, e.g., tissues and/or urinary oxalate levels. Inhibition may be assessed by a decrease in an absolute or relative level of one or more of these variables compared with a control level. The control level may be any type of control level that is utilized in the art, *e.g.*, a pre-dose baseline level, or a level determined from a similar subject, cell, or sample that is untreated or treated with a control (such as, *e.g.*, buffer only control or inactive agent control).

The phrase "contacting a cell with a double stranded RNAi agent," as used herein, includes contacting a cell by any possible means. Contacting a cell with a double stranded RNAi agent includes contacting a cell *in vitro* with the RNAi agent or contacting a cell *in vivo* with the RNAi agent. The contacting may be done directly or indirectly. Thus, for example, the RNAi agent may be put into physical contact with the cell by the individual

performing the method, or alternatively, the RNAi agent may be put into a situation that will permit or cause it to subsequently come into contact with the cell.

Contacting a cell *in vitro* may be done, for example, by incubating the cell with the RNAi agent. Contacting a cell *in vivo* may be done, for example, by injecting the RNAi agent into or near the tissue where the cell is located, or by injecting the RNAi agent into another area, the bloodstream or the subcutaneous space, such that the agent will subsequently reach the tissue where the cell to be contacted is located. For example, the RNAi agent may contain and/or be coupled to a ligand, *e.g.*, a GalNAc3 ligand, that directs the RNAi agent to a site of interest, e.g., the liver. Combinations of *in vitro* and *in vivo* methods of contacting are also possible. In connection with the methods of the invention, a cell might also be contacted *in vitro* with an RNAi agent and subsequently transplanted into a subject.

As used herein, a "subject" includes a human or non-human animal, preferably a vertebrate, and more preferably a mammal. A subject may include a transgenic organism. Most preferably, the subject is a human, such as a human suffering from or predisposed to developing a HAO1 associated disorder.

A "patient" or "subject," as used herein, is intended to include either a human or non-human animal, preferably a mammal, *e.g.*, human or a monkey. Most preferably, the subject or patient is a human.

A "HAO1 associated disorder", as used herein, is intended to include any disorder that can be treated or prevented, or the symptoms of which can be alleviated, by inhibiting the expression of HAO1. Examples include but are not limited to Primary Hyperoxaluria 1 (PH1).

"Therapeutically effective amount," as used herein, is intended to include the amount of an RNAi agent that, when administered to a patient for treating a HAO1 associated disease, is sufficient to effect treatment of the disease (*e.g.*, by diminishing, ameliorating or maintaining the existing disease or one or more symptoms of disease). The "therapeutically effective amount" may vary depending on the RNAi agent, how the agent is administered, the disease and its severity and the history, age, weight, family history, genetic makeup, stage of pathological processes mediated by HAO1 expression, the types of preceding or concomitant treatments, if any, and other individual characteristics of the patient to be treated.

"Prophylactically effective amount," as used herein, is intended to include the amount of an RNAi agent that, when administered to a subject who does not yet experience or display symptoms of a HAO1-associated disease, but who may be predisposed to the disease, is sufficient to prevent or ameliorate the disease or one or more symptoms of the disease. Ameliorating the disease includes slowing the course of the disease or reducing the severity of later-developing disease. The "prophylactically effective amount" may vary depending on the RNAi agent, how the agent is administered, the degree of risk of disease, and the history, age, weight, family history, genetic makeup, the types of preceding or concomitant treatments, if any, and other individual characteristics of the patient to be treated.

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

The term "sample," as used herein, includes a collection of similar fluids, cells, or tissues isolated from a subject, as well as fluids, cells, or tissues present within a subject. Examples of biological fluids include blood, serum and serosal fluids, plasma, cerebrospinal fluid, ocular fluids, lymph, urine, saliva, and the like. Tissue samples may include samples from tissues, organs or localized regions. For example, samples may be derived from particular organs, parts of organs, or fluids or cells within those organs. In certain embodiments, samples may be derived from the liver (*e.g.*, whole liver or certain segments of liver or certain types of cells in the liver, such as, *e.g.*, hepatocytes). In some embodiments, a "sample derived from a subject" refers to blood or plasma drawn from the subject. In further embodiments, a "sample derived from a subject" refers to liver tissue (or subcomponents thereof) derived from the subject.

II. dsRNA iRNA agents of the Invention

Described herein are double-stranded RNAi agents which inhibit the expression of a HAO1 gene in a cell, such as a cell within a subject, *e.g.*, a mammal, such as a human having a HAO1 associated disorder, and uses of such double-stranded RNAi agents.

Accordingly, the invention provides double-stranded RNAi agents with chemical modifications capable of inhibiting the expression of a target gene (*i.e.*, a HAO1 gene) *in vivo*.

As described in more detail below, in certain aspects of the invention, substantially all of the nucleotides of an iRNA of the invention are modified. In other embodiments of the invention, all of the nucleotides of an iRNA of the invention are modified. iRNAs of the invention in which "substantially all of the nucleotides are modified" are largely but not wholly modified and can include not more than 5, 4, 3, 2, or 1 unmodified nucleotides.

The RNAi agent comprises a sense strand and an antisense strand. Each strand of the RNAi agent may range from 12-30 nucleotides in length. For example, each strand may be between 14-30 nucleotides in length, 17-30 nucleotides in length, 19-30 nucleotides in length, 25-30 nucleotides in length, 27-30 nucleotides in length, 17-23 nucleotides in length, 17-21 nucleotides in length, 17-19 nucleotides in length, 19-25 nucleotides in length, 19-23 nucleotides in length, 19-21 nucleotides in length, 21-25 nucleotides in length, or 21-23 nucleotides in length.

Each strand can be 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24,25, 26, 27, 28, 29, or 30 nucleotides in length. Each strand of the RNAi agent can be the same length or can be different lengths.

The sense strand and antisense strand typically form a duplex double stranded RNA ("dsRNA"), also referred to herein as an "RNAi agent." The duplex region of an RNAi agent may be 12-30 nucleotide pairs in length. For example, the duplex region can be between 14-30 nucleotide pairs in length, 17-30 nucleotide pairs in length, 27-30 nucleotide pairs in length, 17 - 23 nucleotide pairs in length, 17-21 nucleotide pairs in length, 17-19 nucleotide pairs in length, 19-25 nucleotide pairs in length, 19-23 nucleotide pairs in length, 19- 21 nucleotide pairs in length, 21-25 nucleotide pairs in length, or 21-23 nucleotide pairs in length. In another example, the duplex region is selected from 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, and 27 nucleotide pairs in length.

In one embodiment, the RNAi agent may contain one or more overhang regions and/or capping groups at the 3'-end, 5'-end, or both ends of one or both strands. The overhang can be 1-6 nucleotides in length, for instance 2-6 nucleotides in length, 1-5 nucleotides in length, 2-5 nucleotides in length, 1-4 nucleotides in length, 2-4 nucleotides in length, 1-3 nucleotides in length, 2-3 nucleotides in length, or 1-2 nucleotides in length. The

overhangs can be the result of one strand being longer than the other, or the result of two strands of the same length being staggered. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence. The first and second strands can also be joined, *e.g.*, by additional bases to form a hairpin, or by other non-base linkers.

In one embodiment, the nucleotides in the overhang region of the RNAi agent can each independently be a modified or unmodified nucleotide including, but not limited to 2'-sugar modified, such as, 2-F, 2'-O-methyl, thymidine (T), 2`-O-methoxyethyl-5-methyluridine (Teo), 2`-O-methoxyethyladenosine (Aeo), 2`-O-methoxyethyl-5-methylcytidine (m5Ceo), and any combinations thereof. For example, TT can be an overhang sequence for either end on either strand. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence.

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

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

Synthesis and modifications

Any of the nucleic acids, e.g., RNAi, featured in the invention can 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, end modifications, *e.g.*, 5'-end modifications (phosphorylation, conjugation, inverted linkages) or 3'-end modifications (conjugation, DNA nucleotides, inverted linkages, *etc.*); base modifications, *e.g.*, replacement with stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, removal of bases (abasic nucleotides), or conjugated bases; sugar modifications (*e.g.*, at the 2'-position or 4'-position) or replacement of the sugar; and/or backbone modifications, including modification or replacement of the phosphodiester linkages. Specific examples of iRNA compounds useful in the embodiments described herein include, but are not limited to RNAs containing modified backbones or no natural internucleoside linkages. RNAs having modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In some embodiments, a modified iRNA 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, the entire contents of each of which are hereby incorporated herein by reference.

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

In other embodiments, suitable RNA mimetics are contemplated for use in iRNAs, in which both the sugar and the internucleoside linkage, *i.e.*, the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an RNA mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar backbone of an RNA is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly 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, the entire contents of each of which are hereby incorporated herein by reference. Additional PNA compounds suitable for use in the iRNAs of the invention are described in, for example, in Nielsen *et al.*, *Science*, 1991, 254, 1497-1500.

Some embodiments featured in the invention 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--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 can 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 can be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Exemplary suitable modifications include O[$(CH_2)_n$O]$_m$$CH_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)_n$ON[$(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$(CH_2)_2$ON$(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples herein below, 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$(CH_2)_2$.

Other modifications include 2'-methoxy (2'-OCH_3), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications can 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 can also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative U.S. patents that teach the preparation of such modified sugar structures

include, but are not limited to, U.S. Pat. Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, certain of which are commonly owned with the instant application,. The entire contents of each of the foregoing are hereby incorporated herein by reference.

An iRNA can also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as deoxy-thymine (dT), 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. Pat. No. 3,687,808, those disclosed in Modified Nucleosides in Biochemistry, Biotechnology and Medicine, Herdewijn, P. ed. Wiley-VCH, 2008; those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. L, ed. John Wiley & Sons, 1990, these disclosed by Englisch *et al.*, 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 invention. 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 Nos. 3,687,808, 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,681,941; 5,750,692; 6,015,886; 6,147,200; 6,166,197; 6,222,025; 6,235,887; 6,380,368; 6,528,640; 6,639,062; 6,617,438; 7,045,610; 7,427,672; and 7,495,088, the entire contents of each of which are hereby incorporated herein by reference.

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

Representative U.S. Patents that teach the preparation of locked nucleic acid nucleotides 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; and 7,399,845, the entire contents of each of which are hereby incorporated herein by reference.

Potentially stabilizing modifications to the ends of RNA molecules can include N-(acetylaminocaproyl)-4-hydroxyprolinol (Hyp-C6-NHAc), N-(caproyl-4-hydroxyprolinol (Hyp-C6), N-(acetyl-4-hydroxyprolinol (Hyp-NHAc), thymidine-2'-0-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.

Modified iRNAs Comprising Motifs of the Invention

In certain aspects of the invention, the double-stranded RNAi agents of the invention include agents with chemical modifications as disclosed, for example, in U.S. Provisional Application No. 61/561,710, filed on November 18, 2011, or in PCT/US2012/065691, filed on November 16, 2012, and published as WO2013075035 A1, the entire contents of each of which are incorporated herein by reference.

As shown herein and in Provisional Application No. 61/561,710, a superior result may be obtained by introducing one or more motifs of three identical modifications on three consecutive nucleotides into a sense strand and/or antisense strand of a 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 and/or antisense strand. The RNAi agent may be optionally conjugated with a GalNAc derivative ligand, for instance on the sense strand. The resulting RNAi agents present superior gene silencing activity.

More specifically, it has been surprisingly discovered that when the sense strand and antisense strand of the double-stranded RNAi agent are modified to have one or more motifs of three identical modifications on three consecutive nucleotides at or near the cleavage site of at least one strand of an RNAi agent, the gene silencing activity of the RNAi agent was superiorly enhanced.

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

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

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

In one embodiment, the RNAi agent comprises a 21 nucleotide sense strand and a 23 nucleotide antisense strand, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 9, 10, 11 from the 5'end; the antisense strand contains at least one motif of three 2'-O-methyl modifications on three

consecutive nucleotides at positions 11, 12, 13 from the 5'end, wherein one end of the RNAi agent is blunt, while the other end comprises a 2 nucleotide overhang. Preferably, the 2 nucleotide overhang is at the 3'-end of the antisense strand. When the 2 nucleotide overhang is at the 3'-end of the antisense strand, there may be two phosphorothioate internucleotide linkages between the terminal three nucleotides, wherein two of the three nucleotides are the overhang nucleotides, and the third nucleotide is a paired nucleotide next to the overhang nucleotide. In one embodiment, the RNAi agent additionally has two phosphorothioate internucleotide linkages between the terminal three nucleotides at both the 5'-end of the sense strand and at the 5'-end of the antisense strand. In one embodiment, every nucleotide in the sense strand and the antisense strand of the RNAi agent, including the nucleotides that are part of the motifs are modified nucleotides. In one embodiment each residue is independently modified with a 2'-O-methyl or 3'-fluoro, *e.g.*, in an alternating motif. Optionally, the RNAi agent further comprises a ligand (preferably $GalNAc_3$).

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

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

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

For an RNAi agent having a duplex region of 17-23 nucleotides in length, the cleavage site of the antisense strand is typically around the 10, 11 and 12 positions from the 5'-end. Thus the motifs of three identical modifications may occur at the 9, 10, 11 positions; 10, 11, 12 positions; 11, 12, 13 positions; 12, 13, 14 positions; or 13, 14, 15 positions of the antisense strand, the count starting from the 1st nucleotide from the 5'-end of the antisense strand, or, the count starting from the 1st paired nucleotide within the duplex region from the 5'- end of the antisense strand. The cleavage site in the antisense strand may also change according to the length of the duplex region of the RNAi from the 5'-end.

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

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

Like the sense strand, the antisense strand of the RNAi agent may contain more than one motifs of three identical modifications on three consecutive nucleotides, with at least one of the motifs occurring at or near the cleavage site of the strand. This antisense strand may

also contain one or more wing modifications in an alignment similar to the wing modifications that may be present on the sense strand.

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

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

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

When the sense strand and the antisense strand of the RNAi agent each contain at least two wing modifications, the sense strand and the antisense strand can be so aligned that two modifications each from one strand fall on one end of the duplex region, having an overlap of one, two or three nucleotides; two modifications each from one strand fall on the other end of the duplex region, having an overlap of one, two or three nucleotides; two modifications one strand fall on each side of the lead motif, having an overlap of one, two or three nucleotides in the duplex region.

In one embodiment, every nucleotide in the sense strand and antisense strand of the RNAi agent, including the nucleotides that are part of the motifs, 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 and/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 a RNA or may only occur in a single strand region of a RNA. For example, 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. For example, 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 one embodiment, 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, 2'-hydroxyl, or 2'-fluoro. The strands can contain more than one modification. In one embodiment, each residue of the sense strand and antisense strand is independently modified with 2'- O-methyl or 2'-fluoro.

At least two different modifications are typically present on the sense strand and antisense strand. Those two modifications may be the 2'- O-methyl or 2'-fluoro modifications, or others.

In one embodiment, the N_a and/or N_b comprise modifications of an alternating pattern. The term "alternating motif" 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 one embodiment, the RNAi agent of the invention 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 5'-3'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 5'-3' 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.

In one embodiment, the RNAi agent comprises the pattern of the alternating motif of 2'-O-methyl modification and 2'-F modification on the sense strand initially has a shift relative to the pattern of the alternating motif of 2'-O-methyl modification and 2'-F modification on the antisense strand initially, *i.e.*, the 2'-O-methyl modified nucleotide on the sense strand base pairs with a 2'-F modified nucleotide on the antisense strand and vice versa. The 1 position of the sense strand may start with the 2'-F modification, and the 1 position of the antisense strand may start with the 2'- O-methyl modification.

The introduction of one or more motifs of three identical modifications on three consecutive nucleotides to the sense strand and/or antisense strand interrupts the initial modification pattern present in the sense strand and/or antisense strand. This interruption of the modification pattern of the sense and/or antisense strand by introducing one or more

motifs of three identical modifications on three consecutive nucleotides to the sense and/or antisense strand surprisingly enhances the gene silencing activity to the target gene.

In one embodiment, when the motif of three identical modifications on three consecutive nucleotides is introduced to any of the strands, the modification of the nucleotide next to the motif is a different modification than the modification of the motif. For example, the portion of the sequence containing the motif is "...N_aYYYN_b...," where "Y" represents the modification of the motif of three identical modifications on three consecutive nucleotide, and "N_a" and "N_b" represent a modification to the nucleotide next to the motif "YYY" that is different than the modification of Y, and where N_a and N_b can be the same or different modifications. Alternatively, N_a and/or N_b may be present or absent when there is a wing modification present.

The RNAi agent 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 strands in any position of the strand. For instance, the internucleotide linkage modification may occur on every nucleotide on the sense strand and/or antisense strand; each internucleotide linkage modification may occur in an alternating pattern on the sense strand and/or antisense strand; or the sense strand or antisense strand may contain 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 one embodiment, the RNAi comprises a phosphorothioate or methylphosphonate internucleotide linkage modification in the overhang region. For example, the overhang region may contain 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 the 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. These terminal three nucleotides may be at the 3'-end of the antisense strand, the 3'-end of the sense strand, the 5'-end of the antisense strand, and/or the 5'end of the antisense strand.

In one embodiment, the 2 nucleotide overhang is at the 3'-end of the antisense strand, and there are two phosphorothioate internucleotide linkages between the terminal three nucleotides, wherein two of the three nucleotides are the overhang nucleotides, and the third nucleotide is a paired nucleotide next to the overhang nucleotide. Optionally, the RNAi agent may additionally have two phosphorothioate internucleotide linkages between the terminal three nucleotides at both the 5'-end of the sense strand and at the 5'-end of the antisense strand.

In one embodiment, the RNAi agent comprises mismatch(es) with the target, within the duplex, or combinations thereof. The mismatch may occur in the overhang region or the duplex region. The base pair may be ranked on the basis of their propensity to promote dissociation or melting (*e.g.*, on the free energy of association or dissociation of a particular pairing, the simplest approach is to examine the pairs on an individual pair basis, though next neighbor or 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 one embodiment, the RNAi agent comprises at least one of the first 1, 2, 3, 4, or 5 base pairs within the duplex regions from the 5'- end of the antisense strand independently selected from the group of: A:U, G:U, I:C, and mismatched pairs, *e.g.*, non-canonical or other than canonical pairings or pairings which include a universal base, to promote the dissociation of the antisense strand at the 5'-end of the duplex.

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

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

5' n_p-N_a-(X X X)$_i$-N_b-Y Y Y -N_b-(Z Z Z)$_j$-N_a-n_q 3' (I)

wherein:

i and j are each independently 0 or 1;

p and q are each independently 0-6;

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

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

each n_p and n_q independently represent an overhang nucleotide;

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

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

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

In one embodiment, the YYY motif occurs at or near the cleavage site of the sense strand. For example, when the 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 one embodiment, i is 1 and j is 0, or i is 0 and j is 1, or both i and j are 1. The sense strand can therefore be represented by the following formulas:

5' n_p-N_a-YYY-N_b-ZZZ-N_a-n_q 3' (Ib);

5' n_p-N_a-XXX-N_b-YYY-N_a-n_q 3' (Ic); or

5' n_p-N_a-XXX-N_b-YYY-N_b-ZZZ-N_a-n_q 3' (Id).

When the sense strand is represented by formula (Ib), N_b represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Each

N_a independently can represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the sense strand is represented as formula (Ic), N_b 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 can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.

When the sense strand is represented as formula (Id), each N_b independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Preferably, N_b is 0, 1, 2, 3, 4, 5 or 6 Each N_a 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 one embodiment, the antisense strand sequence of the RNAi may be represented by formula (II):

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' (II)

wherein:

k and l are each independently 0 or 1;

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

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

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

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

wherein 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 motif of three identical modifications on three consecutive nucleotides.

In one embodiment, the N_a' and/or N_b' comprise modifications of alternating pattern.

The Y′Y′Y′ motif occurs at or near the cleavage site of the antisense strand. For example, when the RNAi agent has a duplex region of 17-23nucleotidein 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. Preferably, the Y′Y′Y′ motif occurs at positions 11, 12, 13.

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

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

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

5' $n_{q'}$-N_a′-Z′Z′Z′-N_b′-Y′Y′Y′-N_a′-$n_{p'}$ 3' (IIb);

5' $n_{q'}$-N_a′-Y′Y′Y′-N_b′-X′X′X′-$n_{p'}$ 3' (IIc); or

5' $n_{q'}$-N_a′- Z′Z′Z′-N_b′-Y′Y′Y′-N_b′- X′X′X′-N_a′-$n_{p'}$ 3' (IId).

When the antisense strand is represented by formula (IIb), N_b 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.

When the antisense strand is represented as formula (IIc), N_b' 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.

When the antisense strand is represented as formula (IId), 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' n_p'-N_a'-Y'Y'Y'- N_a'-n_q' 3' (Ia).

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

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

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

In one embodiment, the sense strand of the RNAi agent may contain YYY motif occurring at 9, 10 and 11 positions of the strand when the duplex region is 21 nt, the count starting from the 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 one embodiment the antisense strand may contain Y'Y'Y' motif occurring at positions 11, 12, 13 of the strand, the count starting from the 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 (IIa), (IIb), (IIc), and (IId), respectively.

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

sense: 5' n_p-N_a-(X X X)$_i$-N_b- Y Y Y -N_b-(Z Z Z)$_j$-N_a-n_q 3'

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

(III)

wherein:

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

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

each N_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 modifications on three consecutive nucleotides.

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

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

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'

(IIIa)

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

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

(IIIb)

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

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

(IIIc)

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

(IIId)

When the RNAi agent is represented by formula (IIIa), 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 (IIIb), 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 (IIIc), each N_b, N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0modified 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 (IIId), each N_b, N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0modified 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 (III), (IIIa), (IIIb), (IIIc), and (IIId) may be the same or different from each other.

When the RNAi agent is represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId), 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 (IIIb) or (IIId), 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 (IIIc) or (IIId), 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 one embodiment, 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 one embodiment, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications. In another embodiment, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications and $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide a via phosphorothioate linkage. In yet another embodiment, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications , $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide via phosphorothioate linkage, and the sense strand is conjugated to one or more GalNAc derivatives attached through a bivalent or trivalent branched linker. In another embodiment, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications , $n_p' > 0$ and at least one n_p' 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 GalNAc derivatives attached through a bivalent or trivalent branched linker.

In one embodiment, when the RNAi agent is represented by formula (IIIa), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications , $n_p' > 0$ and at least one n_p' 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 GalNAc derivatives attached through a bivalent or trivalent branched linker.

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

In one embodiment, the RNAi agent is a multimer containing three, four, five, six or more duplexes represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId), wherein the duplexes are connected by a linker. The linker can be cleavable or non-cleavable.

Optionally, the multimer further comprises a ligand. Each of the duplexes can target the same gene or two different genes; or each of the duplexes can target same gene at two different target sites.

In one embodiment, two RNAi agents represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId) 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 invention. Such publications include WO2007/091269, US Patent No. 7858769, WO2010/141511, WO2007/117686, WO2009/014887 and WO2011/031520 the entire contents of each of which are hereby incorporated herein by reference.

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 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 invention is an agent selected from the group of agents listed in any one of Tables 1 and 2. In one embodiment, when the agent is an agent listed in Table 1, the agent may lack a terminal dT.

The present invention further includes double-stranded RNAi agents comprising any one of the sequences listed in any one of Tables 1 or 2 which comprise a 5' phosphate or phosphate mimetic on the antisense strand (see, *e.g.*, PCT Publication No. WO 2011005860). Further, the present invention includes double-stranded RNAi agents comprising any one of the sequences listed in any one of Tables 1 or 2 which include a 2'fluoro group in place of a 2'-OMe group at the 5'end of the sense strand.

Additional motifs

In certain aspects, the double-stranded RNAi agents described herein comprises a sense strand and an antisense strand wherein said sense strand and an antisense strand comprise less than eleven, ten, nine, eight, seven, six, or five 2'-deoxyflouro.

In certain aspects, the double-stranded RNAi agents described herein comprises a sense strand and an antisense strand, wherein said sense strand and an antisense strand comprise less than ten, nine, eight, seven, six, five, four phosphorothioate internucleotide linkages.

In certain aspects, the double-stranded RNAi agents described herein comprises a sense strand and an antisense strand, wherein said sense strand and an antisense strand

comprise less than ten 2'-deoxyflouro and less than six phosphorothioate internucleotide linkages.

In certain aspects, the double-stranded RNAi agents described herein comprises a sense strand and an antisense strand, wherein said sense strand and an antisense strand comprise less than eight 2'-deoxyflouro and less than six phosphorothioate internucleotide linkages.

In certain aspects, the double-stranded RNAi agents described herein comprises a sense strand and an antisense strand, wherein said sense strand and an antisense strand comprise less than nine 2'-deoxyflouro and less than six phosphorothioate internucleotide linkages.

Ligands

The double-stranded RNAi agents of the invention may optionally be conjugated to one or more ligands. 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 some embodiments, the ligand is conjugated to the 3'-end of the sense strand. In one embodiment, the ligand is a GalNAc ligand. In particularly some embodiments, the ligand is $GalNAc_3$. The ligands are coupled, preferably covalently, either directly or indirectly *via* an intervening tether.

In some embodiments, a ligand alters the distribution, targeting or lifetime of the molecule 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, receptor *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. Ligands providing enhanced affinity for a selected target are also termed targeting ligands.

Some ligands can have endosomolytic properties. The endosomolytic ligands promote the lysis of the endosome and/or transport of the composition of the invention, or its components, from the endosome to the cytoplasm of the cell. The endosomolytic ligand may be a polyanionic peptide or peptidomimetic which shows pH-dependent membrane activity and fusogenicity. In one embodiment, the endosomolytic ligand assumes its active conformation at endosomal pH. The "active" conformation is that conformation in which the endosomolytic ligand promotes lysis of the endosome and/or transport of the composition of the invention, or its components, from the endosome to the cytoplasm of the cell. Exemplary

endosomolytic ligands include the GALA peptide (Subbarao *et al.*, *Biochemistry*, 1987, 26: 2964-2972), the EALA peptide (Vogel *et al.*, *J. Am. Chem. Soc.*, 1996, 118: 1581-1586), and their derivatives (Turk *et al.*, *Biochem. Biophys. Acta*, 2002, 1559: 56-68). In one embodiment, the endosomolytic component may contain a chemical group (*e.g.*, an amino acid) which will undergo a change in charge or protonation in response to a change in pH. The endosomolytic component may be linear or branched.

Ligands can improve transport, hybridization, and specificity properties and may also improve nuclease resistance of the resultant natural or modified oligoribonucleotide, or a polymeric molecule comprising any combination of monomers described herein and/or natural or modified ribonucleotides.

Ligands in general can include therapeutic modifiers, *e.g.*, for enhancing uptake; diagnostic compounds or reporter groups *e.g.*, for monitoring distribution; cross-linking agents; and nuclease-resistance conferring moieties. General examples include lipids, steroids, vitamins, sugars, proteins, peptides, polyamines, and peptide mimics.

Ligands can include a naturally occurring substance, such as a protein (*e.g.*, human serum albumin (HSA), low-density lipoprotein (LDL), high-density lipoprotein (HDL), or globulin); a 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, an oligonucleotide (*e.g.*, an aptamer). 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. Example of polyamines include: polyethylenimine, polylysine (PLL), spermine, spermidine, polyamine, pseudopeptide-polyamine, peptidomimetic polyamine, dendrimer polyamine, arginine, amidine, protamine, cationic lipid, cationic porphyrin, quaternary salt of a polyamine, or an alpha 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-gulucosamine multivalent mannose, multivalent fucose, glycosylated polyaminoacids, multivalent galactose, transferrin, bisphosphonate, polyglutamate, polyaspartate, a lipid, cholesterol, a steroid, bile acid, folate, vitamin B12, biotin, an RGD peptide, an RGD peptide mimetic or an aptamer.

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 or a chelator (*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 a cancer cell, endothelial cell, or bone cell. Ligands may also include hormones and hormone receptors. They can also include non-peptidic species, such as lipids, lectins, carbohydrates, vitamins, cofactors, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-gulucosamine multivalent mannose, multivalent fucose, or aptamers. 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.

The ligand can increase the uptake of the oligonucleotide into the cell by, for example, activating an inflammatory response. Exemplary ligands that would have such an effect include tumor necrosis factor alpha (TNFalpha), interleukin-1 beta, or gamma interferon.

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

A lipid based ligand can be used to modulate, *e.g.*, control 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 one embodiment, the lipid based ligand binds HSA. Preferably, it binds HSA with a sufficient affinity such that the conjugate will be preferably distributed to a non-kidney tissue. In one embodiment, the affinity is such that that the HSA-ligand binding can be reversed. In another embodiment, the lipid based ligand binds HSA weakly or not at all, such that the conjugate will be preferably distributed to the kidney. 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 B vitamins, *e.g.*, folic acid, B12, riboflavin, biotin, pyridoxal or other vitamins or nutrients taken up by cancer cells. Also included are HAS, low density lipoprotein (LDL) and high-density lipoprotein (HDL).

In another aspect, the ligand is a cell-permeation agent, preferably a helical cell-permeation agent. Preferably, 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 preferably an alpha-helical agent, which preferably has 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 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). Preferably the peptide or peptidomimetic tethered to an iRNA 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 moiety can be used to target 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 iRNA 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). Preferably, the RGD peptide will facilitate targeting of an iRNA agent to the kidney. The RGD peptide can be linear or cyclic, and can be modified, *e.g.*, glycosylated or methylated to facilitate targeting to specific tissues. For example, a glycosylated RGD peptide can deliver an iRNA agent to a tumor cell expressing $\alpha_v\beta_3$ (Haubner *et al.*, *Jour. Nucl. Med.*, 42:326-336, 2001). Peptides that target markers enriched in proliferating cells can be used. For example, RGD containing peptides and peptidomimetics can target cancer cells, in particular cells that exhibit an integrin. Thus, one could use RGD peptides, cyclic peptides containing RGD, RGD peptides that include D-amino acids, as well as synthetic RGD mimics. In addition to RGD, one can use other moieties that target the integrin ligand. Generally, such ligands can be used to control proliferating cells and angiogenesis. Some conjugates of this type of ligand target PECAM-1, VEGF, or other cancer gene, *e.g.*, a cancer gene described herein.

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., Nucl. Acids Res. 31:2717-2724, 2003).

In one embodiment, a targeting peptide can be an amphipathic α-helical peptide. Exemplary amphipathic α-helical peptides include, but are not limited to, cecropins, lycotoxins, paradaxins, buforin, CPF, bombinin-like peptide (BLP), cathelicidins, ceratotoxins, S. clava peptides, hagfish intestinal antimicrobial peptides (HFIAPs), magainines, brevinins-2, dermaseptins, melittins, pleurocidin, H_2A peptides, Xenopus peptides, esculentinis-1, and caerins. A number of factors will preferably be considered to maintain the integrity of helix stability. For example, a maximum number of helix stabilization residues will be utilized (*e.g.*, leu, ala, or lys), and a minimum number helix destabilization residues will be utilized (*e.g.*, proline, or cyclic monomeric units. The capping residue will be considered (for example Gly is an exemplary N-capping residue and/or C-terminal amidation can be used to provide an extra H-bond to stabilize the helix.

Formation of salt bridges between residues with opposite charges, separated by i ± 3, or i ± 4 positions can provide stability. For example, cationic residues such as lysine, arginine, homo-arginine, ornithine or histidine can form salt bridges with the anionic residues glutamate or aspartate.

Peptide and peptidomimetic ligands include those having naturally occurring or modified peptides, *e.g.*, D or L peptides; α, β, or γ peptides; N-methyl peptides; azapeptides; peptides having one or more amide, *i.e.*, peptide, linkages replaced with one or more urea, thiourea, carbamate, or sulfonyl urea linkages; or cyclic peptides.

The targeting ligand can be any ligand that is capable of targeting a specific receptor. Examples are: folate, GalNAc, galactose, mannose, mannose-6P, clusters of sugars such as GalNAc cluster, mannose cluster, galactose cluster, or an aptamer. A cluster is a combination of two or more sugar units. The targeting ligands also include integrin receptor ligands, Chemokine receptor ligands, transferrin, biotin, serotonin receptor ligands, PSMA, endothelin, GCPII, somatostatin, LDL and HDL ligands. The ligands can also be based on nucleic acid, *e.g.*, an aptamer. The aptamer can be unmodified or have any combination of modifications disclosed herein.

Endosomal release agents include imidazoles, poly or oligoimidazoles, PEIs, peptides, fusogenic peptides, polycaboxylates, polyacations, masked oligo or poly cations or anions, acetals, polyacetals, ketals/polyketyals, orthoesters, polymers with masked or unmasked cationic or anionic charges, dendrimers with masked or unmasked cationic or anionic charges.

PK modulator stands for pharmacokinetic 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 phosphorothioate linkages in the backbone are also amenable to the present invention as ligands (*e.g.*, as PK modulating ligands).

In addition, aptamers that bind serum components (*e.g.*, serum proteins) are also amenable to the present invention as PK modulating ligands.

Other ligand conjugates amenable to the invention are described in U.S. Patent Applications USSN: 10/916,185, filed August 10, 2004; USSN: 10/946,873, filed September 21, 2004; USSN: 10/833,934, filed August 3, 2007; USSN: 11/115,989 filed April 27, 2005 and USSN: 11/944,227 filed November 21, 2007, which are incorporated by reference in their entireties for all purposes.

When two or more ligands are present, the ligands can all have same properties, all have different properties or some ligands have the same properties while others have different properties. For example, a ligand can have targeting properties, have endosomolytic activity or have PK modulating properties. In one embodiment, all the ligands have different properties.

Ligands can be coupled to the oligonucleotides at various places, for example, 3'-end, 5'-end, and/or at an internal position. In some embodiments, the ligand is attached to the oligonucleotides *via* an intervening tether, *e.g.*, a carrier described herein. The ligand or tethered ligand may be present on a monomer when the monomer is incorporated into the growing strand. In some embodiments, the ligand may be incorporated via coupling to a "precursor" monomer after the "precursor" monomer has been incorporated into the growing strand. For example, a monomer having, *e.g.*, an amino-terminated tether (*i.e.*, having no associated ligand), *e.g.*, TAP-$(CH_2)_nNH_2$ may be incorporated into a growing oligonucleotides strand. In a subsequent operation, *i.e.*, after incorporation of the precursor monomer into the strand, a ligand having an electrophilic group, *e.g.*, a pentafluorophenyl ester or aldehyde group, can subsequently be attached to the precursor monomer by coupling the electrophilic group of the ligand with the terminal nucleophilic group of the precursor monomer's tether.

In another example, a monomer having a chemical group suitable for taking part in Click Chemistry reaction may be incorporated, *e.g.*, an azide or alkyne terminated tether/linker. In a subsequent operation, *i.e.*, after incorporation of the precursor monomer into the strand, a ligand having complementary chemical group, *e.g.* an alkyne or azide can be attached to the precursor monomer by coupling the alkyne and the azide together.

In some embodiments, a ligand can be conjugated to nucleobases, sugar moieties, or internucleosidic linkages of nucleic acid molecules. Conjugation to purine nucleobases or derivatives thereof can occur at any position including, endocyclic and exocyclic atoms. In some embodiments, the 2-, 6-, 7-, or 8-positions of a purine nucleobase are attached to a

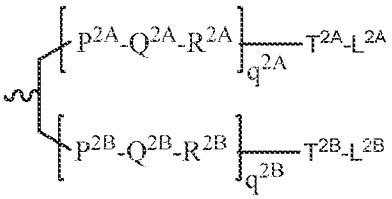
conjugate moiety. Conjugation to pyrimidine nucleobases or derivatives thereof can also occur at any position. In some embodiments, the 2-, 5-, and 6-positions of a pyrimidine nucleobase can be substituted with a conjugate moiety. Conjugation to sugar moieties of nucleosides can occur at any carbon atom. Example carbon atoms of a sugar moiety that can be attached to a conjugate moiety include the 2', 3', and 5' carbon atoms. The 1' position can also be attached to a conjugate moiety, such as in an abasic residue. Internucleosidic linkages can also bear conjugate moieties. For phosphorus-containing linkages (*e.g.*, phosphodiester, phosphorothioate, phosphorodithiotate, phosphoroamidate, and the like), the conjugate moiety can be attached directly to the phosphorus atom or to an O, N, or S atom bound to the phosphorus atom. For amine- or amide-containing internucleosidic linkages (*e.g.*, PNA), the conjugate moiety can be attached to the nitrogen atom of the amine or amide or to an adjacent carbon atom.

GalNAc ligands and linkers

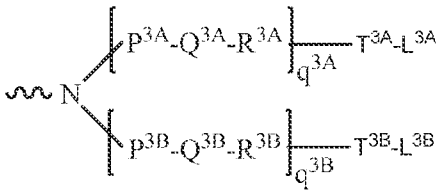
In some embodiment, an siRNA targeting an HAO1 gene is conjugated to a carbohydrate *e.g.* monosaccharide (such as GalNAc), disaccharide, trisaccharide, tetrasaccharide, polysaccharide. In some embodiments, the siRNA is conjugated to N-acetylgalactosamine (GalNAc) ligand. The enhances efficient delivery to hepatocytes following subcutaneous administration. Methods of conjugation of carbohydrates, e.g., N-acetylgalactosamine, to, e.g., an siRNA are well known to one of skill in the art. Examples can be found in US8,106,022 and WO2014/025805.

In some embodiments, an siRNA targeting an HAO1 gene is conjugated to a ligand, e.g., to GalNac, via a linker. For example, the ligand can be one or more GalNAc (*N*-acetylglucosamine) derivatives attached through a bivalent or trivalent branched linker.

In one embodiment, the dsRNA of the invention is conjugated to a bivalent and trivalent branched linkers include the structures shown in any of formula (IV) – (VII):

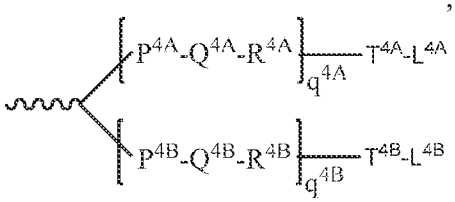


Formula (IV)



Formula (V)

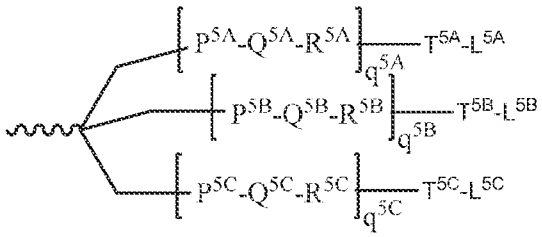
,



Formula (VI)

,

or



Formula (VII)

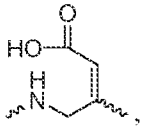
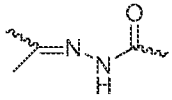
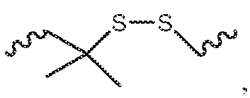
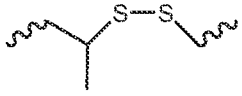
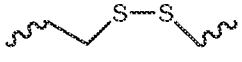
;

wherein:

q^{2A}, q^{2B}, q^{3A}, q^{3B}, $q4^{A}$, q^{4B}, q^{5A}, q^{5B} and q^{5C} 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;

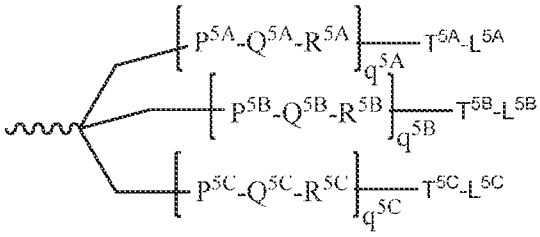
Q^{2A}, Q^{2B}, Q^{3A}, Q^{3B}, Q^{4A}, Q^{4B}, Q^{5A}, Q^{5B}, Q^{5C} are independently for each occurrence absent, alkylene, substituted alkylene wherein one or more methylenes can be interrupted or terminated by one or more of O, S, S(O), SO_2, $N(R^N)$, C(R')=C(R''), C≡C or C(O);

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.

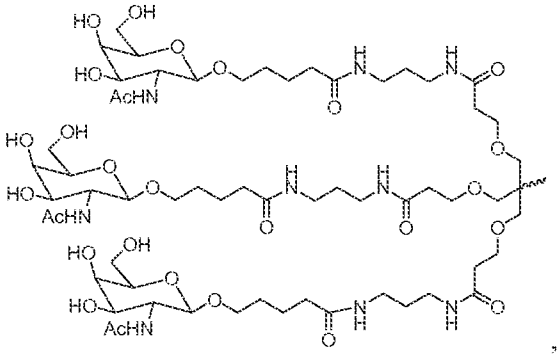
Trivalent conjugating GalNAc derivatives are particularly useful for use with RNAi agents for inhibiting the expression of a target gene, such as those of formula (VII):

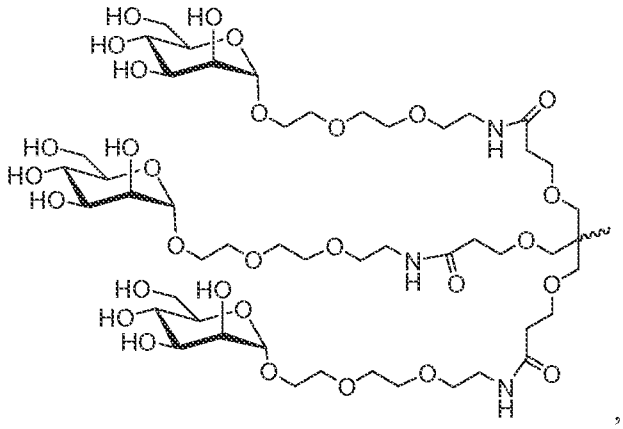


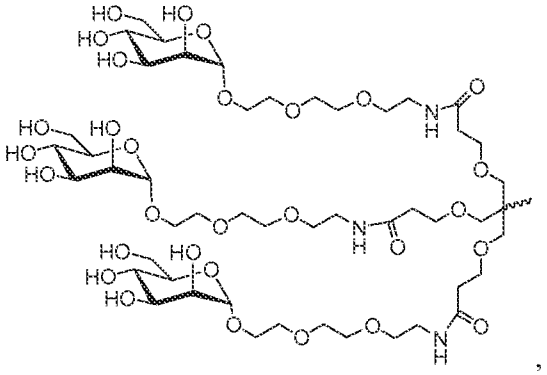
Formula (VII)

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

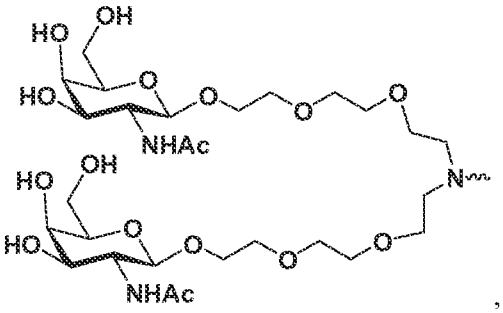
Examples of suitable bivalent and trivalent branched linker groups conjugating GalNAc derivatives include, but are not limited to, the following compounds:



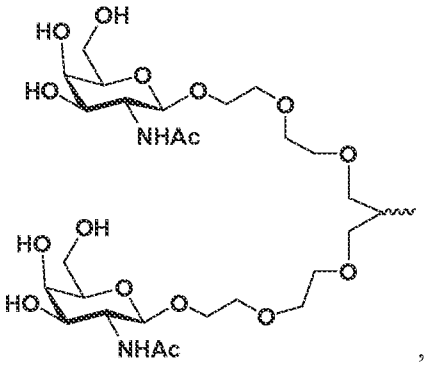




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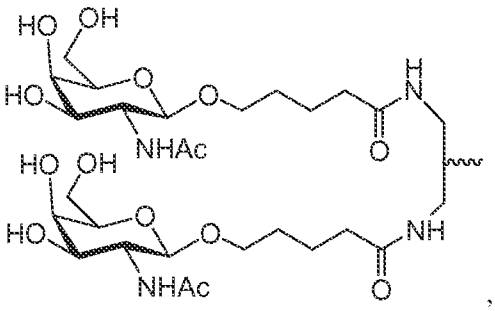


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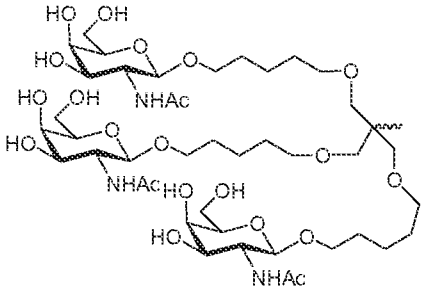


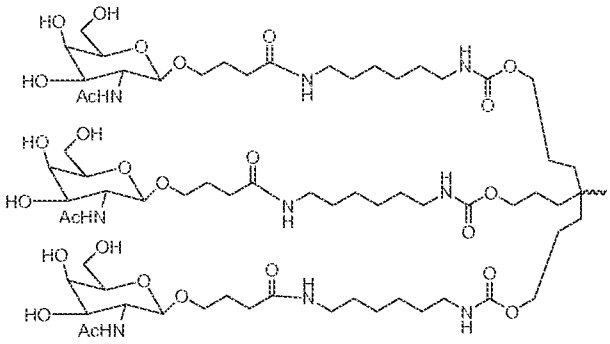
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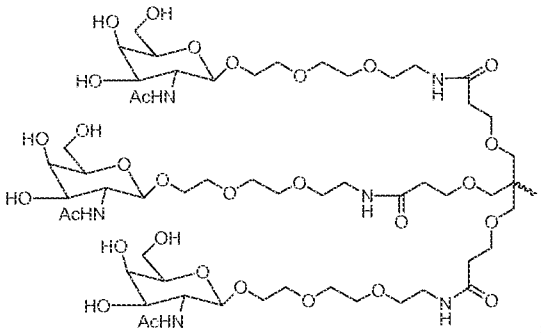


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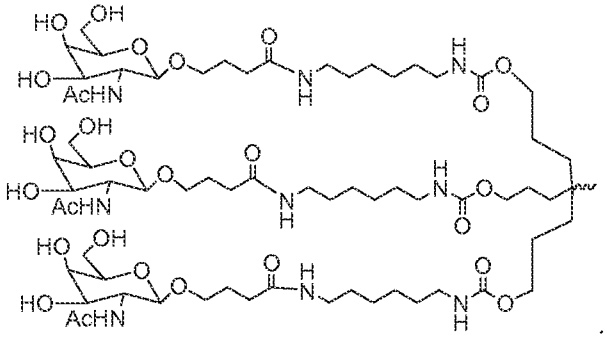




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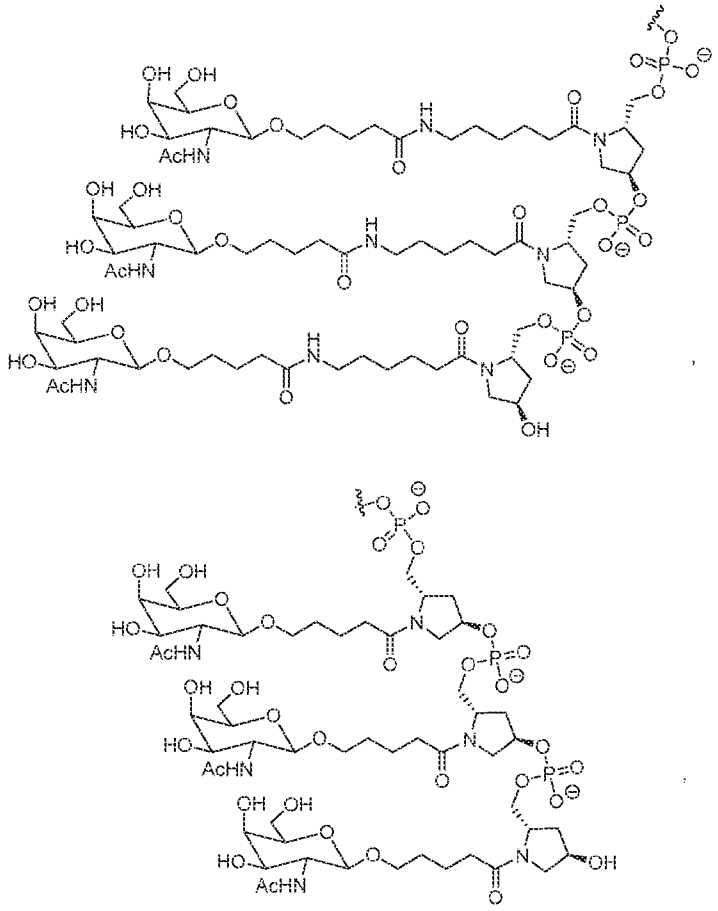
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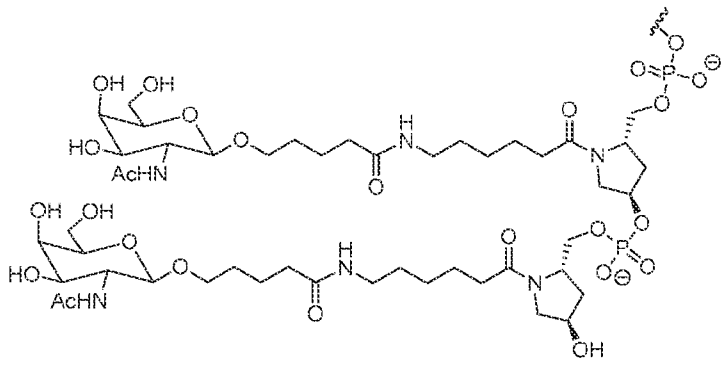
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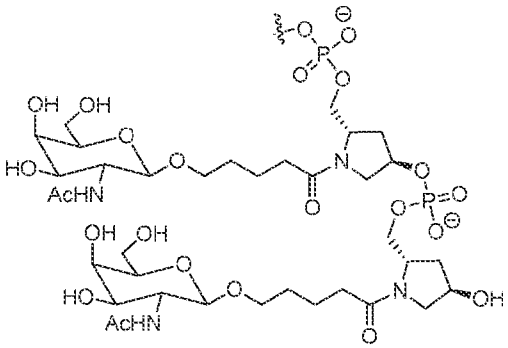
Additional ligands

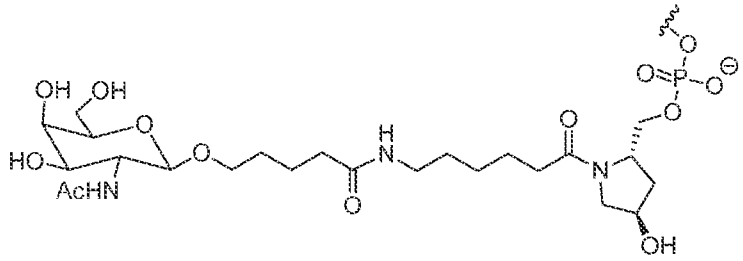
In some embodiments the ligand is selected from one of the following:



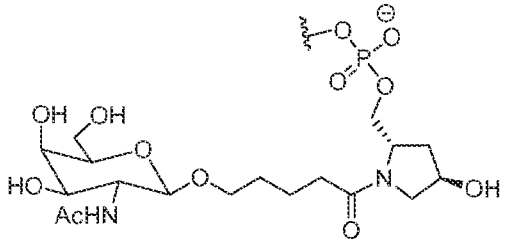
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III. Delivery of an iRNA of the Invention

The delivery of an iRNA agent of the invention to a cell *e.g.*, a cell within a subject, such as a human subject (*e.g.*, a subject in need thereof, such as a subject having a HAO1 associated disorder)can be achieved in a number of different ways. For example, delivery may be performed by contacting a cell with an iRNA of the invention either *in vitro* or *in vivo*. *In vivo* delivery may also be performed directly by administering a composition

comprising an iRNA, *e.g.*, a dsRNA, to a subject. Alternatively, *in vivo* delivery may be performed indirectly by administering one or more vectors that encode and direct the expression of the iRNA. These alternatives are discussed further below.

In general, any method of delivering a nucleic acid molecule (*in vitro* or *in vivo*) can be adapted for use with an iRNA of the invention (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). For *in vivo* delivery, factors to consider in order to deliver an iRNA molecule include, for example, biological stability of the delivered molecule, prevention of non-specific effects, and 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 or topically administering the preparation. Local administration to a treatment site maximizes local concentration of the agent, limits the exposure of the agent to systemic tissues that can otherwise be harmed by the agent or that can degrade the agent, and permits a lower total dose of the 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 VEGF 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 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.

Vector encoded iRNAs of the Invention

iRNA targeting the HAO1 gene 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. Pat. 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.*, *Proc. Natl. Acad. Sci. USA* (1995) 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 one embodiment, a dsRNA is expressed as inverted repeat polynucleotides joined by a linker polynucleotide sequence such that the dsRNA has a stem and loop structure.

iRNA expression vectors are generally DNA plasmids or viral vectors. Expression vectors compatible with eukaryotic cells, preferably those compatible with vertebrate cells, can be used to produce recombinant constructs for the expression of 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 are provided containing 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.

iRNA expression plasmids can be transfected into target cells as a complex with cationic lipid carriers (*e.g.*, Oligofectamine) or non-cationic lipid-based carriers (*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 invention. 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) SV 40 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 can 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-beta-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.

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.*, *Meth. Enzymol.* 217:581-599 (1993)). 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 facilitate delivery of the nucleic acid into a patient. More detail about retroviral vectors can be found, for example, in Boesen *et al.*, *Biotherapy* 6:291-302 (1994), 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.*, *J. Clin. Invest.* 93:644-651 (1994); Kiem *et al.*, *Blood* 83:1467-1473 (1994); Salmons and Gunzberg, *Human Gene Therapy* 4:129-141 (1993); and Grossman and Wilson, *Curr. Opin. in Genetics and Devel.* 3:110-114 (1993). 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 of the invention. 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, *Current Opinion in Genetics and Development* 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout *et al.*, *Human Gene Therapy* 5:3-10 (1994) 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.*, *Science* 252:431-434 (1991); Rosenfeld *et al.*, *Cell* 68:143-155 (1992); Mastrangeli *et al.*, *J. Clin. Invest.* 91:225-234 (1993); PCT Publication WO94/12649; and Wang, *et al.*, *Gene Therapy* 2:775-783 (1995). A suitable AV vector for expressing an iRNA featured in the invention, 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.

Adeno-associated virus (AAV) vectors may also be used to delivery an iRNA of the invention (Walsh *et al.*, Proc. Soc. Exp. Biol. Med. 204:289-300 (1993); U.S. Pat. No. 5,436,146). In one embodiment, 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 invention, 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. Pat. No. 5,252,479; U.S. Pat. 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 viral vector suitable for delivery of an iRNA of the invention 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.

IV. Pharmaceutical Compositions of the Invention

The present invention also includes pharmaceutical compositions and formulations which include the iRNAs of the invention. In one embodiment, provided herein are pharmaceutical compositions containing an iRNA, as described herein, and a pharmaceutically acceptable carrier. The pharmaceutical compositions containing the iRNA are useful for treating a HAO1 associated disease or disorder. Such pharmaceutical compositions are formulated based on the mode of delivery.

The pharmaceutical compositions comprising RNAi agents of the invention may be, for example, solutions with or without a buffer, or compositions containing pharmaceutically acceptable carriers. Such compositions include, for example, aqueous or crystalline compositions, liposomal formulations, micellar formulations, emulsions, and gene therapy vectors.

In the methods of the invention, the RNAi agent may be administered in a solution. A free RNAi agent may be administered in an unbuffered solution, e.g., in saline or in water. Alternatively, the free siRNA may also be administered in a suitable buffer solution. The buffer solution may comprise acetate, citrate, prolamine, carbonate, or phosphate, or any combination thereof. In one embodiment, the buffer solution is phosphate buffered saline (PBS). The pH and osmolarity of the buffer solution containing the RNAi agent can be adjusted such that it is suitable for administering to a subject.

In some embodiments, the buffer solution further comprises an agent for controlling the osmolarity of the solution, such that the osmolarity is kept at a desired value, *e.g.*, at the physiologic values of the human plasma. Solutes which can be added to the buffer solution to control the osmolarity include, but are not limited to, proteins, peptides, amino acids, non-metabolized polymers, vitamins, ions, sugars, metabolites, organic acids, lipids, or salts. In some embodiments, the agent for controlling the osmolarity of the solution is a salt. In certain embodiments, the agent for controlling the osmolarity of the solution is sodium chloride or potassium chloride.

The pharmaceutical compositions of the invention may be administered in dosages sufficient to inhibit expression of a HAO1 gene.

Dosages

In general, a suitable dose of an iRNA of the invention will be in the range of about 0.001 to about 200.0 milligrams per kilogram body weight of the recipient per day, generally in the range of about 0.1 to 10 or 1 to 50 mg per kilogram body weight per day. For example, the dsRNA can be administered at about 0.01 mg/kg, about 0.05 mg/kg, about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 3 mg/kg, about 4 mg/kg, about 5 mg/kg, about 6 mg/kg, about 7 mg/kg, about 8 mg/kg, about 9 mg/kg about 10 mg/kg, about 20 mg/kg, about 30 mg/kg, about 40 mg/kg, or about 50 mg/kg per single dose.

In another embodiment, the RNAi agent, *e.g.*, dsRNA, is administered at a dose of about 0.1 to about 50 mg/kg, about 0.25 to about 50 mg/kg, about 0.5 to about 50 mg/kg, about 0.75 to about 50 mg/kg, about 1 to about 50 mg/mg, about 1.5 to about 50 mg/kb, about 2 to about 50 mg/kg, about 2.5 to about 50 mg/kg, about 3 to about 50 mg/kg, about 3.5 to about 50 mg/kg, about 4 to about 50 mg/kg, about 4.5 to about 50 mg/kg, about 5 to about 50 mg/kg, about 7.5 to about 50 mg/kg, about 10 to about 50 mg/kg, about 15 to about 50 mg/kg, about 20 to about 50 mg/kg, about 20 to about 50 mg/kg, about 25 to about 50 mg/kg,

about 25 to about 50 mg/kg, about 30 to about 50 mg/kg, about 35 to about 50 mg/kg, about 40 to about 50 mg/kg, about 45 to about 50 mg/kg, about 0.1 to about 45 mg/kg, about 0.25 to about 45 mg/kg, about 0.5 to about 45 mg/kg, about 0.75 to about 45 mg/kg, about 1 to about 45 mg/mg, about 1.5 to about 45 mg/kb, about 2 to about 45 mg/kg, about 2.5 to about 45 mg/kg, about 3 to about 45 mg/kg, about 3.5 to about 45 mg/kg, about 4 to about 45 mg/kg, about 4.5 to about 45 mg/kg, about 5 to about 45 mg/kg, about 7.5 to about 45 mg/kg, about 10 to about 45 mg/kg, about 15 to about 45 mg/kg, about 20 to about 45 mg/kg, about 20 to about 45 mg/kg, about 25 to about 45 mg/kg, about 25 to about 45 mg/kg, about 30 to about 45 mg/kg, about 35 to about 45 mg/kg, about 40 to about 45 mg/kg, about 0.1 to about 40 mg/kg, about 0.25 to about 40 mg/kg, about 0.5 to about 40 mg/kg, about 0.75 to about 40 mg/kg, about 1 to about 40 mg/mg, about 1.5 to about 40 mg/kb, about 2 to about 40 mg/kg, about 2.5 to about 40 mg/kg, about 3 to about 40 mg/kg, about 3.5 to about 40 mg/kg, about 4 to about 40 mg/kg, about 4.5 to about 40 mg/kg, about 5 to about 40 mg/kg, about 7.5 to about 40 mg/kg, about 10 to about 40 mg/kg, about 15 to about 40 mg/kg, about 20 to about 40 mg/kg, about 20 to about 40 mg/kg, about 25 to about 40 mg/kg, about 25 to about 40 mg/kg, about 30 to about 40 mg/kg, about 35 to about 40 mg/kg, about 0.1 to about 30 mg/kg, about 0.25 to about 30 mg/kg, about 0.5 to about 30 mg/kg, about 0.75 to about 30 mg/kg, about 1 to about 30 mg/mg, about 1.5 to about 30 mg/kb, about 2 to about 30 mg/kg, about 2.5 to about 30 mg/kg, about 3 to about 30 mg/kg, about 3.5 to about 30 mg/kg, about 4 to about 30 mg/kg, about 4.5 to about 30 mg/kg, about 5 to about 30 mg/kg, about 7.5 to about 30 mg/kg, about 10 to about 30 mg/kg, about 15 to about 30 mg/kg, about 20 to about 30 mg/kg, about 20 to about 30 mg/kg, about 25 to about 30 mg/kg, about 0.1 to about 20 mg/kg, about 0.25 to about 20 mg/kg, about 0.5 to about 20 mg/kg, about 0.75 to about 20 mg/kg, about 1 to about 20 mg/mg, about 1.5 to about 20 mg/kb, about 2 to about 20 mg/kg, about 2.5 to about 20 mg/kg, about 3 to about 20 mg/kg, about 3.5 to about 20 mg/kg, about 4 to about 20 mg/kg, about 4.5 to about 20 mg/kg, about 5 to about 20 mg/kg, about 7.5 to about 20 mg/kg, about 10 to about 20 mg/kg, or about 15 to about 20 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

For example, the RNAi agent, *e.g.*, dsRNA, may be administered at a dose of about 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3,

7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9.0, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.5, 11, 11.5, 12, 12.5, 13, 13.5, 14, 14.5, 15, 15.5, 16, 16.5, 17, 17.5, 18, 18.5, 19, 19.5, 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or about 50 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

In certain embodiments of the invention, for example, when a double-stranded RNAi agent includes modifications (*e.g.*, one or more motifs of three identical modifications on three consecutive nucleotides, including one such motif at or near the cleavage site of the agent), six phosphorothioate linkages, and a ligand, such an agent is administered at a dose of about 0.01 to about 0.5 mg/kg, about 0.01 to about 0.4 mg/kg, about 0.01 to about 0.3 mg/kg, about 0.01 to about 0.2 mg/kg, about 0.01 to about 0.1 mg/kg, about 0.01 mg/kg to about 0.09 mg/kg, about 0.01 mg/kg to about 0.08 mg/kg, about 0.01 mg/kg to about 0.07 mg/kg, about 0.01 mg/kg to about 0.06 mg/kg, about 0.01 mg/kg to about 0.05 mg/kg, about 0.02 to about 0.5 mg/kg, about 0.02 to about 0.4 mg/kg, about 0.02 to about 0.3 mg/kg, about 0.02 to about 0.2 mg/kg, about 0.02 to about 0.1 mg/kg, about 0.02 mg/kg to about 0.09 mg/kg, about 0.02 mg/kg to about 0.08 mg/kg, about 0.02 mg/kg to about 0.07 mg/kg, about 0.02 mg/kg to about 0.06 mg/kg, about 0.02 mg/kg to about 0.05 mg/kg, about 0.03 to about 0.5 mg/kg, about 0.03 to about 0.4 mg/kg, about 0.03 to about 0.3 mg/kg, about 0.03 to about 0.2 mg/kg, about 0.03 to about 0.1 mg/kg, about 0.03 mg/kg to about 0.09 mg/kg, about 0.03 mg/kg to about 0.08 mg/kg, about 0.03 mg/kg to about 0.07 mg/kg, about 0.03 mg/kg to about 0.06 mg/kg, about 0.03 mg/kg to about 0.05 mg/kg, about 0.04 to about 0.5 mg/kg, about 0.04 to about 0.4 mg/kg, about 0.04 to about 0.3 mg/kg, about 0.04 to about 0.2 mg/kg, about 0.04 to about 0.1 mg/kg, about 0.04 mg/kg to about 0.09 mg/kg, about 0.04 mg/kg to about 0.08 mg/kg, about 0.04 mg/kg to about 0.07 mg/kg, about 0.04 mg/kg to about 0.06 mg/kg, about 0.05 to about 0.5 mg/kg, about 0.05 to about 0.4 mg/kg, about 0.05 to about 0.3 mg/kg, about 0.05 to about 0.2 mg/kg, about 0.05 to about 0.1 mg/kg, about 0.05 mg/kg to about 0.09 mg/kg, about 0.05 mg/kg to about 0.08 mg/kg, or about 0.05 mg/kg to about 0.07 mg/kg. Values and ranges intermediate to the foregoing recited values are also intended to be part of this invention, *e.g.*., the RNAi agent may be administered to the subject at a dose of about 0.015 mg/kg to about 0.45 mg/mg.

For example, the RNAi agent, *e.g.*, RNAi agent in a pharmaceutical composition, may be administered at a dose of about 0.01 mg/kg, 0.0125 mg/kg, 0.015 mg/kg, 0.0175 mg/kg,

0.02 mg/kg, 0.0225 mg/kg, 0.025 mg/kg, 0.0275 mg/kg, 0.03 mg/kg, 0.0325 mg/kg, 0.035 mg/kg, 0.0375 mg/kg, 0.04 mg/kg, 0.0425 mg/kg, 0.045 mg/kg, 0.0475 mg/kg, 0.05 mg/kg, 0.0525 mg/kg, 0.055 mg/kg, 0.0575 mg/kg, 0.06 mg/kg, 0.0625 mg/kg, 0.065 mg/kg, 0.0675 mg/kg, 0.07 mg/kg, 0.0725 mg/kg, 0.075 mg/kg, 0.0775 mg/kg, 0.08 mg/kg, 0.0825 mg/kg, 0.085 mg/kg, 0.0875 mg/kg, 0.09 mg/kg, 0.0925 mg/kg, 0.095 mg/kg, 0.0975 mg/kg, 0.1 mg/kg, 0.125 mg/kg, 0.15 mg/kg, 0.175 mg/kg, 0.2 mg/kg, 0.225 mg/kg, 0.25 mg/kg, 0.275 mg/kg, 0.3 mg/kg, 0.325 mg/kg, 0.35 mg/kg, 0.375 mg/kg, 0.4 mg/kg, 0.425 mg/kg, 0.45 mg/kg, 0.475 mg/kg, or about 0.5 mg/kg. Values intermediate to the foregoing recited values are also intended to be part of this invention.

Treatment regimens

The pharmaceutical composition can be administered once daily, or the iRNA can 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 could be used with the agents of the present invention. In this embodiment, the dosage unit contains a corresponding multiple of the daily dose.

In other embodiments, a single dose of the pharmaceutical compositions 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, or 4 week intervals. In some embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered once per week. In other embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered bi-monthly.

The skilled artisan will appreciate that certain factors can influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health 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 invention can be made using conventional methodologies.

Estimates of effective dosages and *in vivo* half-lives for the individual iRNAs encompassed by the invention can also be made on the basis of *in vivo* testing using an appropriate animal model. For example, advances in mouse genetics have generated a number of mouse models for the study of various human diseases, such as a disorder associated expression of HAO1. Such models can be used for *in vivo* testing of iRNA, as well as for determining a therapeutically effective dose. Suitable mouse models are known in the art and include, for example, the animal models described herein.

Administration methods

The pharmaceutical compositions of the present invention can be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration can be topical (*e.g.*, by a transdermal patch), pulmonary, *e.g.*, by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal, oral 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

The iRNA can be delivered in a manner to target a particular tissue, such as the liver.

Formulations

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

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

The compositions of the present invention can be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention can also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions can further contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension can also contain stabilizers.

The compositions of the present invention can be formulated for oral administration; parenteral, intraparenchymal (into the brain), intrathecal, intraventricular or intrahepatic administration, and/or topical administration.

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders can be desirable. In some embodiments, oral formulations are those in which dsRNAs featured in the invention are administered in conjunction with one or more penetration enhancer 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 invention can be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. DsRNA complexing agents include poly-amino acids; polyimines; polyacrylates; 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, US Publn. 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, intraventricular or intrahepatic administration can include sterile aqueous solutions which can also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Pharmaceutical compositions and formulations for topical administration can include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like can be necessary or desirable. Coated condoms, gloves and the like can also be useful. Suitable topical formulations include those in which the iRNAs featured in the invention 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 invention can be encapsulated within liposomes or can form complexes thereto, in particular to cationic liposomes. Alternatively, iRNAs can be complexed to lipids, in particular to cationic lipids. Suitable fatty acids and esters include but are not limited to arachidonic acid, oleic acid, eicosanoic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-

monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a C_{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.

iRNA Formulations Comprising Membranous Molecular Assemblies

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

A liposome containing a RNAi agent can be prepared by a variety of methods. In one example, the lipid component of a liposome is dissolved in a detergent so that micelles are formed with the lipid component. For example, the lipid component can be an amphipathic cationic lipid or lipid conjugate. The detergent can have a high critical micelle concentration and may be nonionic. Exemplary detergents include cholate, CHAPS, octylglucoside, deoxycholate, and lauroyl sarcosine. The RNAi agent preparation is then added to the micelles that include the lipid component. The cationic groups on the lipid interact with the RNAi agent and condense around the RNAi agent to form a liposome. After condensation, the detergent is removed, *e.g.*, by dialysis, to yield a liposomal preparation of RNAi agent.

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

Methods for producing stable polynucleotide delivery vehicles, which incorporate a polynucleotide/cationic lipid complex as structural components of the delivery vehicle, are further described in, e.g., WO 96/37194, the entire contents of which are incorporated herein by reference. Liposome formation can also include one or more aspects of exemplary methods described in Felgner, P. L. *et al., Proc. Natl. Acad. Sci., USA* 8:7413-7417, 1987; U.S. Pat. No. 4,897,355; U.S. Pat. No. 5,171,678; Bangham, *et al. M. Mol. Biol.* 23:238, 1965; Olson, *et al. Biochim. Biophys. Acta* 557:9, 1979; Szoka, *et al. Proc. Natl. Acad. Sci.* 75: 4194, 1978; Mayhew, *et al. Biochim. Biophys. Acta* 775:169, 1984; Kim, *et al. Biochim. Biophys. Acta* 728:339, 1983; and Fukunaga, *et al. Endocrinol.* 115:757, 1984. Commonly used techniques for preparing lipid aggregates of appropriate size for use as delivery vehicles include sonication and freeze-thaw plus extrusion (see, *e.g.,* Mayer, *et al. Biochim. Biophys. Acta* 858:161, 1986). Microfluidization can be used when consistently small (50 to 200 nm) and relatively uniform aggregates are desired (Mayhew, *et al. Biochim. Biophys. Acta* 775:169, 1984). These methods are readily adapted to packaging RNAi agent preparations into liposomes.

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

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

Examples of other methods to introduce liposomes into cells *in vitro* and *in vivo* include U.S. Pat. No. 5,283,185; U.S. Pat. No. 5,171,678; WO 94/00569; WO 93/24640; WO 91/16024; Felgner, *J. Biol. Chem.* 269:2550, 1994; Nabel, *Proc. Natl. Acad. Sci.* 90:11307, 1993; Nabel, *Human Gene Ther.* 3:649, 1992; Gershon, *Biochem.* 32:7143, 1993; and Strauss *EMBO J.* 11:417, 1992.

Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novasome™ I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novasome™ II (glyceryl distearate/cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver cyclosporin-A into the dermis of mouse skin. Results indicated that such non-ionic liposomal systems were effective in facilitating the deposition of cyclosporine A into different layers of the skin (Hu *et al. S.T.P.Pharma. Sci.*, 1994, 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.*, *FEBS Letters*, 1987, 223, 42; Wu *et al.*, *Cancer Research*, 1993, 53, 3765).

Various liposomes comprising one or more glycolipids are known in the art. Papahadjopoulos *et al.* (*Ann. N.Y. Acad. Sci.*, 1987, 507, 64) reported the ability of monosialoganglioside G_{M1}, galactocerebroside sulfate and phosphatidylinositol to improve blood half-lives of liposomes. These findings were expounded upon by Gabizon *et al.* (*Proc.*

Natl. Acad. Sci. U.S.A., 1988, 85, 6949). U.S. Pat. No. 4,837,028 and WO 88/04924, both to Allen *et al.*, disclose liposomes comprising (1) sphingomyelin and (2) the ganglioside G_{M1} or a galactocerebroside sulfate ester. U.S. Pat. No. 5,543,152 (Webb *et al.*) discloses liposomes comprising sphingomyelin. Liposomes comprising 1,2-sn-dimyristoylphosphatidylcholine are disclosed in WO 97/13499 (Lim *et al*).

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

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

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

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

culture cells. Another commercially available cationic lipid, 1,2-bis(oleoyloxy)-3,3-(trimethylammonia)propane ("DOTAP") (Boehringer Mannheim, Indianapolis, Indiana) differs from DOTMA in that the oleoyl moieties are linked by ester, rather than ether linkages.

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

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

Liposomal formulations are particularly suited for topical administration, liposomes present several advantages over other formulations. Such advantages include reduced side effects related to high systemic absorption of the administered drug, increased accumulation of the administered drug at the desired target, and the ability to administer RNAi agent into the skin. In some implementations, liposomes are used for delivering RNAi agent to epidermal cells and also to enhance the penetration of RNAi agent into dermal tissues, e.g., into skin. For example, the liposomes can be applied topically. Topical delivery of drugs formulated as liposomes to the skin has been documented (see, *e.g.*, Weiner *et al., Journal of Drug Targeting,* 1992, vol. 2,405-410 and du Plessis *et al., Antiviral Research*, 18, 1992, 259-265; Mannino, R. J. and Fould-Fogerite, S., *Biotechniques* 6:682-690, 1988; Itani, T. *et al. Gene* 56:267-276. 1987; Nicolau, C. *et al. Meth. Enz.* 149:157-176, 1987; Straubinger, R.

M. and Papahadjopoulos, D. *Meth. Enz.* 101:512-527, 1983; Wang, C. Y. and Huang, L., *Proc. Natl. Acad. Sci. USA* 84:7851-7855, 1987).

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 a drug into the dermis of mouse skin. Such formulations with RNAi agent are useful for treating a dermatological disorder.

Liposomes that include iRNA can be made highly deformable. Such deformability can enable the liposomes to penetrate through pore that are smaller than the average radius of the liposome. For example, transferosomes are a type of deformable liposomes. Transferosomes can be made by adding surface edge activators, usually surfactants, to a standard liposomal composition. Transferosomes that include RNAi agent can be delivered, for example, subcutaneously by infection in order to deliver RNAi agent to keratinocytes in the skin. In order to cross intact mammalian skin, lipid vesicles must pass through a series of fine pores, each with a diameter less than 50 nm, under the influence of a suitable transdermal gradient. In addition, due to the lipid properties, these transferosomes can be self-optimizing (adaptive to the shape of pores, *e.g.*, in the skin), self-repairing, and can frequently reach their targets without fragmenting, and often self-loading.

Other formulations amenable to the present invention are described in United States provisional application serial Nos. 61/018,616, filed January 2, 2008; 61/018,611, filed January 2, 2008; 61/039,748, filed March 26, 2008; 61/047,087, filed April 22, 2008 and 61/051,528, filed May 8, 2008. PCT application no PCT/US2007/080331, filed October 3, 2007 also describes formulations that are amenable to the present invention.

Transferosomes are yet another type of liposomes, and are highly deformable lipid aggregates which are attractive candidates for drug delivery vehicles. Transferosomes can be described as lipid droplets which are so highly deformable that they are easily able to penetrate through pores which are smaller than the droplet. Transferosomes 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 transferosomes it is possible to add surface edge-activators,

usually surfactants, to a standard liposomal composition. Transferosomes have been used to deliver serum albumin to the skin. The transferosome-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).

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

A mixed micellar formulation suitable for delivery through transdermal membranes may be prepared by mixing an aqueous solution of the siRNA composition, an alkali metal C_8 to C_{22} alkyl sulphate, and a micelle forming compounds. Exemplary micelle forming compounds include lecithin, hyaluronic acid, pharmaceutically acceptable salts of hyaluronic acid, glycolic acid, lactic acid, chamomile extract, cucumber extract, oleic acid, linoleic acid, linolenic acid, monoolein, monooleates, monolaurates, borage oil, evening of primrose oil, menthol, trihydroxy oxo cholanyl glycine and pharmaceutically acceptable salts thereof, glycerin, polyglycerin, lysine, polylysine, triolein, polyoxyethylene ethers and analogues thereof, polidocanol alkyl ethers and analogues thereof, chenodeoxycholate, deoxycholate, and mixtures thereof. The micelle forming compounds may be added at the same time or after addition of the alkali metal alkyl sulphate. Mixed micelles will form with substantially any kind of mixing of the ingredients but vigorous mixing in order to provide smaller size micelles.

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

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

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

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

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

Lipid particles

The iRNAs, *e.g.*, dsRNAs of in the invention may be fully encapsulated in a lipid formulation, *e.g.*, a LNP, or other nucleic acid-lipid particle.

As used herein, the term "LNP" refers to a stable nucleic acid-lipid particle. LNPs contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (*e.g.*, a PEG-lipid conjugate). LNPs are extremely useful for systemic applications, as they exhibit extended circulation lifetimes following intravenous (i.v.) injection and accumulate at distal sites (*e.g.*, sites physically separated from the administration site). LNPs include "pSPLP," which include an encapsulated condensing agent-nucleic acid complex as set forth in PCT Publication No. WO 00/03683. The particles of the present invention 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 invention 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; U.S. Publication No. 2010/0324120 and PCT Publication No. WO 96/40964.

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

The cationic lipid can 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 can comprise from about 20 mol % to about 50 mol % or about 40 mol % of the total lipid present in the particle.

In another embodiment, 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 International application no. PCT/US2009/061897, published as WO/2010/048536, which is herein incorporated by reference.

In one embodiment, 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 ionizable/non-cationic lipid can 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-1-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 can 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 can 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 can be, for example, a PEG-dilauryloxypropyl (C_{12}), a PEG-dimyristyloxypropyl (C_{14}), a PEG-dipalmityloxypropyl (C_{16}), or a PEG-distearyloxypropyl (C_{18}). The conjugated lipid that prevents aggregation of particles can 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 one embodiment, the lipidoid ND98·4HCl (MW 1487) (see U.S. Patent Application No. 12/056,230, filed 3/26/2008, which is incorporated herein by reference), Cholesterol (Sigma-Aldrich), and PEG-Ceramide C16 (Avanti Polar Lipids) can be used to prepare lipid-dsRNA nanoparticles (*i.e.*, 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. 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 described in Table A.

Table A. Exemplary lipid dsRNA formulations

	Ionizable/Cationic Lipid	cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
LNP_DLinDMA	1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA)	DLinDMA/DPPC/Cholesterol/PEG-cDMA (57.1/7.1/34.4/1.4) lipid:siRNA ~ 7:1
2-XTC	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DPPC/Cholesterol/PEG-cDMA 57.1/7.1/34.4/1.4 lipid:siRNA ~ 7:1
LNP05	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 57.5/7.5/31.5/3.5 lipid:siRNA ~ 6:1
LNP06	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 57.5/7.5/31.5/3.5 lipid:siRNA ~ 11:1
LNP07	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 60/7.5/31/1.5, lipid:siRNA ~ 6:1
LNP08	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 60/7.5/31/1.5, lipid:siRNA ~ 11:1
LNP09	2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC)	XTC/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1

LNP10	(3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-cyclopenta[d][1,3]dioxol-5-amine (ALN100)	ALN100/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP11	(6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3)	MC-3/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP12	1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (C12-200>	Tech G1/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP13	XTC	XTC/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 33:1
LNP14	MC3	MC3/DSPC/Chol/PEG-DMG 40/15/40/5 Lipid:siRNA: 11:1
LNP15	MC3	MC3/DSPC/Chol/PEG-DSG/GalNAc-PEG-DSG 50/10/35/4.5/0.5 Lipid:siRNA: 11:1
LNP16	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP17	MC3	MC3/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP18	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 12:1
LNP19	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/35/5 Lipid:siRNA: 8:1
LNP20	MC3	MC3/DSPC/Chol/PEG-DPG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP21	C12-200	C12-200/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP22	XTC	XTC/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1

Abbreviations in Table A include the following: 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).

DLinDMA (l,2-Dilinolenyloxy-N,N-dimethylaminopropane) 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. 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. Publication No. 2010/0324120, filed June 10, 2010, the entire contents of 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.

Additional Formulations

i. Emulsions

The compositions of the present invention can be prepared and formulated as emulsions. Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1μm 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 can be of either the water-in-oil (w/o) or the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase, the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase, the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions can contain additional components in addition to the dispersed phases, and the active drug which can be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants can also be present in emulsions as needed. Pharmaceutical emulsions can also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion can be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that can be incorporated into either phase of the emulsion. Emulsifiers can broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich 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 can be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic and amphoteric (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich 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 can readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation. Antioxidants used can be free radical 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.

ii. Microemulsions

In one embodiment of the present invention, the compositions of iRNAs and nucleic acids are formulated as microemulsions. A microemulsion can be defined as a system of water, oil and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich 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, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: Controlled Release of Drugs: Polymers and Aggregate Systems, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 185-215). Microemulsions commonly are prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used and on the structure and geometric packing of the polar heads and hydrocarbon tails of the surfactant molecules (Schott, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 271).

The phenomenological approach utilizing phase diagrams has been extensively studied and has yielded a comprehensive knowledge, to one skilled in the art, of how to formulate microemulsions (see *e.g.*, Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich 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 can, however, be prepared without the use of cosurfactants and alcohol-free self-emulsifying microemulsion systems are known in the art. The aqueous phase can typically be, but is not limited to, water, an aqueous solution of the drug, glycerol, PEG300, PEG400, polyglycerols, propylene glycols, and derivatives of ethylene glycol. The oil phase can include, but is not limited to, materials such as Captex 300, Captex 355, Capmul MCM, fatty acid esters, medium chain (C8-C12) mono, di, and tri-glycerides, polyoxyethylated glyceryl fatty acid esters, fatty alcohols, polyglycolized glycerides, saturated polyglycolized C8-C10 glycerides, vegetable oils and silicone oil.

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (see *e.g.*, U.S. Patent Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides *et al.*, *Pharmaceutical Research*, 1994, 11, 1385-1390; Ritschel, *Meth. Find. Exp. Clin. Pharmacol.*, 1993, 13, 205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of drug absorption due to surfactant-induced alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (see *e.g.*, U.S. Patent Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides *et al.*, *Pharmaceutical Research*, 1994, 11, 1385; Ho *et al.*, *J. Pharm. Sci.*, 1996, 85, 138-143). Often microemulsions can form spontaneously when their components are brought together at ambient temperature. This can be particularly advantageous when formulating thermolabile drugs, peptides or 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 invention 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 invention can also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the iRNAs and nucleic acids of the present invention. Penetration enhancers used in the microemulsions of the present invention can be classified as belonging to one of five broad categories--

surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee *et al., Critical Reviews in Therapeutic Drug Carrier Systems*, 1991, p. 92). Each of these classes has been discussed above.

iii. Microparticles

An RNAi agent of the invention may be incorporated into a particle, *e.g.*, a microparticle. Microparticles can be produced by spray-drying, but may also be produced by other methods including lyophilization, evaporation, fluid bed drying, vacuum drying, or a combination of these techniques.

iv. Penetration Enhancers

In one embodiment, the present invention 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 can cross cell membranes if the membrane to be crossed is treated with a penetration enhancer. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs.

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

Surfactants (or "surface-active agents") are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous solution and another liquid, with the result that absorption of 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., J. Pharm. Pharmacol.*, 1988, 40, 252).

Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C_{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, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; El Hariri *et al.*, *J. Pharm. Pharmacol.*, 1992, 44, 651-654).

The physiological role of bile includes the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (see *e.g.*, Malmsten, M. Surfactants and polymers in drug 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, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Yamamoto *et al.*, *J. Pharm. Exp. Ther.*, 1992, 263, 25; Yamashita *et al.*, *J. Pharm. Sci.*, 1990, 79, 579-583).

Chelating agents, as used in connection with the present invention, 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 invention, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for catalysis and are thus inhibited by chelating agents (Jarrett, *J. Chromatogr.*, 1993, 618, 315-339). Suitable chelating agents include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (*e.g.*, sodium salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones (enamines)(see *e.g.*, Katdare, A. *et al.*, Excipient development for pharmaceutical, biotechnology, and drug delivery, CRC Press, Danvers, MA, 2006; Lee *et al.*, Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Buur *et al.*, *J. Control Rel.*, 1990, 14, 43-51).

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

Agents that enhance uptake of iRNAs at the cellular level can also be added to the pharmaceutical and other compositions of the present invention. For example, cationic lipids, such as lipofectin (Junichi *et al*, U.S. Pat. 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™ (Invitrogen; 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 can be utilized to enhance the penetration of the administered nucleic acids, including glycols such as ethylene glycol and propylene glycol, pyrrols such as 2-pyrrol, azones, and terpenes such as limonene and menthone.

v. Carriers

Certain compositions of the present invention also incorporate carrier compounds in the formulation. As used herein, "carrier compound" or "carrier" 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.*, DsRNA Res. Dev., 1995, 5, 115-121; Takakura *et al.*, DsRNA & Nucl. Acid Drug Dev., 1996, 6, 177-183.

vi. Excipients

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

Pharmaceutically acceptable organic or inorganic excipients suitable for non-parenteral administration which do not deleteriously react with nucleic acids can also be used to formulate the compositions of the present invention. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, polyethylene glycols, gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose, polyvinylpyrrolidone and the like.

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

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

vii. Other Components

The compositions of the present invention can additionally contain other adjunct components conventionally found in pharmaceutical compositions, at their art-established usage levels. Thus, for example, the compositions can contain additional, compatible, pharmaceutically-active materials such as, for example, antipruritics, astringents, local anesthetics or anti-inflammatory agents, or can contain additional materials useful in physically formulating various dosage forms of the compositions of the present invention, 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 invention. 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 can contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension can also contain stabilizers.

In some embodiments, pharmaceutical compositions featured in the invention include (a) one or more iRNA compounds and (b) one or more agents which function by a non-RNAi mechanism and which are useful in treating, e.g., PH1.

Testing of compositions

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 preferred.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of compositions featured herein in the invention lies generally within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used

in the methods featured in the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range of the compound or, when appropriate, of the polypeptide product of a target sequence (*e.g.*, achieving a decreased concentration of the polypeptide) that includes the IC_{50} (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

In addition to their administration, as discussed above, the iRNAs featured in the invention can be administered in combination with other known agents effective in treatment of pathological processes that are mediated by iron overload and that can be treated by inhibiting HAO1 expression. 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.

V. Methods For Inhibiting HAO1 Expression

The present invention provides methods of inhibiting expression of HAO1 (hydroxyacid oxidase 1) in a cell. The methods include contacting a cell with an RNAi agent, *e.g.*, a double stranded RNAi agent, in an amount effective to inhibit expression of the HAO1 in the cell, thereby inhibiting expression of the HAO1 in the cell.

Contacting of a cell with a double stranded RNAi agent may be done *in vitro* or *in vivo*. Contacting a cell *in vivo* with the RNAi agent includes contacting a cell or group of cells within a subject, *e.g.*, a human subject, with the RNAi agent. Combinations of *in vitro* and *in vivo* methods of contacting are also possible. Contacting may be direct or indirect, as discussed above. Furthermore, contacting a cell may be accomplished via a targeting ligand, including any ligand described herein or known in the art. In some embodiments, the targeting ligand is a carbohydrate moiety, *e.g.*, a $GalNAc_3$ ligand, or any other ligand that directs the RNAi agent to a site of interest, *e.g.*, the liver of a subject.

The term "inhibiting," as used herein, is used interchangeably with "reducing," "silencing," "downregulating" and other similar terms, and includes any level of inhibition.

The phrase "inhibiting expression of a HAO1" is intended to refer to inhibition of expression of any HAO1 gene (such as, *e.g.*, a mouse HAO1 gene, a rat HAO1 gene, a monkey HAO1 gene, or a human HAO1 gene) as well as variants or mutants of a HAO1

gene. Thus, the HAO1 gene may be a wild-type HAO1 gene, a mutant HAO1 gene, or a transgenic HAO1 gene in the context of a genetically manipulated cell, group of cells, or organism.

"Inhibiting expression of a HAO1 gene" includes any level of inhibition of a HAO1 gene, *e.g.*, at least partial suppression of the expression of a HAO1 gene. The expression of the HAO1 gene may be assessed based on the level, or the change in the level, of any variable associated with HAO1 gene expression, *e.g.*, HAO1 mRNA level, HAO1 protein level. This level may be assessed in an individual cell or in a group of cells, including, for example, a sample derived from a subject.

Inhibition may be assessed by a decrease in an absolute or relative level of one or more variables that are associated with HAO1 expression compared with a control level. The control level may be any type of control level that is utilized in the art, *e.g.*, a pre-dose baseline level, or a level determined from a similar subject, cell, or sample that is untreated or treated with a control (such as, *e.g.*, buffer only control or inactive agent control).

In some embodiments of the methods of the invention, expression of a HAO1 gene is inhibited by at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%. at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%.

Inhibition of the expression of a HAO1 gene may be manifested by a reduction of the amount of mRNA expressed by a first cell or group of cells (such cells may be present, for example, in a sample derived from a subject) in which a HAO1 gene is transcribed and which has or have been treated (*e.g.*, by contacting the cell or cells with an RNAi agent of the invention, or by administering an RNAi agent of the invention to a subject in which the cells are or were present) such that the expression of a HAO1 gene is inhibited, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has not or have not been so treated (control cell(s)). In some embodiments, the inhibition is assessed by expressing the level of mRNA in treated cells as a percentage of the level of mRNA in control cells, using the following formula:

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

Alternatively, inhibition of the expression of a HAO1 gene may be assessed in terms of a reduction of a parameter that is functionally linked to HAO1 gene expression, *e.g.*, HAO1 protein expression. HAO1 gene silencing may be determined in any cell expressing HAO1, either constitutively or by genomic engineering, and by any assay known in the art. The liver is the major site of HAO1 expression. Other significant sites of expression include the kidneys and the uterus.

Inhibition of the expression of a HAO1 protein may be manifested by a reduction in the level of the HAO1 protein that is expressed by a cell or group of cells (*e.g.*, the level of protein expressed in a sample derived from a subject). As explained above for the assessment of mRNA suppression, the inhibition of protein expression levels in a treated cell or group of cells may similarly be expressed as a percentage of the level of protein in a control cell or group of cells.

A control cell or group of cells that may be used to assess the inhibition of the expression of a HAO1 gene includes a cell or group of cells that has not yet been contacted with an RNAi agent of the invention. For example, the control cell or group of cells may be derived from an individual subject (*e.g.*, a human or animal subject) prior to treatment of the subject with an RNAi agent.

The level of HAO1 mRNA that is expressed by a cell or group of cells may be determined using any method known in the art for assessing mRNA expression. In one embodiment, the level of expression of HAO1 in a sample is determined by detecting a transcribed polynucleotide, or portion thereof, *e.g.*, mRNA of the HAO1 gene. RNA may be extracted from cells using RNA extraction techniques including, for example, using acid phenol/guanidine isothiocyanate extraction (RNAzol B; Biogenesis), RNeasy RNA preparation kits (Qiagen) or PAXgene (PreAnalytix, Switzerland). Typical assay formats utilizing ribonucleic acid hybridization include nuclear run-on assays, RT-PCR, RNase protection assays (Melton *et al.*, *Nuc. Acids Res.* 12:7035), Northern blotting, *in situ* hybridization, and microarray analysis.

In one embodiment, the level of expression of HAO1 is determined using a nucleic acid probe. The term "probe", as used herein, refers to any molecule that is capable of selectively binding to a specific HAO1. Probes can be synthesized by one of skill in the art,

or derived from appropriate biological preparations. Probes may be specifically designed to be labeled. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

Isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction (PCR) analyses and probe arrays. One method for the determination of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to HAO1 mRNA. In one embodiment, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative embodiment, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in determining the level of HAO1 mRNA.

An alternative method for determining the level of expression of HAO1 in a sample involves the process of nucleic acid amplification and/or reverse transcriptase (to prepare cDNA) of for example mRNA in the sample, *e.g.*, by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Pat. No. 4,683,202), ligase chain reaction (Barany (1991) *Proc. Natl. Acad. Sci. USA* 88:189-193), self-sustained sequence replication (Guatelli et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.* (1988) *Bio/Technology* 6:1197), rolling circle replication (Lizardi et al., U.S. Pat. No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. In particular aspects of the invention, the level of expression of HAO1 is determined by quantitative fluorogenic RT-PCR (*i.e.*, the TaqMan™ System).

The expression levels of HAO1 mRNA may be monitored using a membrane blot (such as used in hybridization analysis such as Northern, Southern, dot, and the like), or microwells, sample tubes, gels, beads or fibers (or any solid support comprising bound nucleic acids). See U.S. Pat. Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, which are incorporated herein by reference. The determination of HAO1 expression level may also comprise using nucleic acid probes in solution.

In some embodiments, the level of mRNA expression is assessed using branched DNA (bDNA) assays or real time PCR (qPCR). The use of these methods is described and exemplified in the Examples presented herein.

The level of HAO1 protein expression may be determined using any method known in the art for the measurement of protein levels. Such methods include, for example, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, fluid or gel precipitin reactions, absorption spectroscopy, a colorimetric assays, spectrophotometric assays, flow cytometry, immunodiffusion (single or double), immunoelectrophoresis, Western blotting, radioimmunoassay (RIA), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, electrochemiluminescence assays, and the like.

The term "sample" as used herein refers to a collection of similar fluids, cells, or tissues isolated from a subject, as well as fluids, cells, or tissues present within a subject. Examples of biological fluids include blood, serum and serosal fluids, plasma, lymph, urine, cerebrospinal fluid, saliva, ocular fluids, and the like. Tissue samples may include samples from tissues, organs or localized regions. For example, samples may be derived from particular organs, parts of organs, or fluids or cells within those organs. In certain embodiments, samples may be derived from the liver (*e.g.*, whole liver or certain segments of liver or certain types of cells in the liver, such as, *e.g.*, hepatocytes). In some embodiments, a "sample derived from a subject" refers to blood or plasma drawn from the subject. In further embodiments, a "sample derived from a subject" refers to liver tissue derived from the subject.

In some embodiments of the methods of the invention, the RNAi agent is administered to a subject such that the RNAi agent is delivered to a specific site within the subject. The inhibition of expression of HAO1 may be assessed using measurements of the level or change in the level of HAO1 mRNA or HAO1 protein in a sample derived from fluid or tissue from the specific site within the subject. In some embodiments, the site is the liver. The site may also be a subsection or subgroup of cells from any one of the aforementioned sites. The site may also include cells that express a particular type of receptor.

VI. Methods for Treating or Preventing a HAO1 Associated Disorder

The present invention also provides methods for treating or preventing diseases and conditions that can be modulated by HAO1 gene expression. For example, the compositions described herein can be used to treat any disorder associated with PH1.

Efficacy of treatment or prevention of disease can be assessed, for example by measuring disease progression, disease remission, symptom severity, reduction in pain, quality of life, dose of a medication required to sustain a treatment effect, level of a disease marker or any other measurable parameter appropriate for a given disease being treated or targeted for prevention. It is well within the ability of one skilled in the art to monitor efficacy of treatment or prevention by measuring any one of such parameters, or any combination of parameters.

A treatment or preventive effect is evident when there is a statistically significant improvement in one or more parameters of disease status, or by a failure to worsen or to develop symptoms where they would otherwise be anticipated. As an example, a favorable change of at least 10% in a measurable parameter of disease, and preferably at least 20%, 30%, 40%, 50% or more can be indicative of effective treatment. Efficacy for a given iRNA drug or formulation of that drug can also be judged using an experimental animal model for the given disease as known in the art. When using an experimental animal model, efficacy of treatment is evidenced when a statistically significant reduction in a marker or symptom is observed.

Alternatively, the efficacy can be measured by a reduction in the severity of disease as determined by one skilled in the art of diagnosis based on a clinically accepted disease severity grading scale.

In some embodiments of the methods of the invention, HAO1 expression is decreased for an extended duration, *e.g.*, at least one week, two weeks, three weeks, or four weeks or longer. For example, in certain instances, expression of the HAO1 gene is suppressed by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 100% by administration of an iRNA agent described herein. In some embodiments, the HAO1 gene is suppressed by at least about 60%, 70%, or 80% by administration of the iRNA agent. In some embodiments, the HAO1 gene is suppressed by at least about 85%, 90%, or 95% by administration of the double-stranded oligonucleotide. In another embodiment, the HAO1 gene remains suppressed for 7 days, 10 days, 20 days, 30 days, or more following administration.

Administration

The RNAi agents of the invention may be administered to a subject using any mode of administration known in the art, including, but not limited to subcutaneous, intravenous, intramuscular, intraocular, intrabronchial, intrapleural, intraperitoneal, intraarterial, lymphatic, cerebrospinal, and any combinations thereof. In some embodiments, the agents are administered subcutaneously.

In some embodiments, the administration is via a depot injection. A depot injection may release the RNAi agent in a consistent way over a prolonged time period. Thus, a depot injection may reduce the frequency of dosing needed to obtain a desired effect, *e.g.*, a desired inhibition of HAO1, or a therapeutic or prophylactic effect. A depot injection may also provide more consistent serum concentrations. Depot injections may include subcutaneous injections or intramuscular injections. In some embodiments, the depot injection is a subcutaneous injection.

In some embodiments, the administration is via a pump. The pump may be an external pump or a surgically implanted pump. In certain embodiments, the pump is a subcutaneously implanted osmotic pump. In other embodiments, the pump is an infusion pump. An infusion pump may be used for intravenous, subcutaneous, arterial, or epidural infusions. In some embodiments, the infusion pump is a subcutaneous infusion pump. In other embodiments, the pump is a surgically implanted pump that delivers the RNAi agent to the liver.

Other modes of administration include epidural, intracerebral, intracerebroventricular, nasal administration, intraarterial, intracardiac, intraosseous infusion, intrathecal, and intravitreal, and pulmonary. The mode of administration may be chosen based upon whether local or systemic treatment is desired and based upon the area to be treated. The route and site of administration may be chosen to enhance targeting.

The method includes administering an iRNA agent, *e.g.*, a dose sufficient to depress levels of HAO1 mRNA for at least 5, more preferably 7, 10, 14, 21, 25, 30 or 40 days; and optionally, administering a second single dose of dsRNA, wherein the second single dose is administered at least 5, more preferably 7, 10, 14, 21, 25, 30 or 40 days after the first single dose is administered, thereby inhibiting the expression of the HAO1 gene in a subject.

In one embodiment, doses of iRNA agent of the invention are administered not more than once every four weeks, not more than once every three weeks, not more than once every

two weeks, or not more than once every week. In another embodiment, the administrations can be maintained for one, two, three, or six months, or one year or longer. In another embodiment, doses of iRNA agent of the invention are administered once a week for three weeks.

In general, the iRNA agent does not activate the immune system, *e.g.*, it does not increase cytokine levels, such as TNF-alpha or IFN-alpha levels. For example, when measured by an assay, such as an in vitro PBMC assay, such as described herein, the increase in levels of TNF-alpha or IFN-alpha, is less than 30%, 20%, or 10% of control cells treated with a control dsRNA, such as a dsRNA that does not target HAO1.

For example, a subject can be administered a therapeutic amount of an iRNA agent, such as 0.3 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 1.5 mg/kg, 2.0 mg/kg, 2.5 mg/kg, or 3 mg/kg of dsRNA. The iRNA agent can be administered by intravenous infusion over a period of time, such as over a 5 minute, 10 minute, 15 minute, 20 minute, or 25 minute period. The administration is repeated, for example, on a regular basis, such as biweekly (*i.e.*, every two weeks) for one month, two months, three months, four 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. Administration of the iRNA agent can reduce HAO1 levels, *e.g.*, in a cell, tissue, blood, urine or other compartment of the patient by at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80 % or at least 90% or more.

Before administration of a full dose of the iRNA agent, patients can be administered a smaller dose, such as a dose resulting in less than 5% infusion reaction, 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 immunostimulatory effects, such as increased cytokine (*e.g.*, TNF-alpha or INF-alpha) levels.

A patient in need of a HAO1 RNAi agent may be identified by taking a family history. A healthcare provider, such as a doctor, nurse, or family member, can take a family history before prescribing or administering a HAO1 dsRNA. A DNA test may also be performed on the patient to identify a mutation in the AGT1 gene, before a HAO1 RNAi agent is administered to the patient. Diagnosis of PH1 can be confirmed by any test well-known to one of skill in the art.

A treatment or preventive effect is evident when there is a statistically significant improvement in one or more parameters of disease status, or by a failure to worsen or to develop symptoms where they would otherwise be anticipated. As an example, a favorable change of at least 10% in a measurable parameter of disease, and preferably at least 20%, 30%, 40%, 50% or more can be indicative of effective treatment. Efficacy for a given iRNA agent of the invention or formulation of that iRNA agent can also be judged using an experimental animal model for the given disease as known in the art. When using an experimental animal model, efficacy of treatment is evidenced when a statistically significant reduction in a marker or symptom is observed.

The dose of an RNAi agent that is administered to a subject may be tailored to balance the risks and benefits of a particular dose, for example, to achieve a desired level of HAO1 gene suppression (as assessed, *e.g.*, based on HAO1 mRNA suppression, HAO1 protein expression, or a reduction in oxalate levels) or a desired therapeutic or prophylactic effect, while at the same time avoiding undesirable side effects.

In some embodiments, the RNAi agent is administered in two or more doses. If desired to facilitate repeated or frequent infusions, implantation of a delivery device, *e.g.*, a pump, semi-permanent stent (*e.g.*, intravenous, intraperitoneal, intracisternal or intracapsular), or reservoir may be advisable. In some embodiments, the number or amount of subsequent doses is dependent on the achievement of a desired effect, *e.g.*, the suppression of a HAO1 gene, or the achievement of a therapeutic or prophylactic effect, *e.g.*, reducing iron overload. In some embodiments, the RNAi agent is administered according to a schedule. For example, the RNAi 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 other 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 RNAi agent is not administered. In one embodiment, the RNAi agent is initially administered hourly and is

later administered at a longer interval (*e.g.*, daily, weekly, biweekly, or monthly). In another embodiment, the RNAi 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. In a specific embodiment, the RNAi agent is administered once daily during a first week, followed by weekly dosing starting on the eighth day of administration. In another specific embodiment, the RNAi agent is administered every other day during a first week followed by weekly dosing starting on the eighth day of administration.

In some embodiments, the RNAi agent is administered in a dosing regimen that includes a "loading phase" of closely spaced administrations that may be followed by a "maintenance phase", in which the RNAi agent is administered at longer spaced intervals. In one embodiment, the loading phase comprises five daily administrations of the RNAi agent during the first week. In another embodiment, the maintenance phase comprises one or two weekly administrations of the RNAi agent. In a further embodiment, the maintenance phase lasts for 5 weeks.

Any of these schedules may optionally be repeated for one or more iterations. The number of iterations may depend on the achievement of a desired effect, *e.g.*, the suppression of a HAO1 gene, and/or the achievement of a therapeutic or prophylactic effect, *e.g.*, reducing oxalate levels or reducing a symptom of PH1.

In another aspect, the invention features, a method of instructing an end user, *e.g.*, a caregiver or a subject, on how to administer an iRNA agent described herein. The method includes, optionally, providing the end user with one or more doses of the iRNA agent, and instructing the end user to administer the iRNA agent on a regimen described herein, thereby instructing the end user.

VII. Kits

The present invention also provides kits for using any of the iRNA agents and/or performing any of the methods of the invention. Such kits include one or more RNAi agent(s) and instructions for use, *e.g.*, instructions for inhibiting expression of a HAO1 in a cell by contacting the cell with the RNAi agent(s) in an amount effective to inhibit expression of the HAO1. The kits may optionally further comprise means for contacting the cell with the RNAi agent (*e.g.*, an injection device), or means for measuring the inhibition of HAO1 (*e.g.*, means for measuring the inhibition of HAO1 mRNA or protein). Such means for

measuring the inhibition of HAO1 may comprise a means for obtaining a sample from a subject, such as, *e.g.*, a plasma sample. The kits of the invention may optionally further comprise means for administering the RNAi agent(s) to a subject or means for determining the therapeutically effective or prophylactically effective amount.

VII. Diagnostic markers for PH1 and related conditions

Also described herein are markers and methods for the diagnosis of disease conditions caused by oxalate overproduction, particularly PH1 and related conditions, as well as with agents for the treatment of said conditions.

According to another aspect, the invention relates to a method for the treatment of a PH1 condition in a subject (stone forming diseases, especially PH1). The diagnostic method comprises the steps of: (a) knocking down the HAO1 expression in a subject (b) obtaining a biological serum from said subject; and (b) determining the level of glycolate in said serum. It should be appreciated that elevated level of glycolate in serum, in comparison with negative control, indicates the inhibition of the glycolate oxidase enzyme to prevent oxalate production that is caused the PH1 conditions.

In one embodiment, described herein is a kit for the diagnosis of PH1 condition, said kit including the following: (a) an agent for determining the presence of an analyte of interest in serum, wherein said analyte of interest is one of glycolate; and (b) calibration means. For example, said analyte of interest is glycolate, said agent is an siRNA targeting HAO1.

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

EXAMPLES

Materials and Methods

The following materials and methods were used in the Examples. As used herein, "HAO" and "GO" are used interchangeably.

siRNA synthesis

Single-stranded RNAs were produced by solid phase synthesis on a scale of 1 µmole using an Expedite 8909 synthesizer (Applied Biosystems, Applera Deutschland GmbH, Darm-stadt, Germany) and controlled pore glass (CPG, 500Å, Proligo Biochemie GmbH, Hamburg, Germany) as solid support. RNA and RNA containing 2'-O-methyl nucleotides were generated by solid phase synthesis employing the corresponding phosphoramidites and 2'-O-methyl phos-phoramidites, respectively (Proligo Biochemie GmbH, Hamburg, Germany). These building blocks were incorporated at selected sites within the sequence of the oligoribonucleotide chain using standard nucleoside phosphoramidite chemistry such as described in Current protocols in nucleic acid chemistry, Beaucage, S.L. et al. (Edrs.), John Wiley & Sons, Inc., New York, NY, USA. Phosphorothioate linkages were introduced by replacement of the iodine oxidizer solution with a solution of the Beaucage reagent (Chruachem Ltd, Glasgow, UK) in acetonitrile (1%). Further ancillary reagents were obtained from Mallinckrodt Baker (Griesheim, Germany).

Deprotection and purification of the crude oligoribonucleotides by anion exchange HPLC were carried out according to established procedures. Yields and concentrations were determined by UV absorption of a solution of the respective RNA at a wavelength of 260 nm using a spectral photometer (DU 640B, Beckman Coulter GmbH, Unterschleißheim, Germany).

Double stranded RNA was generated by mixing an equimolar solution of complementary strands in annealing buffer (20 mM sodium phosphate, pH 6.8; 100 mM sodium chloride), heated in a water bath at 85 - 90°C for 3 minutes and cooled to room temperature over a period of 3 - 4 hours. The annealed RNA solution was stored at –20 °C until use.

In some instances, a duplex (dsRNA) was synthesized more than once. Different batches are labeled with different extensions. For example, AD-62933.1 and AD-62933.2 are different batches of the same duplex.

Cell culture and transfections

Primary Cynomolgus monkey hepatocytes (PCH) and primary mouse hepatocytes (PMH) were used. PCHs (Celsis # M003055, lot CBT) or PMH (freshly isolated) were transfected by adding 14.8µl of Opti-MEM plus 0.2µl of Lipofectamine RNAiMax per well (Invitrogen, Carlsbad CA. cat # 13778-150) to 5µl of siRNA duplexes per well into a 96-well plate and incubated at room temperature for 15 minutes. 80µl of InVitroGRO CP Rat media (InVitro Technologies) containing ~2 x10^4 PCH or PMH cells were then added to the siRNA mixture. Cells were incubated for 24 hours prior to RNA purification. Single dose experiments were performed at 10 or 20nM and 0.1 or 0.2nM final duplex concentration and dose response experiments were done over a range of doses from 10nM to 36fM final duplex concentration over 8, 6-fold dilutions.

Total RNA isolation

Total RNA was isolated using DYNABEADS mRNA Isolation Kit (Invitrogen, part #: 610-12). Cells were harvested and lysed in 150µl of Lysis/Binding Buffer then mixed for 5 minute at 850rpm using an Eppendorf Thermomixer (the mixing speed was the same throughout the process). Ten microliters of magnetic beads and 80µl Lysis/Binding Buffer mixture were added to a round bottom plate and mixed for 1 minute. Magnetic beads were captured using magnetic stand and the supernatant was removed without disturbing the beads. After removing supernatant, the lysed cells were added to the remaining beads and mixed for 5 minutes. After removing supernatant, magnetic beads were washed 2 times with 150µl Wash Buffer A and mixed for 1 minute. Beads were capture again and supernatant removed. Beads were then washed with 150µl Wash Buffer B, captured and supernatant was removed. Beads were next washed with 150µl Elution Buffer, captured and supernatant removed. Beads were allowed to dry for 2 minutes. After drying, 50µl of Elution Buffer was added and mixed for 5 minutes at 70°C. Beads were captured on magnet for 5 minutes. 40µl of supernatant was removed and added to another 96 well plate.

cDNA synthesis

Synthesis of cDNA was performed using the ABI High capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA, Cat #4368813).

A master mix of 2µl 10X Buffer, 0.8µl 25X dNTPs, 2µl Random primers, 1µl Reverse Transcriptase, 1µl RNase inhibitor and 3.2µl of H2O per reaction were added into

10µl total RNA. cDNA was generated using a Bio-Rad C-1000 or S-1000 thermal cycler (Hercules, CA) through the following steps: 25°C 10 min, 37°C 120 min, 85°C 5 sec, 4°C hold.

Real time PCR

2µl of cDNA were added to a master mix containing 0.5µl of mouse GAPDH (cat # 4352339E Life Technologies) or custom designed Cynomolgus monkey GAPDH TaqMan Probes: (F- GCATCCTGGGCTACACTGA, (SEQ ID NO: 13) R-TGGGTGTCGCTGTTGAAGTC (SEQ ID NO: 14), Probe- CCAGGTGGTCTCCTCC (SEQ ID NO: 15)), 0.5µl human or mouse HAO1 (HS00213909_M1- which is cross reactive with Cynomolgus monkey HOA1, Mm 00439249_m1 for mouse assays, life technologies) and 5µl Lightcycler 480 probe master mix (Roche Cat # 04887301001) per well in a 384 well 50 plates (Roche cat # 04887301001). Real time PCR was done in a LightCycler480 Real Time PCR system (Roche) using the ΔΔCt(RQ) assay. Each duplex was tested in two independent transfections and each transfection was assayed in duplicate, unless otherwise noted in the summary tables.

To calculate relative fold change, real time data were analyzed using the ΔΔCt method and normalized to assays performed with cells transfected with 10nM AD-1955, or mock transfected cells. IC50s were calculated using a 4 parameter fit model using XLFit and normalized to cells transfected with AD-1955 or naïve cells.

The sense and antisense sequences of AD-1955 are: SENSE: 5'-cuuAcGcuGAGuAcuucGAdTsdT-3' (SEQ ID NO: 16); and ANTISENSE: 5'-UCGAAGuACUcAGCGuAAGdTsdT-3' (SEQ ID NO: 17).

Table B: Abbreviations of nucleotide monomers used in nucleic acid sequence representation.

Abbreviation	Nucleotide(s)
A	Adenosine-3'-phosphate
Ab	beta-L-adenosine-3`-phosphate
Af	2'-fluoroadenosine-3'-phosphate
Afs	2'-fluoroadenosine-3'-phosphorothioate
As	adenosine-3'-phosphorothioate
C	cytidine-3'-phosphate
Cb	beta-L-cytidine-3'-phosphate
Cf	2'-fluorocytidine-3'-phosphate
Cfs	2'-fluorocytidine-3'-phosphorothioate
Cs	cytidine-3'-phosphorothioate

Abbreviation	Nucleotide(s)
G	guanosine-3'-phosphate
Gb	beta-L-guanosine-3`-phosphate
Gbs	beta-L-guanosine-3`-phosphorothioate
Gf	2'-fluoroguanosine-3'-phosphate
Gfs	2'-fluoroguanosine-3'-phosphorothioate
Gs	guanosine-3'-phosphorothioate
T	5'-methyluridine-3'-phosphate
Tf	2'-fluoro-5-methyluridine-3'-phosphate
Tfs	2'-fluoro-5-methyluridine-3'-phosphorothioate
Ts	5-methyluridine-3'-phosphorothioate
U	Uridine-3'-phosphate
Uf	2'-fluorouridine-3'-phosphate
Ufs	2'-fluorouridine -3'-phosphorothioate
Us	uridine -3'-phosphorothioate
N	any nucleotide (G, A, C, T or U)
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
dT	2'-deoxythymidine
dTs	2`-deoxythymidine-3`-phosphorothioate
dU	2`-deoxyuridine
s	phosphorothioate linkage
L96	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
(A3m)	3`-O-methyladenosine-2`-phosphate
(A3mx)	3'-O-methyl-xylofuranosyladenosine-2'-phosphate
(G3m)	3`-O-methylguanosine-2`-phosphate
(G3mx)	3'-O-methyl-xylofuranosylguanosine-2'-phosphate
(C3m)	3`-O-methylcytidine-2`-phosphate
(C3mx)	3'-O-methyl-xylofuranosylcytidine-2'-phosphate
(U3m)	3`-O-methyluridine-2`-phosphate
(U3mx)	3'-O-methylxylouridine-2'-phosphate

Abbreviation	Nucleotide(s)
(Chd)	2'-O-hexadecyl-cytidine-3'-phosphate
(pshe)	Hydroxyethylphosphorothioate
(Uhd)	2'-O-hexadecyl-uridine-3'-phosphate
(Tgn)	Thymidine-glycol nucleic acid (GNA) S-Isomer
(Cgn)	Cytidine-glycol nucleic acid (GNA)
(Chd)	2'-O-hexadecyl-cytidine-3'-phosphate
(Ggn)	2'-O-hexadecyl-cytidine-3'-phosphate
(Agn)	Adenosine-glycol nucleic acid (GNA)
P	5'-phosphate
(m5Cam)	2`-O-(N-methylacetamide)-5-methylcytidine-3`-phosphate
(m5Cams)	2`-O-(N-methylacetamide)-5-methylcytidine-3`-phosphorothioate
(Tam)	2`-O-(N-methylacetamide)thymidine-3`-phosphate
(Tams)	2`-O-(N-methylacetamide)thymidine-3`-phosphorothioate
(Aam)	2`-O-(N-methylacetamide)adenosine-3`-phosphate
(Aams)	2`-O-(N-methylacetamide)adenosine-3`-phosphorothioate
(Gam)	2`-O-(N-methylacetamide)guanosine-3`-phosphate
(Gams)	2`-O-(N-methylacetamide)guanosine-3`-phosphorothioate
Y34	abasic 2'-O-Methyl
Y44	2-hydroxymethyl-tetrahydrofurane-5-phosphate

Example 1. Design, Specificity and Efficacy Prediction of siRNA

siRNA design was carried out to identify siRNAs targeting human, cynomolgus monkey, mouse, and rat HAO1 transcripts annotated in the NCBI Gene database (http://www.ncbi.nlm.nih.gov/gene/).

Design used the following transcripts from the NCBI RefSeq collection: human (*Homo sapiens*) HAO1 mRNA is NM_017545.2; cynomolgus monkey (*Macaca fascicularis)* HAO1 mRNA is XM_005568381.1; Mouse (*Mus musculus)* HAO1 mRNA is NM_010403.2; Rat (*Rattus norvegicus)* HAO1 mRNA is XM_006235096.1.

Due to high primate/rodent sequence divergence, siRNA duplexes were designed in several separate batches, including but not limited to batches containing duplexes matching human and cyno transcripts only; human, cyno, mouse, and rat transcripts only; and mouse and rat transcripts only. All siRNA duplexes were designed that shared 100% identity with the listed human transcript and other species transcripts considered in each design batch (above).

The specificity of all possible 19mers was predicted from each sequence. Candidate 19mers that lacked repeats longer than 7 nucleotides were then selected. These 1069 candidate human/cyno, 184 human/cyno/mouse/rat, and 579 mouse/rat siRNAs were used in

comprehensive searches against the appropriate transcriptomes (defined as the set of NM_ and XM_ records within the human, cyno, mouse, or rat NCBI Refseq sets) using an exhaustive "brute-force" algorithm implemented in the python script 'BruteForce.py'. The script next parsed the transcript-oligo alignments to generate a score based on the position and number of mismatches between the siRNA and any potential 'off-target' transcript. The off-target score is weighted to emphasize differences in the 'seed' region of siRNAs, in positions 2-9 from the 5' end of the molecule. Each oligo-transcript pair from the brute-force search was given a mismatch score by summing the individual mismatch scores; mismatches in the position 2-9 were counted as 2.8, mismatches in the cleavage site positions 10-11 were counted as 1.2, and mismatches in region 12-19 counted as 1.0. An additional off-target prediction was carried out by comparing the frequency of heptamers and octomers derived from 3 distinct, seed-derived hexamers of each oligo. The hexamers from positions 2-7 relative to the 5' start were used to create 2 heptamers and one octomer. Heptamer1 was created by adding a 3' A to the hexamer; heptamer2 was created by adding a 5' A to the hexamer; the octomer was created by adding an A to both 5' and 3' ends of the hexamer. The frequency of octomers and heptamers in the human, cyno, mouse, or rat 3'UTRome (defined as the subsequence of the transcriptome from NCBI's Refseq database where the end of the coding region, the 'CDS', is clearly defined) was pre-calculated. The octomer frequency was normalized to the heptamer frequency using the median value from the range of octomer frequencies. A 'mirSeedScore' was then calculated by calculating the sum of ((3 X normalized octomer count) + (2 X heptamer2 count) + (1 X heptamer1 count)).

Both siRNA strands were assigned to a category of specificity according to the calculated scores: a score above 3 qualified as highly specific, equal to 3 as specific and between 2.2 and 2.8 qualified as moderately specific. The siRNAs were sorted by the specificity of the antisense strand. Duplexes from the human/cyno and mouse/rat sets whose antisense oligos lacked GC at the first position, lacked G at both positions 13 and 14, and had 3 or more Us or As in the seed region (characteristics of duplexes with high predicted efficacy) were then selected. Similarly, duplexes from the human/cyno/mouse and human/cyno/mouse/rat sets that had had 3 or more Us or As in the seed region were selected.

Candidate GalNAc-conjugated duplexes, 21 and 23 nucleotides long on the sense and antisense strands respectively, were designed by extending antisense 19mers 4 additional nucleotides in the 3' direction (preserving perfect complementarity with the target transcript). The sense strand was specified as the reverse complement of the first 21 nucleotides of the

antisense 23mer. Duplexes were selected that maintained perfect matches to all selected species transcripts across all 23 nucleotides.

Antisense strands that contained C or G at the first 5' position were modified to have a U at the first 5' position, unless doing so would introduce a run of 4 or more contiguous Us (5' → 3'), in which case they were modified to have an A at the first 5' position. Sense strands to be paired into duplexes with these "UA swapped" antisense strands were correspondingly modified to preserve complementarity. Examples described below include AD-62989 and AD-62993.

A total of 31 sense and 31 antisense derived human/cyno, 19 sense and 19 antisense derived human/cyno/mouse/rat, and 48 sense and 48 antisense derived mouse/rat 21/23mer oligos were synthesized and formed into GalNAc-conjugated duplexes.

The sequences of the sense and antisense strands of the modified duplexes are shown in Table 1, and the sequences of the sense and antisense strands of the unmodified duplexes are shown in Table 2.

Table 1a. HAO1 modified sequences

Duplex Name	Sense strand sequence	SEQ ID NO:	Antisense strand sequence	SEQ ID NO:	Species
AD-62933	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	18	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	89	Hs/Mm
AD-62939	UfsusUfuCfaAfuGfGfGfuGfuCfcUfaGfgAfL96	19	usCfscUfaGfgAfcAfcccAfuUfgAfaAfasgsu	90	Hs/Mm
AD-62944	GfsasAfaGfuCfaUfCfGfaCfaAfgAfcAfuUfL96	20	asAfsuGfuCfuUfgUfcgaUfgAfcUfuUfcsasc	91	Hs/Mm
AD-62949	UfscsAfuCfgAfcAfAfGfaCfaUfuGfgUfgAfL96	21	usCfsaCfcAfaUfgUfcuuGfuCfgAfuGfascsu	92	Hs/Mm
AD-62954	UfsusUfcAfaUfgGfGfUfgUfcCfuAfgGfaAfL96	22	usUfscCfuAfgGfaCfaccCfaUfuGfaAfasasg	93	Hs/Mm
AD-62959	AfsasUfgGfgUfgUfCfCfuAfgGfaAfcCfuUfL96	23	asAfsgGfuUfcCfuAfggaCfaCfcCfaUfusgsa	94	Hs/Mm
AD-62964	GfsasCfaGfuGfcAfCfAfaUfaUfuUfuCfcAfL96	24	usGfsgAfaAfaUfaUfuguGfcAfcUfgUfcsasg	95	Hs/Mm
AD-62969	AfscsUfuUfuCfaAfUfGfgGfuGfuCfcUfaAfL96	25	usUfsaGfgAfcAfcCfcauUfgAfaAfaGfuscsa	96	Hs/Mm
AD-62934	AfsasGfuCfaUfcGfAfCfaAfgAfcAfuUfgAfL96	26	usCfsaAfuGfuCfuUfgucGfaUfgAfcUfususc	97	Hs/Mm
AD-62940	AfsusCfgAfcAfaGfAfCfaUfuGfgUfgAfgAfL96	27	usCfsuCfaCfcAfaUfgucUfuGfuCfgAfusgsa	98	Hs/Mm
AD-62945	GfsgsGfaGfaAfaGfGfUfgUfuCfaAfgAfuAfL96	28	usAfsuCfuUfgAfaCfaccUfuUfcUfcCfcscsc	99	Hs/Mm
AD-62950	CfsusUfuUfcAfaUfGfGfgUfgUfcCfuAfgAfL96	29	usCfsuAfgGfaCfaCfccaUfuGfaAfaAfgsusc	100	Hs/Mm
AD-62955	UfscsAfaUfgGfgUfGfUfcCfuAfgGfaAfcAfL96	30	usGfsuUfcCfuAfgGfacaCfcCfaUfuGfasasa	101	Hs/Mm
AD-62960	UfsusGfaCfuUfuUfCfAfaUfgGfgUfgUfcAfL96	31	usGfsaCfaCfcCfaUfugaAfaAfgUfcAfasasa	102	Hs/Mm
AD-62965	AfsasAfgUfcAfuCfGfAfcAfaGfaCfaUfuAfL96	32	usAfsaUfgUfcUfuGfucgAfuGfaCfuUfuscsa	103	Hs/Mm
AD-62970	CfsasGfgGfgGfaGfAfAfaGfgUfgUfuCfaAfL96	33	usUfsgAfaCfaCfcUfuucUfcCfcCfcUfgsgsa	104	Hs/Mm
AD-62935	CfsasUfuGfgUfgAfGfGfaAfaAfaUfcCfuUfL96	34	asAfsgGfaUfuUfuUfccuCfaCfcAfaUfgsusc	105	Hs/Mm
AD-62941	AfscsAfuUfgGfuGfAfGfgAfaAfaAfuCfcUfL96	35	asGfsgAfuUfuUfuCfcucAfcCfaAfuGfuscsu	106	Hs/Mm
AD-62946	AfsgsGfgGfgAfgAfAfAfgGfuGfuUfcAfaAfL96	36	usUfsuGfaAfcAfcCfuuuCfuCfcCfcCfusgsg	107	Hs/Mm
AD-62951	AfsusGfgUfgGfuAfAfUfuUfgUfgAfuUfuUfL96	37	asAfsaAfuCfaCfaAfauuAfcCfaCfcAfuscsc	108	Hs
AD-62956	GfsasCfuUfgCfaUfCfCfuGfgAfaAfuAfuAfL96	38	usAfsuAfuUfuCfcAfggaUfgCfaAfgUfcscsa	109	Hs
AD-62961	GfsgsAfaGfgGfaAfGfGfuAfgAfaGfuCfuUfL96	39	asAfsgAfcUfuCfuAfccuUfcCfcUfuCfcsasc	110	Hs
AD-62966	UfsgsUfcUfuCfuGfUfUfuAfgAfuUfuCfcUfL96	40	asGfsgAfaAfuCfuAfaacAfgAfaGfaCfasgsg	111	Hs
AD-62971	CfsusUfuGfgCfuGfUfUfuCfcAfaGfaUfcUfL96	41	asGfsaUfcUfuGfgAfaacAfgCfcAfaAfgsgsa	112	Hs
AD-62936	AfsasUfgUfgUfuUfGfGfgCfaAfcGfuCfaUfL96	42	asUfsgAfcGfuUfgCfccaAfaCfaCfaUfususu	113	Hs
AD-62942	UfsgsUfgAfcUfgUfGfGfaCfaCfcCfcUfuAfL96	43	usAfsaGfgGfgUfgUfccaCfaGfuCfaCfasasa	114	Hs
AD-62947	GfsasUfgGfgGfuGfCfCfaGfcUfaCfuAfuUfL96	44	asAfsuAfgUfaGfcUfggcAfcCfcCfaUfcscsa	115	Hs
AD-62952	GfsasAfaAfuGfuGfUfUfuGfgGfcAfaCfgUfL96	45	asCfsgUfuGfcCfcAfaacAfcAfuUfuUfcsasa	116	Hs
AD-62957	GfsgsCfuGfuUfuCfCfAfaGfaUfcUfgAfcAfL96	46	usGfsuCfaGfaUfcUfuggAfaAfcAfgCfcsasa	117	Hs
AD-62962	UfscsCfaAfcAfaAfAfUfaGfcCfaCfcCfcUfL96	47	asGfsgGfgUfgGfcUfauuUfuGfuUfgGfasasa	118	Hs
AD-62967	GfsusCfuUfcUfgUfUfUfaGfaUfuUfcCfuUfL96	48	asAfsgGfaAfaUfcUfaaaCfaGfaAfgAfcsasg	119	Hs
AD-62972	UfsgsGfaAfgGfgAfAfGfgUfaGfaAfgUfcUfL96	49	asGfsaCfuUfcUfaCfcuuCfcCfuUfcCfascsa	120	Hs
AD-62937	UfscsCfuUfuGfgCfUfGfuUfuCfcAfaGfaUfL96	50	asUfscUfuGfgAfaAfcagCfcAfaAfgGfasusu	121	Hs
AD-62943	CfsasUfcUfcUfcAfGfCfuGfgGfaUfgAfuAfL96	51	usAfsuCfaUfcCfcAfgcuGfaGfaGfaUfgsgsg	122	Hs
AD-62948	GfsgsGfgUfgCfcAfGfCfuAfcUfaUfuGfaUfL96	52	asUfscAfaUfaGfuAfgcuGfgCfaCfcCfcsasu	123	Hs
AD-62953	AfsusGfuGfuUfuGfGfGfcAfaCfgUfcAfuAfL96	53	usAfsuGfaCfgUfuGfcccAfaAfcAfcAfususu	124	Hs
AD-62958	CfsusGfuUfuAfgAfUfUfuCfcUfuAfaGfaAfL96	54	usUfscUfuAfaGfgAfaauCfuAfaAfcAfgsasa	125	Hs
AD-62963	AfsgsAfaAfgAfaAfUfGfgAfcUfuGfcAfuAfL96	55	usAfsuGfcAfaGfuCfcauUfuCfuUfuCfusasg	126	Hs
AD-62968	GfscsAfuCfcUfgGfAfAfaUfaUfuUfuAfaAfL96	56	usUfsuAfaUfaUfaUfuuuCfaGfgAfuGfcsasa	127	Hs
AD-62973	CfscsUfgUfcAfgAfCfCfaUfgGfgAfaCfuAfL96	57	usAfsgUfuCfcCfaUfgguCfuGfaCfaGfgscsu	128	Hs

AD-62938	AfsasAfcAfuGfgUfGfUfgGfaUfgGfgAfuAfL96	58	usAfsuCfcCfaUfcCfacaCfcAfuGfuUfusasa	129	Hs
AD-62974	CfsusCfaGfgAfuGfAfAfaAfaUfuUfuGfaAfL96	59	usUfscAfaAfaUfuUfuucAfuCfcUfgAfgsusu	130	Hs
AD-62978	CfsasGfcAfuGfuAfUfUfaCfuUfgAfcAfaAfL96	60	usUfsuGfuCfaAfgUfaauAfcAfuGfcUfgsasa	131	Hs
AD-62982	UfsasUfgAfaCfaAfCfAfuGfcUfaAfaUfcAfL96	61	usGfsaUfuUfaGfcAfuguUfgUfuCfaUfasasu	132	Hs
AD-62986	AfsusAfuAfuCfcAfAfAfuGfuUfuUfaGfgAfL96	62	usCfscUfaAfaAfcAfuuuGfgAfuAfuAfususc	133	Hs
AD-62990	CfscsAfgAfuGfgAfAfGfcUfgUfaUfcCfaAfL96	63	usUfsgGfaUfaCfaGfcuuCfcAfuCfuGfgsasa	134	Hs
AD-62994	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	64	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	135	Hs
AD-62998	CfscsCfcGfgCfuAfAfUfuUfgUfaUfcAfaUfL96	65	asUfsuGfaUfaCfaAfauuAfgCfcGfgGfgsgsa	136	Hs
AD-63002	UfsusAfaAfcAfuGfGfCfuUfgAfaUfgGfgAfL96	66	usCfscCfaUfuCfaAfgccAfuGfuUfuAfascsa	137	Hs
AD-62975	AfsasUfgUfgUfuUfAfGfaCfaAfcGfuCfaUfL96	67	asUfsgAfcGfuUfgUfcuaAfaCfaCfaUfususu	138	Mm
AD-62979	AfscsUfaAfaGfgAfAfGfaAfuUfcCfgGfuUfL96	68	asAfscCfgGfaAfuUfcuuCfcUfuUfaGfusasu	139	Mm
AD-62983	UfsasUfaUfcCfaAfAfUfgUfuUfuAfgGfaUfL96	69	asUfscCfuAfaAfaCfauuUfgGfaUfaUfasusu	140	Mm
AD-62987	GfsusGfcGfgAfaAfGfGfcAfcUfgAfuGfuUfL96	70	asAfscAfuCfaGfuGfccuUfuCfcGfcAfcsasc	141	Mm
AD-62991	UfsasAfaAfcAfgUfGfGfuUfcUfuAfaAfuUfL96	71	asAfsuUfuAfaGfaAfccaCfuGfuUfuUfasasa	142	Mm
AD-62995	AfsusGfaAfaAfaUfUfUfuGfaAfaCfcAfgUfL96	72	asCfsuGfgUfuUfcAfaaaUfuUfuUfcAfuscsc	143	Mm
AD-62999	AfsasCfaAfaAfuAfGfCfaAfuCfcCfuUfuUfL96	73	asAfsaAfgGfgAfuUfgcuAfuUfuUfgUfusgsg	144	Mm
AD-63003	CfsusGfaAfaCfaGfAfUfcUfgUfcGfaCfuUfL96	74	asAfsgUfcGfaCfaGfaucUfgUfuUfcAfgscsa	145	Mm
AD-62976	UfsusGfuUfgCfaAfAfGfgGfcAfuUfuUfgAfL96	75	usCfsaAfaAfuGfcCfcuuUfgCfaAfcAfasusu	146	Mm
AD-62980	CfsusCfaUfuGfuUfUfAfuUfaAfcCfuGfuAfL96	76	usAfscAfgGfuUfaAfuaaAfcAfaUfgAfgsasu	147	Mm
AD-62984	CfsasAfcAfaAfaUfAfGfcAfaUfcCfcUfuUfL96	77	asAfsaGfgGfaUfuGfcuaUfuUfuGfuUfgsgsa	148	Mm
AD-62992	CfsasUfuGfuUfuAfUfUfaAfcCfuGfuAfuUfL96	78	asAfsuAfcAfgGfuUfaauAfaAfcAfaUfgsasg	149	Mm
AD-62996	UfsasUfcAfgCfuGfGfGfaAfgAfuAfuCfaAfL96	79	usUfsgAfuAfuCfuUfcccAfgCfuGfaUfasgsa	150	Mm
AD-63000	UfsgsUfcCfuAfgGfAfAfcCfuUfuUfaGfaAfL96	80	usUfscUfaAfaAfgGfuucCfuAfgGfaCfascsc	151	Mm
AD-63004	UfscsCfaAfcAfaAfAfUfaGfcAfaUfcCfcUfL96	81	asGfsgGfaUfuGfcUfauuUfuGfuUfgGfasasa	152	Mm
AD-62977	GfsgsUfgUfgCfgGfAfAfaGfgCfaCfuGfaUfL96	82	asUfscAfgUfgCfcUfuucCfgCfaCfaCfcscsc	153	Mm
AD-62981	UfsusGfaAfaCfcAfGfUfaCfuUfuAfuCfaUfL96	83	asUfsgAfuAfaAfgUfacuGfgUfuUfcAfasasa	154	Mm
AD-62985	UfsasCfuUfcCfaAfAfGfuCfuAfuAfuAfuAfL96	84	usAfsuAfuAfuAfgAfcuuUfgGfaAfgUfascsu	155	Mm
AD-62989	UfscsCfuAfgGfaAfCfCfuUfuUfaGfaAfaUfL96	85	asUfsuUfcUfaAfaAfgguUfcCfuAfgGfascsa	156	Mm
AD-62993	CfsusCfcUfgAfgGfAfAfaAfuUfuUfgGfaAfL96	86	usUfscCfaAfaAfuUfuucCfuCfaGfgAfgsasa	157	Mm
AD-62997	GfscsUfcCfgGfaAfUfGfuUfgCfuGfaAfaUfL96	87	asUfsuUfcAfgCfaAfcauUfcCfgGfaGfcsasu	158	Mm
AD-63001	GfsusGfuUfuGfuGfGfGfgAfgAfcCfaAfuAfL96	88	usAfsuUfgGfuCfuCfcccAfcAfaAfcAfcsasg	159	Mm

Table 1b: Additional HAO1 modified sequences.

Duplex Name	Sense strand sequence	SEQ ID NO:	Antisense strand sequence	SEQ ID NO:	Species
AD-62933.2	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	18	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	89	Hs/Mm
AD-62939.2	UfsusUfuCfaAfuGfGfGfuGfuCfcUfaGfgAfL96	19	usCfscUfaGfgAfcAfcccAfuUfgAfaAfasgsu	90	Hs/Mm
AD-62944.2	GfsasAfaGfuCfaUfCfCfGfaCfaAfgAfcAfuUfL96	20	asAfsuGfuCfuUfgUfcgaUfgAfcUfuUfcsasc	91	Hs/Mm
AD-62949.2	UfscsAfuCfgAfcAfAfGfaCfaUfuGfgUfgAfL96	21	usCfsaCfcAfaUfgUfcuuGfuCfgAfuGfascsu	92	Hs/Mm
AD-62954.2	UfsusUfcAfaUfgGfGfUfgUfcCfuAfgGfaAfL96	22	usUfscCfuAfgGfaCfaccCfaUfuGfaAfasasg	93	Hs/Mm
AD-62959.2	AfsasUfgGfgUfgUfCfCfuAfgGfaAfcCfuUfL96	23	asAfsgGfuUfcCfuAfggaCfaCfcCfaUfusgsa	94	Hs/Mm
AD-62964.2	GfsasCfaGfuGfcAfCfAfaUfaUfuUfuCfcAfL96	24	usGfsgAfaAfaUfaUfuguGfcAfcUfgUfcsasg	95	Hs/Mm
AD-62969.2	AfscsUfuUfuCfaAfUfGfgGfuGfuCfcUfaAfL96	25	usUfsaGfgAfcAfcCfcauUfgAfaAfaGfuscsa	96	Hs/Mm
AD-62934.2	AfsasGfuCfaUfcGfAfCfaAfgAfcAfuUfgAfL96	26	usCfsaAfuGfuCfuUfgucGfaUfgAfcUfususc	97	Hs/Mm
AD-62940.2	AfsusCfgAfcAfaGfAfCfaUfuGfgUfgAfgAfL96	27	usCfsuCfaCfcAfaUfgucUfuGfuCfgAfusgsa	98	Hs/Mm
AD-62945.2	GfsgsGfaGfaAfaGfGfUfgUfuCfaAfgAfuAfL96	28	usAfsuCfuUfgAfaCfaccUfuUfcUfcCfcscsc	99	Hs/Mm
AD-62950.2	CfsusUfuUfcAfaUfGfGfgUfgUfcCfuAfgAfL96	29	usCfsuAfgGfaCfaCfccaUfuGfaAfaAfgsusc	100	Hs/Mm
AD-62955.2	UfscsAfaUfgGfgUfGfUfcCfuAfgGfaAfcAfL96	30	usGfsuUfcCfuAfgGfacaCfcCfaUfuGfasasa	101	Hs/Mm
AD-62960.2	UfsusGfaCfuUfuUfCfAfaUfgGfgUfgUfcAfL96	31	usGfsaCfaCfcCfaUfugaAfaAfgUfcAfasasa	102	Hs/Mm
AD-62965.2	AfsasAfgUfcAfuCfGfAfcAfaGfaCfaUfuAfL96	32	usAfsaUfgUfcUfuGfucgAfuGfaCfuUfuscsa	103	Hs/Mm
AD-62970.2	CfsasGfgGfgGfaGfAfAfaGfgUfgUfuCfaAfL96	33	usUfsgAfaCfaCfcUfuucUfcCfcCfcUfgsgsa	104	Hs/Mm
AD-62935.2	CfsasUfuGfgUfgAfGfGfaAfaAfaUfcCfuUfL96	34	asAfsgGfaUfuUfuUfccuCfaCfcAfaUfgsusc	105	Hs/Mm
AD-62941.2	AfscsAfuUfgGfuGfAfGfgAfaAfaAfuCfcUfL96	35	asGfsgAfuUfuUfuCfcucAfcCfaAfuGfuscsu	106	Hs/Mm
AD-62946.2	AfsgsGfgGfgAfgAfAfAfgGfuGfuUfcAfaAfL96	36	usUfsuGfaAfcAfcCfuuuCfuCfcCfcCfusgsg	107	Hs/Mm
AD-62951.2	AfsusGfgUfgGfuAfAfUfuUfgUfgAfuUfuUfL96	37	asAfsaAfuCfaCfaAfauuAfcCfaCfcAfuscsc	108	Hs
AD-62956.2	GfsasCfuUfgCfaUfCfCfuGfgAfaAfuAfuAfL96	38	usAfsuAfuUfuCfcAfggaUfgCfaAfgUfcscsa	109	Hs
AD-62961.2	GfsgsAfaGfgGfaAfGfGfuAfgAfaGfuCfuUfL96	39	asAfsgAfcUfuCfuAfccuUfcCfcUfuCfcsasc	110	Hs
AD-62966.2	UfsgsUfcUfuCfuGfUfUfuAfgAfuUfuCfcUfL96	40	asGfsgAfaAfuCfuAfaacAfgAfaGfaCfasgsg	111	Hs
AD-62971.2	CfsusUfuGfgCfuGfUfUfuCfcAfaGfaUfcUfL96	41	asGfsaUfcUfuGfgAfaacAfgCfcAfaAfgsgsa	112	Hs
AD-62936.2	AfsasUfgUfgUfuUfGfGfgCfaAfcGfuCfaUfL96	42	asUfsgAfcGfuUfgCfccaAfaCfaCfaUfususu	113	Hs
AD-62942.2	UfsgsUfgAfcUfgUfGfGfaCfaCfcCfcUfuAfL96	43	usAfsaGfgGfgUfgUfccaCfaGfuCfaCfasasa	114	Hs
AD-62947.2	GfsasUfgGfgGfuGfCfCfaGfcUfaCfuAfuUfL96	44	asAfsuAfgUfaGfcUfggcAfcCfcCfaUfcscsa	115	Hs
AD-62952.2	GfsasAfaAfuGfuGfUfUfuGfgGfcAfaCfgUfL96	45	asCfsgUfuGfcCfcAfaacAfcAfuUfuUfcsasa	116	Hs
AD-62957.2	GfsgsCfuGfuUfuCfCfAfaGfaUfcUfgAfcAfL96	46	usGfsuCfaGfaUfcUfuggAfaAfcAfgCfcsasa	117	Hs
AD-62962.2	UfscsCfaAfcAfaAfAfUfaGfcCfaCfcCfcUfL96	47	asGfsgGfgUfgGfcUfauuUfuGfuUfgGfasasa	118	Hs
AD-62967.2	GfsusCfuUfcUfgUfUfUfaGfaUfuUfcCfuUfL96	48	asAfsgGfaAfaUfcUfaaaCfaGfaAfgAfcsasg	119	Hs
AD-62972.2	UfsgsGfaAfgGfgAfAfGfgUfaGfaAfgUfcUfL96	49	asGfsaCfuUfcUfaCfcuuCfcCfuUfcCfascsa	120	Hs
AD-62937.2	UfscsCfuUfuGfgCfUfGfuUfuCfcAfaGfaUfL96	50	asUfscUfuGfgAfaAfcagCfcAfaAfgGfasusu	121	Hs
AD-62943.2	CfsasUfcUfcUfcAfGfCfuGfgGfaUfgAfuAfL96	51	usAfsuCfaUfcCfcAfgcuGfaGfaGfaUfgsgsg	122	Hs
AD-62948.2	GfsgsGfgUfgCfcAfGfCfuAfcUfaUfuGfaUfL96	52	asUfscAfaUfaGfuAfgcuGfgCfaCfcCfcsasu	123	Hs
AD-62953.2	AfsusGfuGfuUfuGfGfGfcAfaCfgUfcAfuAfL96	53	usAfsuGfaCfgUfuGfcccAfaAfcAfcAfususu	124	Hs
AD-62958.2	CfsusGfuUfuAfgAfUfUfuCfcUfuAfaGfaAfL96	54	usUfscUfuAfaGfgAfaauCfuAfaAfcAfgsasa	125	Hs
AD-62963.2	AfsgsAfaAfgAfaAfUfGfgAfcUfuGfcAfuAfL96	55	usAfsuGfcAfaGfuCfcauUfuCfuUfuCfusasg	126	Hs
AD-62968.2	GfscsAfuCfcUfgGfAfAfaUfaUfuUfuAfaAfL96	56	usUfsuAfaUfaUfaUfuucCfaGfgAfuGfcsasa	127	Hs
AD-62973.2	CfscsUfgUfcAfgAfCfCfaUfgGfgAfaCfuAfL96	57	usAfsgUfuCfcCfaUfgguCfuGfaCfaGfgscsu	128	Hs
AD-62938.2	AfsasAfcAfuGfgUfGfUfgGfaUfgGfgAfuAfL96	58	usAfsuCfcCfaUfcCfacaCfcAfuGfuUfusasa	129	Hs

AD-62974.2	CfsusCfaGfgAfuGfAfAfaAfaUfuUfuGfaAfL96	59	usUfscAfaAfaUfuUfuucAfuCfcUfgAfgsusu	130	Hs
AD-62978.2	CfsasGfcAfuGfuAfUfUfaCfuUfgAfcAfaAfL96	60	usUfsuGfuCfaAfgUfaauAfcAfuGfcUfgsasa	131	Hs
AD-62982.2	UfsasUfgAfaCfaAfCfAfuGfcUfaAfaUfcAfL96	61	usGfsaUfuUfaGfcAfuguUfgUfuCfaUfasasu	132	Hs
AD-62986.2	AfsusAfuAfuCfcAfAfAfuGfuUfuUfaGfgAfL96	62	usCfscUfaAfaAfcAfuuuGfgAfuAfuAfususc	133	Hs
AD-62990.2	CfscsAfgAfuGfgAfAfGfcUfgUfaUfcCfaAfL96	63	usUfsgGfaUfaCfaGfcuuCfcAfuCfuGfgsasa	134	Hs
AD-62994.2	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	64	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	135	Hs
AD-62998.2	CfscsCfcGfgCfuAfAfUfuUfgUfaUfcAfaUfL96	65	asUfsuGfaUfaCfaAfauuAfgCfcGfgGfgsgsa	136	Hs
AD-63002.2	UfsusAfaAfcAfuGfGfCfuUfgAfaUfgGfgAfL96	66	usCfscCfaUfuCfaAfgccAfuGfuUfuAfascsa	137	Hs
AD-62975.2	AfsasUfgUfgUfuUfAfGfaCfaAfcGfuCfaUfL96	67	asUfsgAfcGfuUfgUfcuaAfaCfaCfaUfususu	138	Mm
AD-62979.2	AfscsUfaAfaGfgAfAfGfaAfuUfcCfgGfuUfL96	68	asAfscCfgGfaAfuUfcuuCfcUfuUfaGfusasu	139	Mm
AD-62983.2	UfsasUfaUfcCfaAfAfUfgUfuUfuAfgGfaUfL96	69	asUfscCfuAfaAfaCfauuUfgGfaUfaUfasusu	140	Mm
AD-62987.2	GfsusGfcGfgAfaAfGfGfcAfcUfgAfuGfuUfL96	70	asAfscAfuCfaGfuGfccuUfuCfcGfcAfcsasc	141	Mm
AD-62991.2	UfsasAfaAfcAfgUfGfGfuUfcUfuAfaAfuUfL96	71	asAfsuUfuAfaGfaAfccaCfuGfuUfuUfasasa	142	Mm
AD-62995.2	AfsusGfaAfaAfaUfUfUfuGfaAfaCfcAfgUfL96	72	asCfsuGfgUfuUfcAfaaaUfuUfuUfcAfuscsc	143	Mm
AD-62999.2	AfsasCfaAfaAfuAfGfCfaAfuCfcCfuUfuUfL96	73	asAfsaAfgGfgAfuUfgcuAfuUfuUfgUfusgsg	144	Mm
AD-63003.2	CfsusGfaAfaCfaGfAfUfcUfgUfcGfaCfuUfL96	74	asAfsgUfcGfaCfaGfaucUfgUfuUfcAfgscsa	145	Mm
AD-62976.2	UfsusGfuUfgCfaAfAfGfgGfcAfuUfuUfgAfL96	75	usCfsaAfaAfuGfcCfcuuUfgCfaAfcAfasusu	146	Mm
AD-62980.2	CfsusCfaUfuGfuUfUfAfuUfaAfcCfuGfuAfL96	76	usAfscAfgGfuUfaAfuaaAfcAfaUfgAfgsasu	147	Mm
AD-62984.2	CfsasAfcAfaAfaUfAfGfcAfaUfcCfcUfuUfL96	77	asAfsaGfgGfaUfuGfcuaUfuUfuGfuUfgsgsa	148	Mm
AD-62992.2	CfsasUfuGfuUfuAfUfUfaAfcCfuGfuAfuUfL96	78	asAfsuAfcAfgGfuUfaauAfaAfcAfaUfgsasg	149	Mm
AD-62996.2	UfsasUfcAfgCfuGfGfGfaAfgAfuAfuCfaAfL96	79	usUfsgAfuAfuCfuUfcccAfgCfuGfaUfasgsa	150	Mm
AD-63000.2	UfsgsUfcCfuAfgGfAfAfcCfuUfuUfaGfaAfL96	80	usUfscUfaAfaAfgGfuucCfuAfgGfaCfascsc	151	Mm
AD-63004.2	UfscsCfaAfcAfaAfAfUfaGfcAfaUfcCfcUfL96	81	asGfsgGfaUfuGfcUfauuUfuGfuUfgGfasasa	152	Mm
AD-62977.2	GfsgsUfgUfgCfgGfAfAfaGfgCfaCfuGfaUfL96	82	asUfscAfgUfgCfcUfuucCfgCfaCfaCfcscsc	153	Mm
AD-62981.2	UfsusGfaAfaCfcAfGfUfaCfuUfuAfuCfaUfL96	83	asUfsgAfuAfaAfgUfacuGfgUfuUfcAfasasa	154	Mm
AD-62985.2	UfsasCfuUfcCfaAfAfGfuCfuAfuAfuAfuAfL96	84	usAfsuAfuAfuAfgAfcuuUfgGfaAfgUfascsu	155	Mm
AD-62989.2	UfscsCfuAfgGfaAfCfCfuUfuUfuAfgAfaAfL96	85	asUfsuUfcUfaAfaAfgguUfcCfuAfgGfascsa	156	Mm
AD-62993.2	CfsusCfcUfgAfgGfAfAfaAfuUfuUfgGfaAfL96	86	usUfscCfaAfaAfuUfuucCfuCfaGfgAfgsasa	157	Mm
AD-62997.2	GfscsUfcCfgGfaAfUfGfuUfgCfuGfaAfaUfL96	87	asUfsuUfcAfgCfaAfcauUfcCfgGfaGfcsasu	158	Mm
AD-63001.2	GfsusGfuUfuGfuGfGfGfgAfgAfcCfaAfuAfL96	88	usAfsuUfgGfuCfuCfcccAfcAfaAfcAfcsasg	159	Mm
AD-62933.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	160	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	277	
AD-65630.1	Y44gsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	161	PusUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	278	
AD-65636.1	gsasauguGfaAfAfGfucauCfgacaaL96	162	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	279	
AD-65642.1	gsasauguGfaAfAfGfucaucgacaaL96	163	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	280	
AD-65647.1	gsasauguGfaaAfGfucaucgacaaL96	164	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	281	
AD-65652.1	gsasauguGfaaaGfucaucGfacaaL96	165	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	282	
AD-65657.1	gsasaugugaaaGfucaucGfacaaL96	166	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	283	
AD-65662.1	gsasauguGfaaaGfucaucgacaaL96	167	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	284	
AD-65625.1	AfsusGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	168	usUfsgUfcGfaUfgAfcuuUfcAfcAfususc	285	
AD-65631.1	asusguGfaAfAfGfucaucgacaaL96	169	usUfsgucGfaugacuuUfcAfcaususc	286	
AD-65637.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	170	usUfsgucGfaUfgAfcuuUfcAfcauucsusg	287	
AD-65643.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	171	usUfsgucGfaUfGfacuuUfcAfcauucsusg	288	
AD-65648.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	172	usUfsgucGfaugacuuUfcAfcauucsusg	289	
AD-65653.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	173	usUfsgucGfaugacuuUfcacauucsusg	290	
AD-65658.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	174	usUfsgucgaugacuuUfcacauucsusg	291	

AD-65663.1	gsasauguGfaAfAfGfucaucgacaaL96	175	usUfsgucGfaUfgAfcuuUfcAfcauucsusg	292	
AD-65626.1	gsasauguGfaAfAfGfucaucgacaaL96	176	usUfsgucGfaUfGfacuuUfcAfcauucsusg	293	
AD-65638.1	gsasauguGfaaAfGfucaucgacaaL96	177	usUfsgucGfaUfgAfcuuUfcAfcauucsusg	294	
AD-65644.1	gsasauguGfaaAfGfucaucgacaaL96	178	usUfsgucGfaUfGfacuuUfcAfcauucsusg	295	
AD-65649.1	gsasauguGfaaAfGfucaucgacaaL96	179	usUfsgucGfaugacuuUfcAfcauucsusg	296	
AD-65654.1	gsasaugugaaagucau(Cgn)gacaaL96	180	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	297	
AD-65659.1	gsasaugdTgaaagucau(Cgn)gacaaL96	181	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	298	
AD-65627.1	gsasaudGugaaadGucau(Cgn)gacaaL96	182	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	299	
AD-65633.1	gsasaugdTgaaadGucau(Cgn)gacaaL96	183	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	300	
AD-65639.1	gsasaugudGaaadGucau(Cgn)gacaaL96	184	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	301	
AD-65645.1	gsasaugugaaadGucaucdGacaaL96	185	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	302	
AD-65650.1	gsasaugugaaadGucaucdTacaaL96	186	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	303	
AD-65655.1	gsasaugugaaadGucaucY34acaaL96	187	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	304	
AD-65660.1	gsasaugugaaadGucadTcdTacaaL96	188	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	305	
AD-65665.1	gsasaugugaaadGucaucdGadCaaL96	189	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	306	
AD-65628.1	gsasaugugaaadGucaucdTadCaaL96	190	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	307	
AD-65634.1	gsasaugugaaadGucaucY34adCaaL96	191	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	308	
AD-65646.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	192	usdTsgucgaugdAcuudTcacauucsusg	309	
AD-65656.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	193	usUsgucgaugacuudTcacauucsusg	310	
AD-65661.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	194	usdTsgucdGaugacuudTcacauucsusg	311	
AD-65666.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	195	usUsgucdGaugacuudTcacauucsusg	312	
AD-65629.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	196	usdTsgucgaugacuudTcdAcauucsusg	313	
AD-65635.1	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	197	usdTsgucdGaugacuudTcdAcauucsusg	314	
AD-65641.1	gsasaugugaaadGucau(Cgn)gacaaL96	198	usdTsgucgaugdAcuudTcacauucsusg	315	
AD-62994.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	199	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	316	
AD-65595.1	gsascuuuCfaUfCfCfuggaAfauauaL96	200	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	317	
AD-65600.1	gsascuuuCfaUfCfCfuggaaauauaL96	201	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	318	
AD-65610.1	gsascuuuCfaucCfuggaaAfuauaL96	202	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	319	
AD-65615.1	gsascuuucaucCfuggaaAfuauaL96	203	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	320	
AD-65620.1	gsascuuuCfaucCfuggaaauauaL96	204	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	321	
AD-65584.1	CfsusUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	205	usAfsuAfuUfuCfcAfggaUfgAfaAfgsusc	322	
AD-65590.1	csusuuCfaUfCfCfuggaaauauaL96	206	usAfsuauUfuccaggaUfgAfaagsusc	323	
AD-65596.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	207	usAfsuauUfuCfcAfggaUfgAfaagucscsa	324	
AD-65601.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	208	usAfsuauUfuCfCfaggaUfgAfaagucscsa	325	
AD-65606.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	209	usAfsuauUfuccaggaUfgAfaagucscsa	326	
AD-65611.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	210	usAfsuauUfuccaggaUfgaaagucscsa	327	
AD-65616.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	211	usAfsuauuuccaggaUfgaaagucscsa	328	
AD-65621.1	gsascuuuCfaUfCfCfuggaaauauaL96	212	usAfsuauUfuCfcAfggaUfgAfaagucscsa	329	
AD-65585.1	gsascuuuCfaUfCfCfuggaaauauaL96	213	usAfsuauUfuCfCfaggaUfgAfaagucscsa	330	
AD-65591.1	gsascuuuCfaUfCfCfuggaaauauaL96	214	usAfsuauUfuccaggaUfgAfaagucscsa	331	
AD-65597.1	gsascuuuCfauCfCfuggaaauauaL96	215	usAfsuauUfuCfcAfggaUfgAfaagucscsa	332	
AD-65602.1	gsascuuuCfauCfCfuggaaauauaL96	216	usAfsuauUfuCfCfaggaUfgAfaagucscsa	333	
AD-65607.1	gsascuuuCfauCfCfuggaaauauaL96	217	usAfsuauUfuccaggaUfgAfaagucscsa	334	
AD-65612.1	gsascuuucauccuggaa(Agn)uauaL96	218	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	335	
AD-65622.1	gsascuuucaucdCuggaa(Agn)uauaL96	219	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	336	

AD-65586.1	gsascudTucaucdCuggaa(Agn)uauaL96	220	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	337	
AD-65592.1	gsascuudTcaucdCuggaa(Agn)uauaL96	221	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	338	
AD-65598.1	gsascuuudCaucdCuggaa(Agn)uauaL96	222	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	339	
AD-65603.1	gsascuuucaucdCuggaadAuauaL96	223	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	340	
AD-65608.1	gsascuuucaucdCuggaadTuauaL96	224	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	341	
AD-65613.1	gsascuuucaucdCuggaaY34uauaL96	225	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	342	
AD-65618.1	gsascuuucaucdCuggdAadTuauaL96	226	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	343	
AD-65623.1	gsascuuucaucdCuggaadTudAuaL96	227	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	344	
AD-65587.1	gsascuuucaucdCuggaa(Agn)udAuaL96	228	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	345	
AD-65593.1	gsascuudTcaucdCuggaadAudAuaL96	229	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	346	
AD-65599.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	230	usdAsuauuuccdAggadTgaaagucscsa	347	
AD-65604.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	231	usdAsuauuuccaggadTgaaagucscsa	348	
AD-65609.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	232	usAsuauuuccaggadTgaaagucscsa	349	
AD-65614.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	233	usdAsuaudTuccaggadTgaaagucscsa	350	
AD-65619.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	234	usAsuaudTuccaggadTgaaagucscsa	351	
AD-65624.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	235	usdAsuauuuccaggadTgdAaagucscsa	352	
AD-65588.1	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	236	usdAsuaudTuccaggadTgdAaagucscsa	353	
AD-65594.1	gsascuuucaucdCuggaa(Agn)uauaL96	237	usdAsuauuuccdAggadTgaaagucscsa	354	
AD-68309.1	asgsaaagGfuGfUfUfcaagaugucaL96	238	usGfsacaUfcUfUfgaacAfcCfuuucuscsc	355	
AD-68303.1	csasuccuGfgAfAfAfuauauuaacuL96	239	asGfsuuaAfuAfUfauuuCfcAfggaugsasa	356	
AD-65626.5	gsasauguGfaAfAfGfucaucgacaaL96	240	usUfsgucGfaUfGfacuuUfcAfcauucsusg	357	
AD-68295.1	asgsugcaCfaAfUfAfuuuucccauaL96	241	usAfsuggGfaAfAfauauUfgUfgcacusgsu	358	
AD-68273.1	gsasaaguCfaUfCfGfacaagacauuL96	242	asAfsuguCfuUfGfucgaUfgAfcuuucsasc	359	
AD-68297.1	asasugugAfaAfGfUfcaucgacaaaL96	243	usUfsuguCfgAfUfgacuUfuCfacauuscsu	360	
AD-68287.1	csusggaaAfuAfUfAfuuaacuguuaL96	244	usAfsacaGfuUfAfauauAfuUfuccagsgsa	361	
AD-68300.1	asusuuucCfcAfUfCfuguauuauuuuL96	245	asAfsauaAfuAfCfagauGfgGfaaaausasu	362	
AD-68306.1	usgsucguUfcUfUfUfuccaacaaaaL96	246	usUfsuugUfuGfGfaaaaGfaAfcgacascsc	363	
AD-68292.1	asusccugGfaAfAfUfauauuaacuaL96	247	usAfsguuAfaUfAfuauuUfcCfaggausgsa	364	
AD-68298.1	gscsauuuUfgAfGfAfggugaugauaL96	248	usAfsucaUfcAfCfcucuCfaAfaaugcscsc	365	
AD-68277.1	csasggggGfaGfAfAfagguguucaaL96	249	usUfsgaaCfaCfCfuuucUfcCfcccugsgsa	366	
AD-68289.1	gsgsaaauAfuAfUfUfaacuguuaaaL96	250	usUfsuaaCfaGfUfuaauAfuAfuuuccsasg	367	
AD-68272.1	csasuuggUfgAfGfGfaaaaauccuuL96	251	asAfsggaUfuUfUfuccuCfaCfcaaugsusc	368	
AD-68282.1	gsgsgagaAfaGfGfUfguucaagauaL96	252	usAfsucuUfgAfAfcaccUfuUfcucccscsc	369	
AD-68285.1	gsgscauuUfuGfAfGfaggugaugauL96	253	asUfscauCfaCfCfucucAfaAfaugccscsu	370	
AD-68290.1	usascaaaGfgGfUfGfucguucuuuuL96	254	asAfsaagAfaCfGfacacCfcUfuuguasusu	371	
AD-68296.1	usgsggauCfuUfGfGfugucgaaucaL96	255	usGfsauuCfgAfCfaccaAfgAfucccasusu	372	
AD-68288.1	csusgacaGfuGfCfAfcaauauuuuaL96	256	usAfsaaaUfaUfUfgugcAfcUfgucagsasu	373	
AD-68299.1	csasgugcAfcAfAfUfauuuucccauL96	257	asUfsgggAfaAfAfuauuGfuGfcacugsusc	374	
AD-68275.1	ascsuuuuCfaAfUfGfgguguccuaaL96	258	usUfsaggAfcAfCfccauUfgAfaaaguscsa	375	
AD-68274.1	ascsauugGfuGfAfGfgaaaaauccuL96	259	asGfsgauUfuUfUfccucAfcCfaauguscsu	376	
AD-68294.1	ususgcuuUfuGfAfCfuuuucaaugaL96	260	usCfsauuGfaAfAfagucAfaAfagcaasusg	377	
AD-68302.1	csasuuuuGfaGfAfGfgugaugaugaL96	261	usCfsaucAfuCfAfccucUfcAfaaaugscsc	378	
AD-68279.1	ususgacuUfuUfCfAfaugggugucaL96	262	usGfsacaCfcCfAfuugaAfaAfgucaasasa	379	
AD-68304.1	csgsacuuCfuGfUfUfuuaggacagaL96	263	usCfsuguCfcUfAfaaacAfgAfagucgsasc	380	
AD-68286.1	csuscugaGfuGfGfGfugccagaauaL96	264	usAfsuucUfgGfCfacccAfcUfcagagscsc	381	

AD-68291.1	gsgsgugcCfaGfAfAfugugaaaguaL96	265	usAfscuuUfcAfCfauucUfgGfcacccsasc	382	
AD-68283.1	uscsaaugGfgUfGfUfccuaggaacaL96	266	usGfsuucCfuAfGfgacaCfcCfauugasasa	383	
AD-68280.1	asasagucAfuCfGfAfcaagacauuaL96	267	usAfsaugUfcUfUfgucgAfuGfacuuuscsa	384	
AD-68293.1	asususuugAfgAfGfGfugaugaugcaL96	268	usGfscauCfaUfCfaccuCfuCfaaaausgsc	385	
AD-68276.1	asuscgacAfaGfAfCfauuggugagaL96	269	usCfsucaCfcAfAfugucUfuGfucgausgsa	386	
AD-68308.1	gsgsugccAfgAfAfUfgugaaagucaL96	270	usGfsacuUfuCfAfcauuCfuGfgcacccsca	387	
AD-68278.1	gsascaguGfcAfCfAfauauuuuccaL96	271	usGfsgaaAfaUfAfuuguGfcAfcugucsasg	388	
AD-68307.1	ascsaaagAfgAfCfAfcugugcagaaL96	272	usUfscugCfaCfAfguguCfuCfuuuguscsa	389	
AD-68284.1	ususuucaAfuGfGfGfuguccuaggaL96	273	usCfscuaGfgAfCfacccAfuUfgaaaasgsu	390	
AD-68301.1	cscsguuuCfcAfAfGfaucugacaguL96	274	asCfsuguCfaGfAfucuuGfgAfaacggscsc	391	
AD-68281.1	asgsggggAfgAfAfAfgguguucaaaL96	275	usUfsugaAfcAfCfcuuuCfuCfccccusgsg	392	
AD-68305.1	asgsucauCfgAfCfAfagacauugguL96	276	asCfscaaUfgUfCfuuguCfgAfugacususu	393	

Table 2a. HAO1 unmodified sequences (human and human/mouse)

Duplex Name	SEQ ID NO:	Sense strand sequence	SEQ ID NO:	Antisense strand sequence	Position in NM_017545.2
AD-62933	394	GAAUGUGAAAGUCAUCGACAA	443	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-62939	395	UUUUCAAUGGGUGUCCUAGGA	444	UCCUAGGACACCCAUUGAAAAGU	1302-1324
AD-62944	396	GAAAGUCAUCGACAAGACAUU	445	AAUGUCUUGUCGAUGACUUUCAC	1078-1100
AD-62949	397	UCAUCGACAAGACAUUGGUGA	446	UCACCAAUGUCUUGUCGAUGACU	1083-1105
AD-62954	398	UUUCAAUGGGUGUCCUAGGAA	447	UUCCUAGGACACCCAUUGAAAAG	1303-1325
AD-62959	399	AAUGGGUGUCCUAGGAACCUU	448	AAGGUUCCUAGGACACCCAUUGA	1307-1329
AD-62964	400	GACAGUGCACAAUAUUUUCCA	449	UGGAAAAUAUUGUGCACUGUCAG	1134-1156_C21A
AD-62969	401	ACUUUUCAAUGGGUGUCCUAA	450	UUAGGACACCCAUUGAAAAGUCA	1300-1322_G21A
AD-62934	402	AAGUCAUCGACAAGACAUUGA	451	UCAAUGUCUUGUCGAUGACUUUC	1080-1102_G21A
AD-62940	403	AUCGACAAGACAUUGGUGAGA	452	UCUCACCAAUGUCUUGUCGAUGA	1085-1107_G21A
AD-62945	404	GGGAGAAAGGUGUUCAAGAUA	453	UAUCUUGAACACCUUUCUCCCCC	996-1018_G21A
AD-62950	405	CUUUUCAAUGGGUGUCCUAGA	454	UCUAGGACACCCAUUGAAAAGUC	1301-1323_G21A
AD-62955	406	UCAAUGGGUGUCCUAGGAACA	455	UGUUCCUAGGACACCCAUUGAAA	1305-1327_C21A
AD-62960	407	UUGACUUUUCAAUGGGUGUCA	456	UGACACCCAUUGAAAAGUCAAAA	1297-1319_C21A
AD-62965	408	AAAGUCAUCGACAAGACAUUA	457	UAAUGUCUUGUCGAUGACUUUCA	1079-1101_G21A
AD-62970	409	CAGGGGGAGAAAGGUGUUCAA	458	UUGAACACCUUUCUCCCCCUGGA	992-1014
AD-62935	410	CAUUGGUGAGGAAAAAUCCUU	459	AAGGAUUUUUUCCUCACCAAUGUC	1095-1117
AD-62941	411	ACAUUGGUGAGGAAAAAUCCU	460	AGGAUUUUUCCUCACCAAUGUCU	1094-1116
AD-62946	412	AGGGGGAGAAAGGUGUUCAAA	461	UUUGAACACCUUUCUCCCCCUGG	993-1015_G21A
AD-62974	413	CUCAGGAUGAAAAAUUUUGAA	462	UUCAAAAUUUUUUCAUCCUGAGUU	563-585
AD-62978	414	CAGCAUGUAUUACUUGACAAA	463	UUUGUCAAGUAAUACAUGCUGAA	1173-1195
AD-62982	415	UAUGAACAACAUGCUAAAUCA	464	UGAUUUAGCAUGUUGUUUCAUAAU	53-75
AD-62986	416	AUAUAUCCAAAUGUUUUAGGA	465	UCCUAAAACAUUUGGAUAUAUUC	1679-1701
AD-62990	417	CCAGAUGGAAGCUGUAUCCAA	466	UUGGAUACAGCUUCCAUCUGGAA	156-178
AD-62994	418	GACUUUCAUCCUGGAAAUAUA	467	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-62998	419	CCCCGGCUAAUUUGUAUCAAU	468	AUUGAUACAAAUUAGCCGGGGGA	29-51
AD-63002	420	UUAAACAUGGCUUGAAUGGGA	469	UCCCAUUCAAGCCAUGUUUAACA	765-787
AD-62975	421	AAUGUGUUUAGACAACGUCAU	470	AUGACGUUGUCUAAACACAUUUU	1388-1410
AD-62979	422	ACUAAAGGAAGAAUUCCGGUU	471	AACCGGAAUUCUUCCUUUAGUAU	1027-1049
AD-62983	423	UAUAUCCAAAUGUUUUAGGAU	472	AUCCUAAAACAUUUGGAUAUAUU	1680-1702
AD-62987	424	GUGCGGAAAGGCACUGAUGUU	473	AACAUCAGUGCCUUUCCGCACAC	902-924
AD-62991	425	UAAAACAGUGGUUCUUAAAUU	474	AAUUUAAGAACCACUGUUUUAAA	1521-1543
AD-62995	426	AUGAAAAAUUUUGAAACCAGU	475	ACUGGUUUCAAAAUUUUUCAUCC	569-591
AD-62999	427	AACAAAAUAGCAAUCCCUUUU	476	AAAAGGGAUUGCUAUUUUGUUGG	1264-1286
AD-63003	428	CUGAAACAGAUCUGUCGACUU	477	AAGUCGACAGAUCUGUUUCAGCA	195-217
AD-62976	429	UUGUUGCAAAGGGCAUUUUGA	478	UCAAAAUGCCCUUUGCAACAAUU	720-742
AD-62980	430	CUCAUUGUUUAUUAACCUGUA	479	UACAGGUUAAUAAACAAUGAGAU	1483-1505
AD-62984	431	CAACAAAAUAGCAAUCCCUUU	480	AAAGGGAUUGCUAUUUUGUUGGA	1263-1285
AD-62992	432	CAUUGUUUAUUAACCUGUAUU	481	AAUACAGGUUAAUAAACAAUGAG	1485-1507
AD-62996	433	UAUCAGCUGGGAAGAUAUCAA	482	UUGAUAUCUUCCCAGCUGAUAGA	670-692
AD-63000	434	UGUCCUAGGAACCUUUUAGAA	483	UUCUAAAAGGUUCCUAGGACACC	1313-1335
AD-63004	435	UCCAACAAAAUAGCAAUCCCU	484	AGGGAUUGCUAUUUUGUUGGAAA	1261-1283
AD-62977	436	GGUGUGCGGAAAGGCACUGAU	485	AUCAGUGCCUUUCCGCACACCCC	899-921
AD-62981	437	UUGAAACCAGUACUUUAUCAU	486	AUGAUAAAGUACUGGUUUCAAAA	579-601
AD-62985	438	UACUUCCAAAGUCUAUAUAUA	487	UAUAUAUAGACUUUGGAAGUACU	75-97_G21A
AD-62989	439	UCCUAGGAACCUUUUAGAAAU	488	AUUUCUAAAAGGUUCCUAGGACA	1315-1337_G21U
AD-62993	440	CUCCUGAGGAAAAUUUUGGAA	489	UUCCAAAAUUUUCCUCAGGAGAA	603-625_G21A
AD-62997	441	GCUCCGGAAUGUUGCUGAAAU	490	AUUUCAGCAACAUUCCGGAGCAU	181-203_C21U
AD-63001	442	GUGUUUGUGGGGAGACCAAUA	491	UAUUGGUCUCCCCACAAACACAG	953-975_C21A

Table 2b. HAO1 unmodified sequences (mouse)

Duplex Name	SEQ ID NO:	Sense strand sequence	SEQ ID NO:	Antisense strand sequence	Position in NM_010403.2
AD-62951	492	AUGGUGGUAAUUUGUGAUUUU	514	AAAAUCACAAAUUACCACCAUCC	1642-1664
AD-62956	493	GACUUGCAUCCUGGAAAUAUA	515	UAUAUUUCCAGGAUGCAAGUCCA	1338-1360
AD-62961	494	GGAAGGGAAGGUAGAAGUCUU	516	AAGACUUCUACCUUCCCUUCCAC	864-886
AD-62966	495	UGUCUUCUGUUUAGAUUUCCU	517	AGGAAAUCUAAACAGAAGACAGG	1506-1528
AD-62971	496	CUUUGGCUGUUUCCAAGAUCU	518	AGAUCUUGGAAACAGCCAAAGGA	1109-1131
AD-62936	497	AAUGUGUUUGGGCAACGUCAU	519	AUGACGUUGCCCAAACACAUUUU	1385-1407
AD-62942	498	UGUGACUGUGGACACCCCUUA	520	UAAGGGGUGUCCACAGUCACAAA	486-508
AD-62947	499	GAUGGGGUGCCAGCUACUAUU	521	AAUAGUAGCUGGCACCCCAUCCA	814-836
AD-62952	500	GAAAAUGUGUUUGGGCAACGU	522	ACGUUGCCCAAACACAUUUUCAA	1382-1404
AD-62957	501	GGCUGUUUCCAAGAUCUGACA	523	UGUCAGAUCUUGGAAACAGCCAA	1113-1135
AD-62962	502	UCCAACAAAAUAGCCACCCCU	524	AGGGGUGGCUAUUUUGUUGGAAA	1258-1280
AD-62967	503	GUCUUCUGUUUAGAUUUCCUU	525	AAGGAAAUCUAAACAGAAGACAG	1507-1529
AD-62972	504	UGGAAGGGAAGGUAGAAGUCU	526	AGACUUCUACCUUCCCUUCCACA	863-885
AD-62937	505	UCCUUUGGCUGUUUCCAAGAU	527	AUCUUGGAAACAGCCAAAGGAUU	1107-1129
AD-62943	506	CAUCUCUCAGCUGGGAUGAUA	528	UAUCAUCCCAGCUGAGAGAUGGG	662-684
AD-62948	507	GGGGUGCCAGCUACUAUUGAU	529	AUCAAUAGUAGCUGGCACCCCAU	817-839
AD-62953	508	AUGUGUUUGGGCAACGUCAUA	530	UAUGACGUUGCCCAAACACAUUU	1386-1408_C21A
AD-62958	509	CUGUUUAGAUUUCCUUAAGAA	531	UUCUUAAGGAAAUCUAAACAGAA	1512-1534_C21A
AD-62963	510	AGAAAGAAAUGGACUUGCAUA	532	UAUGCAAGUCCAUUUCUUUCUAG	1327-1349_C21A
AD-62968	511	GCAUCCUGGAAAUAUAUUAAA	533	UUUAAUAUAUUUCCAGGAUGCAA	1343-1365_C21A
AD-62973	512	CCUGUCAGACCAUGGGAACUA	534	UAGUUCCCAUGGUCUGACAGGCU	308-330_G21A
AD-62938	513	AAACAUGGUGUGGAUGGGAUA	535	UAUCCCAUCCACACCAUGUUUAA	763-785_C21A

Table 2c: Additional HAO1 unmodified sequences

Duplex Name	SEQ ID NO:	Sense strand sequence	SEQ ID NO:	Antisense strand sequence	Position in NM_017545.2
AD-62933.2	394	GAAUGUGAAAGUCAUCGACAA	443	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-62939.2	395	UUUUCAAUGGGUGUCCUAGGA	444	UCCUAGGACACCCAUUGAAAAGU	1302-1324
AD-62944.2	396	GAAAGUCAUCGACAAGACAUU	445	AAUGUCUUGUCGAUGACUUUCAC	1078-1100
AD-62949.2	397	UCAUCGACAAGACAUUGGUGA	446	UCACCAAUGUCUUGUCGAUGACU	1083-1105
AD-62954.2	398	UUUCAAUGGGUGUCCUAGGAA	447	UUCCUAGGACACCCAUUGAAAAG	1303-1325
AD-62959.2	399	AAUGGGUGUCCUAGGAACCUU	448	AAGGUUCCUAGGACACCCAUUGA	1307-1329
AD-62964.2	400	GACAGUGCACAAUAUUUUCCA	449	UGGAAAAUAUUGUGCACUGUCAG	1134-1156_C21A
AD-62969.2	401	ACUUUUCAAUGGGUGUCCUAA	450	UUAGGACACCCAUUGAAAAGUCA	1300-1322_G21A
AD-62934.2	402	AAGUCAUCGACAAGACAUUGA	451	UCAAUGUCUUGUCGAUGACUUUC	1080-1102_G21A
AD-62940.2	403	AUCGACAAGACAUUGGUGAGA	452	UCUCACCAAUGUCUUGUCGAUGA	1085-1107_G21A
AD-62945.2	404	GGGAGAAAGGUGUUCAAGAUA	453	UAUCUUGAACACCUUUCUCCCCC	996-1018_G21A
AD-62950.2	405	CUUUUCAAUGGGUGUCCUAGA	454	UCUAGGACACCCAUUGAAAAGUC	1301-1323_G21A
AD-62955.2	406	UCAAUGGGUGUCCUAGGAACA	455	UGUUCCUAGGACACCCAUUGAAA	1305-1327_C21A
AD-62960.2	407	UUGACUUUUCAAUGGGUGUCA	456	UGACACCCAUUGAAAAGUCAAAA	1297-1319_C21A
AD-62965.2	408	AAAGUCAUCGACAAGACAUUA	457	UAAUGUCUUGUCGAUGACUUUCA	1079-1101_G21A
AD-62970.2	409	CAGGGGGAGAAAGGUGUUCAA	458	UUGAACACCUUUCUCCCCCUGGA	992-1014
AD-62935.2	410	CAUUGGUGAGGAAAAAUCCUU	459	AAGGAUUUUUCCUCACCAAUGUC	1095-1117
AD-62941.2	411	ACAUUGGUGAGGAAAAAUCCU	460	AGGAUUUUUCCUCACCAAUGUCU	1094-1116
AD-62946.2	412	AGGGGGAGAAAGGUGUUCAAA	461	UUUGAACACCUUUCUCCCCCUGG	993-1015_G21A
AD-62974.2	413	CUCAGGAUGAAAAAUUUUGAA	462	UUCAAAAUUUUUCAUCCUGAGUU	563-585
AD-62978.2	414	CAGCAUGUAUUACUUGACAAA	463	UUUGUCAAGUAAUACAUGCUGAA	1173-1195
AD-62982.2	415	UAUGAACAACAUGCUAAAUCA	464	UGAUUUAGCAUGUUGUUCAUAAU	53-75
AD-62986.2	416	AUAUAUCCAAAUGUUUUAGGA	465	UCCUAAAACAUUUGGAUAUAUUC	1679-1701
AD-62990.2	417	CCAGAUGGAAGCUGUAUCCAA	466	UUGGAUACAGCUUCCAUCUGGAA	156-178
AD-62994.2	418	GACUUUCAUCCUGGAAAUAUA	467	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-62998.2	419	CCCCGGCUAAUUUGUAUCAAU	468	AUUGAUACAAAUUAGCCGGGGGA	29-51
AD-63002.2	420	UUAAACAUGGCUUGAAUGGGA	469	UCCCAUUCAAGCCAUGUUUAACA	765-787
AD-62975.2	421	AAUGUGUUUAGACAACGUCAU	470	AUGACGUUGUCUAAACACAUUUU	1388-1410
AD-62979.2	422	ACUAAAGGAAGAAUUCCGGUU	471	AACCGGAAUUCUUCCUUUAGUAU	1027-1049
AD-62983.2	423	UAUAUCCAAAUGUUUUAGGAU	472	AUCCUAAAACAUUUGGAUAUAUU	1680-1702
AD-62987.2	424	GUGCGGAAAGGCACUGAUGUU	473	AACAUCAGUGCCUUUCCGCACAC	902-924
AD-62991.2	425	UAAAACAGUGGUUCUUAAAUU	474	AAUUUAAGAACCACUGUUUUAAA	1521-1543
AD-62995.2	426	AUGAAAAAUUUUGAAACCAGU	475	ACUGGUUUCAAAAUUUUUCAUCC	569-591
AD-62999.2	427	AACAAAAUAGCAAUCCCUUUU	476	AAAAGGGAUUGCUAUUUUGUUGG	1264-1286
AD-63003.2	428	CUGAAACAGAUCUGUCGACUU	477	AAGUCGACAGAUCUGUUUCAGCA	195-217
AD-62976.2	429	UUGUUGCAAAGGGCAUUUUGA	478	UCAAAAUGCCCUUUGCAACAAUU	720-742
AD-62980.2	430	CUCAUUGUUUAUUAACCUGUA	479	UACAGGUUAAUAAACAAUGAGAU	1483-1505
AD-62984.2	431	CAACAAAAUAGCAAUCCCUUU	480	AAAGGGAUUGCUAUUUUGUUGGA	1263-1285
AD-62992.2	432	CAUUGUUUAUUAACCUGUAUU	481	AAUACAGGUUAAUAAACAAUGAG	1485-1507
AD-62996.2	433	UAUCAGCUGGGAAGAUAUCAA	482	UUGAUAUCUUCCCAGCUGAUAGA	670-692
AD-63000.2	434	UGUCCUAGGAACCUUUUAGAA	483	UUCUAAAAGGUUCCUAGGACACC	1313-1335

AD-63004.2	435	UCCAACAAAAUAGCAAUCCCU	484	AGGGAUUGCUAUUUUGUUGGAAA	1261-1283
AD-62977.2	436	GGUGUGCGGAAAGGCACUGAU	485	AUCAGUGCCUUUCCGCACACCCC	899-921
AD-62981.2	437	UUGAAACCAGUACUUUAUCAU	486	AUGAUAAAGUACUGGUUUCAAAA	579-601
AD-62985.2	438	UACUUCCAAAGUCUAUAUAUA	487	UAUAUAUAGACUUUGGAAGUACU	75-97_G21A
AD-62989.2	439	UCCUAGGAACCUUUUAGAAAU	488	AUUUCUAAAAGGUUCCUAGGACA	1315-1337_G21U
AD-62993.2	440	CUCCUGAGGAAAAUUUUGGAA	489	UUCCAAAAUUUUCCUCAGGAGAA	603-625_G21A
AD-62997.2	441	GCUCCGGAAUGUUGCUGAAAU	490	AUUUCAGCAACAUUCCGGAGCAU	181-203_C21U
AD-63001.2	442	GUGUUUGUGGGGAGACCAAUA	491	UAUUGGUCUCCCCACAAACACAG	953-975_C21A
AD-62951.2	492	AUGGUGGUAAUUUGUGAUUUU	514	AAAAUCACAAAUUACCACCAUCC	1642-1664
AD-62956.2	493	GACUUGCAUCCUGGAAAUAUA	515	UAUAUUUCCAGGAUGCAAGUCCA	1338-1360
AD-62961.2	494	GGAAGGGAAGGUAGAAGUCUU	516	AAGACUUCUACCUUCCCUUCCAC	864-886
AD-62966.2	495	UGUCUUCUGUUUAGAUUUCCU	517	AGGAAAUCUAAACAGAAGACAGG	1506-1528
AD-62971.2	496	CUUUGGCUGUUUCCAAGAUCU	518	AGAUCUUGGAAACAGCCAAAGGA	1109-1131
AD-62936.2	497	AAUGUGUUUGGGCAACGUCAU	519	AUGACGUUGCCCAAACACAUUUU	1385-1407
AD-62942.2	498	UGUGACUGUGGACACCCCUUA	520	UAAGGGGUGUCCACAGUCACAAA	486-508
AD-62947.2	499	GAUGGGGUGCCAGCUACUAUU	521	AAUAGUAGCUGGCACCCCAUCCA	814-836
AD-62952.2	500	GAAAAUGUGUUUGGGCAACGU	522	ACGUUGCCCAAACACAUUUUCAA	1382-1404
AD-62957.2	501	GGCUGUUUCCAAGAUCUGACA	523	UGUCAGAUCUUGGAAACAGCCAA	1113-1135
AD-62962.2	502	UCCAACAAAAUAGCCACCCCU	524	AGGGGUGGCUAUUUUGUUGGAAA	1258-1280
AD-62967.2	503	GUCUUCUGUUUAGAUUUCCUU	525	AAGGAAAUCUAAACAGAAGACAG	1507-1529
AD-62972.2	504	UGGAAGGGAAGGUAGAAGUCU	526	AGACUUCUACCUUCCCUUCCACA	863-885
AD-62937.2	505	UCCUUUGGCUGUUUCCAAGAU	527	AUCUUGGAAACAGCCAAAGGAUU	1107-1129
AD-62943.2	506	CAUCUCUCAGCUGGGAUGAUA	528	UAUCAUCCCAGCUGAGAGAUGGG	662-684
AD-62948.2	507	GGGGUGCCAGCUACUAUUGAU	529	AUCAAUAGUAGCUGGCACCCCAU	817-839
AD-62953.2	508	AUGUGUUUGGGCAACGUCAUA	530	UAUGACGUUGCCCAAACACAUUU	1386-1408_C21A
AD-62958.2	509	CUGUUUAGAUUUCCUUAAGAA	531	UUCUUAAGGAAAUCUAAACAGAA	1512-1534_C21A
AD-62963.2	510	AGAAAGAAAUGGACUUGCAUA	532	UAUGCAAGUCCAUUUCUUUCUAG	1327-1349_C21A
AD-62968.2	511	GCAUCCUGGAAAUAUAUUAAA	533	UUUAAUAUAUUUCCAGGAUGCAA	1343-1365_C21A
AD-62973.2	512	CCUGUCAGACCAUGGGAACUA	534	UAGUUCCCAUGGUCUGACAGGCU	308-330_G21A
AD-62938.2	513	AAACAUGGUGUGGAUGGGAUA	535	UAUCCCAUCCACACCAUGUUUAA	763-785_C21A
AD-62933.1	536	GAAUGUGAAAGUCAUCGACAA	653	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65630.1	537	GAAUGUGAAAGUCAUCGACAA	654	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65636.1	538	GAAUGUGAAAGUCAUCGACAA	655	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65642.1	539	GAAUGUGAAAGUCAUCGACAA	656	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65647.1	540	GAAUGUGAAAGUCAUCGACAA	657	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65652.1	541	GAAUGUGAAAGUCAUCGACAA	658	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65657.1	542	GAAUGUGAAAGUCAUCGACAA	659	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65662.1	543	GAAUGUGAAAGUCAUCGACAA	660	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65625.1	544	AUGUGAAAGUCAUCGACAA	661	UUGUCGAUGACUUUCACAUUC	1072-1094
AD-65631.1	545	AUGUGAAAGUCAUCGACAA	662	UUGUCGAUGACUUUCACAUUC	1072-1094
AD-65637.1	546	GAAUGUGAAAGUCAUCGACAA	663	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65643.1	547	GAAUGUGAAAGUCAUCGACAA	664	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65648.1	548	GAAUGUGAAAGUCAUCGACAA	665	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65653.1	549	GAAUGUGAAAGUCAUCGACAA	666	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65658.1	550	GAAUGUGAAAGUCAUCGACAA	667	UUGUCGAUGACUUUCACAUUCUG	1072-1094

AD-65663.1	551	GAAUGUGAAAGUCAUCGACAA	668	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65626.1	552	GAAUGUGAAAGUCAUCGACAA	669	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65638.1	553	GAAUGUGAAAGUCAUCGACAA	670	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65644.1	554	GAAUGUGAAAGUCAUCGACAA	671	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65649.1	555	GAAUGUGAAAGUCAUCGACAA	672	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65654.1	556	GAAUGUGAAAGUCAUCGACAA	673	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65659.1	557	GAAUGTGAAAGUCAUCGACAA	674	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65627.1	558	GAAUGUGAAAGUCAUCGACAA	675	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65633.1	559	GAAUGTGAAAGUCAUCGACAA	676	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65639.1	560	GAAUGUGAAAGUCAUCGACAA	677	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65645.1	561	GAAUGUGAAAGUCAUCGACAA	678	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65650.1	562	GAAUGUGAAAGUCAUCTACAA	679	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65655.1	563	GAAUGUGAAAGUCAUCACAA	680	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65660.1	564	GAAUGUGAAAGUCATCTACAA	681	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65665.1	565	GAAUGUGAAAGUCAUCGACAA	682	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65628.1	566	GAAUGUGAAAGUCAUCTACAA	683	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65634.1	567	GAAUGUGAAAGUCAUCACAA	684	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-65646.1	568	GAAUGUGAAAGUCAUCGACAA	685	UTGUCGAUGACUUTCACAUUCUG	1072-1094
AD-65656.1	569	GAAUGUGAAAGUCAUCGACAA	686	UUGUCGAUGACUUTCACAUUCUG	1072-1094
AD-65661.1	570	GAAUGUGAAAGUCAUCGACAA	687	UTGUCGAUGACUUTCACAUUCUG	1072-1094
AD-65666.1	571	GAAUGUGAAAGUCAUCGACAA	688	UUGUCGAUGACUUTCACAUUCUG	1072-1094
AD-65629.1	572	GAAUGUGAAAGUCAUCGACAA	689	UTGUCGAUGACUUTCACAUUCUG	1072-1094
AD-65635.1	573	GAAUGUGAAAGUCAUCGACAA	690	UTGUCGAUGACUUTCACAUUCUG	1072-1094
AD-65641.1	574	GAAUGUGAAAGUCAUCGACAA	691	UTGUCGAUGACUUTCACAUUCUG	1072-1094
AD-62994.1	575	GACUUUCAUCCUGGAAAUAUA	692	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65595.1	576	GACUUUCAUCCUGGAAAUAUA	693	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65600.1	577	GACUUUCAUCCUGGAAAUAUA	694	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65610.1	578	GACUUUCAUCCUGGAAAUAUA	695	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65615.1	579	GACUUUCAUCCUGGAAAUAUA	696	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65620.1	580	GACUUUCAUCCUGGAAAUAUA	697	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65584.1	581	CUUUCAUCCUGGAAAUAUA	698	UAUAUUUCCAGGAUGAAAGUC	1341-1361
AD-65590.1	582	CUUUCAUCCUGGAAAUAUA	699	UAUAUUUCCAGGAUGAAAGUC	1341-1361
AD-65596.1	583	GACUUUCAUCCUGGAAAUAUA	700	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65601.1	584	GACUUUCAUCCUGGAAAUAUA	701	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65606.1	585	GACUUUCAUCCUGGAAAUAUA	702	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65611.1	586	GACUUUCAUCCUGGAAAUAUA	703	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65616.1	587	GACUUUCAUCCUGGAAAUAUA	704	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65621.1	588	GACUUUCAUCCUGGAAAUAUA	705	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65585.1	589	GACUUUCAUCCUGGAAAUAUA	706	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65591.1	590	GACUUUCAUCCUGGAAAUAUA	707	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65597.1	591	GACUUUCAUCCUGGAAAUAUA	708	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65602.1	592	GACUUUCAUCCUGGAAAUAUA	709	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65607.1	593	GACUUUCAUCCUGGAAAUAUA	710	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65612.1	594	GACUUUCAUCCUGGAAAUAUA	711	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65622.1	595	GACUUUCAUCCUGGAAAUAUA	712	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363

AD-65586.1	596	GACUTUCAUCCUGGAAAUAUA	713	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65592.1	597	GACUUTCAUCCUGGAAAUAUA	714	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65598.1	598	GACUUUCAUCCUGGAAAUAUA	715	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65603.1	599	GACUUUCAUCCUGGAAAUAUA	716	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65608.1	600	GACUUUCAUCCUGGAATUAUA	717	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65613.1	601	GACUUUCAUCCUGGAAUAUA	718	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65618.1	602	GACUUUCAUCCUGGAATUAUA	719	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65623.1	603	GACUUUCAUCCUGGAATUAUA	720	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65587.1	604	GACUUUCAUCCUGGAAAUAUA	721	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65593.1	605	GACUUTCAUCCUGGAAAUAUA	722	UAUAUUUCCAGGAUGAAAGUCCA	1341-1363
AD-65599.1	606	GACUUUCAUCCUGGAAAUAUA	723	UAUAUUUCCAGGATGAAAGUCCA	1341-1363
AD-65604.1	607	GACUUUCAUCCUGGAAAUAUA	724	UAUAUUUCCAGGATGAAAGUCCA	1341-1363
AD-65609.1	608	GACUUUCAUCCUGGAAAUAUA	725	UAUAUUUCCAGGATGAAAGUCCA	1341-1363
AD-65614.1	609	GACUUUCAUCCUGGAAAUAUA	726	UAUAUTUCCAGGATGAAAGUCCA	1341-1363
AD-65619.1	610	GACUUUCAUCCUGGAAAUAUA	727	UAUAUTUCCAGGATGAAAGUCCA	1341-1363
AD-65624.1	611	GACUUUCAUCCUGGAAAUAUA	728	UAUAUUUCCAGGATGAAAGUCCA	1341-1363
AD-65588.1	612	GACUUUCAUCCUGGAAAUAUA	729	UAUAUTUCCAGGATGAAAGUCCA	1341-1363
AD-65594.1	613	GACUUUCAUCCUGGAAAUAUA	730	UAUAUUUCCAGGATGAAAGUCCA	1341-1363
AD-68309.1	614	AGAAAGGUGUUCAAGAUGUCA	731	UGACAUCUUGAACACCUUUCUCC	1001-1022_C21A
AD-68303.1	615	CAUCCUGGAAAUAUAUUAACU	732	AGUUAAUAUAUUUCCAGGAUGAA	1349-1370
AD-65626.5	616	GAAUGUGAAAGUCAUCGACAA	733	UUGUCGAUGACUUUCACAUUCUG	1072-1094
AD-68295.1	617	AGUGCACAAUAUUUUCCCAUA	734	UAUGGGAAAAUAUUGUGCACUGU	1139-1160_C21A
AD-68273.1	618	GAAAGUCAUCGACAAGACAUU	735	AAUGUCUUGUCGAUGACUUUCAC	1080-1100
AD-68297.1	619	AAUGUGAAAGUCAUCGACAAA	736	UUUGUCGAUGACUUUCACAUUCU	1075-1096_G21A
AD-68287.1	620	CUGGAAAUAUAUUAACUGUUA	737	UAACAGUUAAUAUAUUUCCAGGA	1353-1374
AD-68300.1	621	AUUUUCCCAUCUGUAUUAUUU	738	AAAUAAUACAGAUGGGAAAAUAU	1149-1170
AD-68306.1	622	UGUCGUUCUUUUCCAACAAAA	739	UUUUGUUGGAAAAGAACGACACC	1252-1273
AD-68292.1	623	AUCCUGGAAAUAUAUUAACUA	740	UAGUUAAUAUAUUUCCAGGAUGA	1350-1371_G21A
AD-68298.1	624	GCAUUUUGAGAGGUGAUGAUA	741	UAUCAUCACCUCUCAAAAUGCCC	734-755_G21A
AD-68277.1	625	CAGGGGGAGAAAGGUGUUCAA	742	UUGAACACCUUUCUCCCCCUGGA	994-1014
AD-68289.1	626	GGAAAUAUAUUAACUGUUAAA	743	UUUAACAGUUAAUAUAUUUCCAG	1355-1376
AD-68272.1	627	CAUUGGUGAGGAAAAAUCCUU	744	AAGGAUUUUUUCCUCACCAAUGUC	1097-1117
AD-68282.1	628	GGGAGAAAGGUGUUCAAGAUA	745	UAUCUUGAACACCUUUCUCCCCC	998-1018_G21A
AD-68285.1	629	GGCAUUUUGAGAGGUGAUGAU	746	AUCAUCACCUCUCAAAAUGCCCU	733-754
AD-68290.1	630	UACAAAGGGUGUCGUUCUUUU	747	AAAAGAACGACACCCUUUGUAUU	1243-1264
AD-68296.1	631	UGGGAUCUUGGUGUCGAAUCA	748	UGAUUCGACACCAAGAUCCCAUU	783-804
AD-68288.1	632	CUGACAGUGCACAAUAUUUUA	749	UAAAAUAUUGUGCACUGUCAGAU	1134-1155_C21A
AD-68299.1	633	CAGUGCACAAUAUUUUCCCAU	750	AUGGGAAAAUAUUGUGCACUGUC	1138-1159
AD-68275.1	634	ACUUUUCAAUGGGUGUCCUAA	751	UUAGGACACCCAUUGAAAAGUCA	1302-1322_G21A
AD-68274.1	635	ACAUUGGUGAGGAAAAAUCCU	752	AGGAUUUUUUCCUCACCAAUGUCU	1096-1116
AD-68294.1	636	UUGCUUUUGACUUUUCAAUGA	753	UCAUUGAAAAGUCAAAAGCAAUG	1293-1314_G21A
AD-68302.1	637	CAUUUUGAGAGGUGAUGAUGA	754	UCAUCAUCACCUCUCAAAAUGCC	735-756_C21A
AD-68279.1	638	UUGACUUUUCAAUGGGUGUCA	755	UGACACCCAUUGAAAAGUCAAAA	1299-1319_C21A
AD-68304.1	639	CGACUUCUGUUUUAGGACAGA	756	UCUGUCCUAAAACAGAAGUCGAC	212-233
AD-68286.1	640	CUCUGAGUGGGUGCCAGAAUA	757	UAUUCUGGCACCCACUCAGAGCC	1058-1079_G21A

AD-68291.1	641	GGGUGCCAGAAUGUGAAAGUA	758	UACUUUCACAUUCUGGCACCCAC	1066-1087_C21A
AD-68283.1	642	UCAAUGGGUGUCCUAGGAACA	759	UGUUCCUAGGACACCCAUUGAAA	1307-1327_C21A
AD-68280.1	643	AAAGUCAUCGACAAGACAUUA	760	UAAUGUCUUGUCGAUGACUUUCA	1081-1101_G21A
AD-68293.1	644	AUUUUGAGAGGUGAUGAUGCA	761	UGCAUCAUCACCUCUCAAAAUGC	736-757_C21A
AD-68276.1	645	AUCGACAAGACAUUGGUGAGA	762	UCUCACCAAUGUCUUGUCGAUGA	1087-1107_G21A
AD-68308.1	646	GGUGCCAGAAUGUGAAAGUCA	763	UGACUUUCACAUUCUGGCACCCA	1067-1088
AD-68278.1	647	GACAGUGCACAAUAUUUUCCA	764	UGGAAAAUAUUGUGCACUGUCAG	1136-1156_C21A
AD-68307.1	648	ACAAAGAGACACUGUGCAGAA	765	UUCUGCACAGUGUCUCUUUGUCA	1191-1212_G21A
AD-68284.1	649	UUUUCAAUGGGUGUCCUAGGA	766	UCCUAGGACACCCAUUGAAAAGU	1304-1324
AD-68301.1	650	CCGUUUCCAAGAUCUGACAGU	767	ACUGUCAGAUCUUGGAAACGGCC	1121-1142
AD-68281.1	651	AGGGGGAGAAAGGUGUUCAAA	768	UUUGAACACCUUUCUCCCCCUGG	995-1015_G21A
AD-68305.1	652	AGUCAUCGACAAGACAUUGGU	769	ACCAAUGUCUUGUCGAUGACUUU	1083-1104

Example 2. *In vitro* single dose screen in primary monkey hepatocytes.

The modified and conjugated HAO1 siRNA duplexes were evaluated for efficacy by transfection assays in primary monkey hepatocytes. HAO1 siRNAs were transfected at two doses, 10nM and 0.1nM. The results of these assays are shown in Table 3 and the data are expressed as a fraction of the message remaining in cells transfected with siRNAs targeting HAO1, relative to cells transfected with a negative control siRNA, AD-1955 ± the standard deviation (SD).

The results are also shown in Figure 3A. Figure 3B illustrates a dose response with one of the most active conjugates (#31) (AD-62933) from the primary two dose screen; the IC50 was ~19pM.

Table 3a. HAO1 single dose screen in monkey hepatocytes.

DUPLEX ID	Species	10nM PCH	0.1nM PCH	SD 10nM PCH	SD 0.1nM PCH
AD-62974	Hs	5.3	29.8	1.87	11.11
AD-62975	Hs	7.6	31.3	0.34	1.99
AD-62976	Hs	4.7	35.5	0.34	13.90
AD-62977	Hs	29.2	66.9	8.32	43.88
AD-62978	Hs	3.8	8.9	0.15	4.29
AD-62979	Hs	27.5	80.7	1.35	19.58
AD-62980	Hs	7.4	32.2	1.26	1.42
AD-62981	Hs	18.7	49.9	3.46	12.83
AD-62982	Hs	2.2	8.5	0.10	7.71
AD-62983	Hs	19.4	41.0	11.19	6.60
AD-62984	Hs	6.7	13.3	1.05	2.60
AD-62985	Hs	2.3	8.3	0.24	2.68
AD-62986	Hs	39.0	57.2	3.82	16.31

AD-62987	Hs	11.5	17.8	14.62	15.39
AD-62989	Hs	10.6	34.2	2.23	2.68
AD-62990	Hs	12.0	18.4	9.11	5.23
AD-62991	Hs	7.2	14.2	1.30	2.96
AD-62992	Hs	3.9	16.0	1.15	1.80
AD-62993	Hs	22.3	58.4	9.91	6.28
AD-62994	Hs	3.2	10.8	1.21	1.69
AD-62995	Hs	5.5	17.6	4.58	3.25
AD-62996	Hs	3.4	20.7	2.16	3.73
AD-62997	Hs	4.5	24.2	0.67	3.32
AD-62998	Hs	4.3	14.7	0.49	0.29
AD-62999	Hs	11.4	15.5	1.23	2.50
AD-63000	Hs	45.5	90.6	13.41	43.49
AD-63001	Hs	13.3	31.0	0.20	2.13
AD-63002	Hs	6.6	22.0	0.26	5.75
AD-63003	Hs	36.8	5.1	47.09	0.60
AD-63004	Hs	12.7	35.4	1.55	9.42
AD-62933	Hs/Mm	5.8	13.4	0.71	0.13
AD-62934	Hs/Mm	52.2	35.9	6.64	5.08
AD-62935	Hs/Mm	7.7	22.7	1.53	4.97
AD-62939	Hs/Mm	25.1	49.0	9.48	2.88
AD-62940	Hs/Mm	11.9	50.4	4.12	13.91
AD-62941	Hs/Mm	9.6	30.3	7.28	3.11
AD-62944	Hs/Mm	8.0	18.5	1.40	5.63
AD-62945	Hs/Mm	22.9	36.5	17.16	13.81
AD-62946	Hs/Mm	19.3	29.5	15.29	1.74
AD-62949	Hs/Mm	34.1	84.2	18.11	18.42
AD-62950	Hs/Mm	12.7	36.2	5.69	6.54
AD-62954	Hs/Mm	46.0	53.2	37.57	10.61
AD-62955	Hs/Mm	24.6	36.0	0.97	16.36
AD-62959	Hs/Mm	32.3	37.4	12.49	12.08
AD-62960	Hs/Mm	18.1	37.5	2.12	3.12
AD-62964	Hs/Mm	16.2	52.4	5.59	22.40
AD-62965	Hs/Mm	18.5	34.5	3.77	22.38
AD-62969	Hs/Mm	11.7	34.0	0.17	12.55
AD-62970	Hs/Mm	13.6	21.2	1.13	5.85
AD-62936	Mm	91.3	55.6	16.03	0.27
AD-62937	Mm	45.8	77.7	22.77	47.01
AD-62938	Mm	78.3	55.1	8.81	2.70
AD-62942	Mm	18.8	21.7	7.34	8.00
AD-62943	Mm	6.7	31.0	0.79	7.22
AD-62947	Mm	27.9	82.0	14.01	2.01
AD-62948	Mm	21.9	52.5	6.56	21.01
AD-62951	Mm	40.1	77.4	8.76	3.03
AD-62952	Mm	33.7	69.9	17.76	1.71

AD-62953	Mm	79.9	65.1	96.61	22.79
AD-62956	Mm	7.6	16.4	1.01	12.39
AD-62957	Mm	6.7	21.3	0.99	3.02
AD-62958	Mm	38.9	54.4	21.66	29.39
AD-62961	Mm	35.3	66.0	0.35	24.65
AD-62962	Mm	70.7	63.7	21.17	26.36
AD-62963	Mm	35.1	66.5	35.49	9.42
AD-62966	Mm	69.0	100.3	17.07	3.44
AD-62967	Mm	90.7	116.7	22.01	47.77
AD-62968	Mm	46.3	72.2	28.37	67.08
AD-62971	Mm	17.9	46.3	1.23	23.41
AD-62972	Mm	75.6	122.9	24.75	18.00
AD-62973	Mm	102.8	73.9	22.49	14.39

Table 3b. Additional HAO1 single dose screen in primary monkey hepatocytes.

DUPLEX ID	Species	10nM PCH	0.1nM PCH	SD 10nM PCH	SD 0.1nM PCH
AD-62974.2	Hs	5.3	29.8	1.87	11.11
AD-62975.2	Hs	7.6	31.3	0.34	1.99
AD-62976.2	Hs	4.7	35.5	0.34	13.90
AD-62977.2	Hs	29.2	66.9	8.32	43.88
AD-62978.2	Hs	3.8	8.9	0.15	4.29
AD-62979.2	Hs	27.5	80.7	1.35	19.58
AD-62980.2	Hs	7.4	32.2	1.26	1.42
AD-62981.2	Hs	18.7	49.9	3.46	12.83
AD-62982.2	Hs	2.2	8.5	0.10	7.71
AD-62983.2	Hs	19.4	41.0	11.19	6.60
AD-62984.2	Hs	6.7	13.3	1.05	2.60
AD-62985.2	Hs	2.3	8.3	0.24	2.68
AD-62986.2	Hs	39.0	57.2	3.82	16.31
AD-62987.2	Hs	11.5	17.8	14.62	15.39
AD-62989.2	Hs	10.6	34.2	2.23	2.68
AD-62990.2	Hs	12.0	18.4	9.11	5.23
AD-62991.2	Hs	7.2	14.2	1.30	2.96
AD-62992.2	Hs	3.9	16.0	1.15	1.80
AD-62993.2	Hs	22.3	58.4	9.91	6.28
AD-62994.2	Hs	3.2	10.8	1.21	1.69
AD-62995.2	Hs	5.5	17.6	4.58	3.25
AD-62996.2	Hs	3.4	20.7	2.16	3.73
AD-62997.2	Hs	4.5	24.2	0.67	3.32
AD-62998.2	Hs	4.3	14.7	0.49	0.29
AD-62999.2	Hs	11.4	15.5	1.23	2.50
AD-63000.2	Hs	45.5	90.6	13.41	43.49

AD-63001.2	Hs	13.3	31.0	0.20	2.13
AD-63002.2	Hs	6.6	22.0	0.26	5.75
AD-63003.2	Hs	36.8	5.1	47.09	0.60
AD-63004.2	Hs	12.7	35.4	1.55	9.42
AD-62933.2	Hs/Mm	5.8	13.4	0.71	0.13
AD-62934.2	Hs/Mm	52.2	35.9	6.64	5.08
AD-62935.2	Hs/Mm	7.7	22.7	1.53	4.97
AD-62939.2	Hs/Mm	25.1	49.0	9.48	2.88
AD-62940.2	Hs/Mm	11.9	50.4	4.12	13.91
AD-62941.2	Hs/Mm	9.6	30.3	7.28	3.11
AD-62944.2	Hs/Mm	8.0	18.5	1.40	5.63
AD-62945.2	Hs/Mm	22.9	36.5	17.16	13.81
AD-62946.2	Hs/Mm	19.3	29.5	15.29	1.74
AD-62949.2	Hs/Mm	34.1	84.2	18.11	18.42
AD-62950.2	Hs/Mm	12.7	36.2	5.69	6.54
AD-62954.2	Hs/Mm	46.0	53.2	37.57	10.61
AD-62955.2	Hs/Mm	24.6	36.0	0.97	16.36
AD-62959.2	Hs/Mm	32.3	37.4	12.49	12.08
AD-62960.2	Hs/Mm	18.1	37.5	2.12	3.12
AD-62964.2	Hs/Mm	16.2	52.4	5.59	22.40
AD-62965.2	Hs/Mm	18.5	34.5	3.77	22.38
AD-62969.2	Hs/Mm	11.7	34.0	0.17	12.55
AD-62970.2	Hs/Mm	13.6	21.2	1.13	5.85
AD-62936.2	Mm	91.3	55.6	16.03	0.27
AD-62937.2	Mm	45.8	77.7	22.77	47.01
AD-62938.2	Mm	78.3	55.1	8.81	2.70
AD-62942.2	Mm	18.8	21.7	7.34	8.00
AD-62943.2	Mm	6.7	31.0	0.79	7.22
AD-62947.2	Mm	27.9	82.0	14.01	2.01
AD-62948.2	Mm	21.9	52.5	6.56	21.01
AD-62951.2	Mm	40.1	77.4	8.76	3.03
AD-62952.2	Mm	33.7	69.9	17.76	1.71
AD-62953.2	Mm	79.9	65.1	96.61	22.79
AD-62956.2	Mm	7.6	16.4	1.01	12.39
AD-62957.2	Mm	6.7	21.3	0.99	3.02
AD-62958.2	Mm	38.9	54.4	21.66	29.39
AD-62961.2	Mm	35.3	66.0	0.35	24.65
AD-62962.2	Mm	70.7	63.7	21.17	26.36
AD-62963.2	Mm	35.1	66.5	35.49	9.42
AD-62966.2	Mm	69.0	100.3	17.07	3.44
AD-62967.2	Mm	90.7	116.7	22.01	47.77
AD-62968.2	Mm	46.3	72.2	28.37	67.08
AD-62971.2	Mm	17.9	46.3	1.23	23.41
AD-62972.2	Mm	75.6	122.9	24.75	18.00
AD-62973.2	Mm	102.8	73.9	22.49	14.39

Example 3. *In vitro* Single Dose Screen in Primary Mouse Hepatocytes.

The modified and conjugated HAO1 siRNA duplexes were evaluated for efficacy by transfection assays in primary mouse hepatocytes. HAO1 siRNAs were transfected at two doses, 20 nM and 0.2 nM. The results of these assays are shown in Table 4 and the data are expressed as a fraction of the message remaining in cells transfected with siRNAs targeting HAO1, relative to cells transfected with a negative control siRNA, AD-1955 ± the standard deviation (SD).

Table 4a. HAO1 Single Dose Screen in Primary Mouse Hepatocytes.

DUPLEX ID	Species	20nM PMH	0.2nM PMH	SD 20nM PMH	SD 0.2nM PMH
AD-62974	Hs	1.5	11.5	0.3	8.5
AD-62975	Hs	6.2	24.5	1.9	19.4
AD-62976	Hs	8.3	60.0	3.9	7.9
AD-62977	Hs	69.1	106.9	44.8	18.3
AD-62978	Hs	30.0	46.3	26.0	27.3
AD-62979	Hs	50.7	59.5	45.6	43.4
AD-62980	Hs	65.4	89.5	68.9	29.3
AD-62981	Hs	65.8	83.3	31.9	23.7
AD-62982	Hs	86.6	67.0	92.1	65.5
AD-62983	Hs	81.5	103.6	61.3	68.0
AD-62984	Hs	13.5	51.8	1.2	37.7
AD-62985	Hs	53.8	37.7	38.1	26.3
AD-62986	Hs	138.5	153.4	140.7	119.6
AD-62987	Hs	39.0	99.6	44.9	110.7
AD-62989	Hs	17.1	2.2	23.1	1.6
AD-62990	Hs	4.3	46.3	4.6	46.4
AD-62991	Hs	125.2	102.6	111.9	92.9
AD-62992	Hs	64.7	65.6	67.8	55.8
AD-62993	Hs	83.8	79.0	63.0	22.2
AD-62994	Hs	1.9	5.4	1.5	0.2
AD-62995	Hs	2.9	17.4	1.8	13.8
AD-62996	Hs	49.3	61.4	43.6	49.9
AD-62997	Hs	60.2	83.4	19.1	45.7
AD-62998	Hs	73.5	86.7	71.5	69.4
AD-62999	Hs	38.7	50.0	29.5	22.7
AD-63000	Hs	27.3	56.6	26.1	41.4
AD-63001	Hs	56.6	83.8	52.9	13.5
AD-63002	Hs	81.6	74.2	67.4	70.5
AD-63003	Hs	46.4	47.7	42.4	21.4
AD-63004	Hs	28.6	64.5	17.0	44.5

AD-62933	Hs/Mm	1.1	4.6	0.5	4.0
AD-62934	Hs/Mm	7.6	43.4	0.6	32.6
AD-62935	Hs/Mm	1.3	7.0	0.3	3.4
AD-62939	Hs/Mm	6.1	21.4	2.2	14.5
AD-62940	Hs/Mm	6.0	16.9	1.4	3.8
AD-62941	Hs/Mm	5.6	8.5	3.9	6.3
AD-62944	Hs/Mm	3.3	4.3	2.9	4.5
AD-62945	Hs/Mm	6.4	7.0	1.0	7.2
AD-62946	Hs/Mm	18.3	21.4	19.2	21.1
AD-62949	Hs/Mm	11.4	43.7	8.9	38.3
AD-62950	Hs/Mm	9.9	21.9	4.7	20.8
AD-62954	Hs/Mm	9.4	65.5	0.2	64.3
AD-62955	Hs/Mm	5.8	21.8	5.5	5.8
AD-62959	Hs/Mm	4.2	9.6	1.8	5.3
AD-62960	Hs/Mm	5.4	10.1	3.8	2.5
AD-62964	Hs/Mm	3.7	21.2	0.9	12.7
AD-62965	Hs/Mm	8.0	20.8	5.3	23.5
AD-62969	Hs/Mm	6.4	4.7	3.8	5.1
AD-62970	Hs/Mm	19.6	5.2	14.6	6.1
AD-62936	Mm	7.0	17.5	0.1	9.9
AD-62937	Mm	4.0	16.9	0.8	10.2
AD-62938	Mm	4.0	49.1	0.7	42.4
AD-62942	Mm	3.4	4.9	1.2	5.3
AD-62943	Mm	3.8	14.9	2.2	10.6
AD-62947	Mm	10.9	6.4	9.6	1.6
AD-62948	Mm	6.7	18.7	6.9	15.8
AD-62951	Mm	8.1	11.8	8.6	14.5
AD-62952	Mm	9.4	23.2	10.1	29.2
AD-62953	Mm	11.3	10.3	13.7	12.1
AD-62956	Mm	2.2	3.9	1.8	1.6
AD-62957	Mm	3.2	22.5	3.1	20.0
AD-62958	Mm	7.5	16.0	5.8	13.2
AD-62961	Mm	4.3	6.9	2.8	5.6
AD-62962	Mm	17.1	42.4	14.2	49.5
AD-62963	Mm	2.3	10.8	0.6	8.3
AD-62966	Mm	5.7	11.6	5.8	5.6
AD-62967	Mm	3.8	21.7	2.0	23.0
AD-62968	Mm	3.5	9.4	0.3	9.0
AD-62971	Mm	4.6	3.1	5.0	2.7
AD-62972	Mm	13.8	22.7	17.0	24.9
AD-62973	Mm	19.3	51.9	19.7	21.9

Table 4b. Additional HAO1 Single Dose Screen in Primary Mouse Hepatocytes.

DUPLEX ID	Species	senseOligoName	20nM PMH	0.2nM PMH	SD 20nM PMH	SD 0.2nM PMH
AD-62974.2	Hs	A-126176.1	1.5	11.5	0.3	8.5
AD-62975.2	Hs	A-126192.1	6.2	24.5	1.9	19.4
AD-62976.2	Hs	A-126208.1	8.3	60.0	3.9	7.9
AD-62977.2	Hs	A-126224.1	69.1	106.9	44.8	18.3
AD-62978.2	Hs	A-126178.1	30.0	46.3	26.0	27.3
AD-62979.2	Hs	A-126194.1	50.7	59.5	45.6	43.4
AD-62980.2	Hs	A-126210.1	65.4	89.5	68.9	29.3
AD-62981.2	Hs	A-126226.1	65.8	83.3	31.9	23.7
AD-62982.2	Hs	A-126180.1	86.6	67.0	92.1	65.5
AD-62983.2	Hs	A-126196.1	81.5	103.6	61.3	68.0
AD-62984.2	Hs	A-126212.1	13.5	51.8	1.2	37.7
AD-62985.2	Hs	A-126228.1	53.8	37.7	38.1	26.3
AD-62986.2	Hs	A-126182.1	138.5	153.4	140.7	119.6
AD-62987.2	Hs	A-126198.1	39.0	99.6	44.9	110.7
AD-62989.2	Hs	A-126230.1	17.1	2.2	23.1	1.6
AD-62990.2	Hs	A-126184.1	4.3	46.3	4.6	46.4
AD-62991.2	Hs	A-126200.1	125.2	102.6	111.9	92.9
AD-62992.2	Hs	A-126216.1	64.7	65.6	67.8	55.8
AD-62993.2	Hs	A-126232.1	83.8	79.0	63.0	22.2
AD-62994.2	Hs	A-126186.1	1.9	5.4	1.5	0.2
AD-62995.2	Hs	A-126202.1	2.9	17.4	1.8	13.8
AD-62996.2	Hs	A-126218.1	49.3	61.4	43.6	49.9
AD-62997.2	Hs	A-126234.1	60.2	83.4	19.1	45.7
AD-62998.2	Hs	A-126188.1	73.5	86.7	71.5	69.4
AD-62999.2	Hs	A-126204.1	38.7	50.0	29.5	22.7
AD-63000.2	Hs	A-126220.1	27.3	56.6	26.1	41.4
AD-63001.2	Hs	A-126236.1	56.6	83.8	52.9	13.5
AD-63002.2	Hs	A-126190.1	81.6	74.2	67.4	70.5
AD-63003.2	Hs	A-126206.1	46.4	47.7	42.4	21.4
AD-63004.2	Hs	A-126222.1	28.6	64.5	17.0	44.5
AD-62933.2	Hs/Mm	A-126094.1	1.1	4.6	0.5	4.0
AD-62934.2	Hs/Mm	A-126110.1	7.6	43.4	0.6	32.6
AD-62935.2	Hs/Mm	A-126126.1	1.3	7.0	0.3	3.4
AD-62939.2	Hs/Mm	A-126096.1	6.1	21.4	2.2	14.5
AD-62940.2	Hs/Mm	A-126112.1	6.0	16.9	1.4	3.8
AD-62941.2	Hs/Mm	A-126128.1	5.6	8.5	3.9	6.3
AD-62944.2	Hs/Mm	A-126098.1	3.3	4.3	2.9	4.5
AD-62945.2	Hs/Mm	A-126114.1	6.4	7.0	1.0	7.2
AD-62946.2	Hs/Mm	A-126130.1	18.3	21.4	19.2	21.1
AD-62949.2	Hs/Mm	A-126100.1	11.4	43.7	8.9	38.3
AD-62950.2	Hs/Mm	A-126116.1	9.9	21.9	4.7	20.8

AD-62954.2	Hs/Mm	A-126102.1	9.4	65.5	0.2	64.3
AD-62955.2	Hs/Mm	A-126118.1	5.8	21.8	5.5	5.8
AD-62959.2	Hs/Mm	A-126104.1	4.2	9.6	1.8	5.3
AD-62960.2	Hs/Mm	A-126120.1	5.4	10.1	3.8	2.5
AD-62964.2	Hs/Mm	A-126106.1	3.7	21.2	0.9	12.7
AD-62965.2	Hs/Mm	A-126122.1	8.0	20.8	5.3	23.5
AD-62969.2	Hs/Mm	A-126108.1	6.4	4.7	3.8	5.1
AD-62970.2	Hs/Mm	A-126124.1	19.6	5.2	14.6	6.1
AD-62936.2	Mm	A-126142.1	7.0	17.5	0.1	9.9
AD-62937.2	Mm	A-126158.1	4.0	16.9	0.8	10.2
AD-62938.2	Mm	A-126174.1	4.0	49.1	0.7	42.4
AD-62942.2	Mm	A-126144.1	3.4	4.9	1.2	5.3
AD-62943.2	Mm	A-126160.1	3.8	14.9	2.2	10.6
AD-62947.2	Mm	A-126146.1	10.9	6.4	9.6	1.6
AD-62948.2	Mm	A-126162.1	6.7	18.7	6.9	15.8
AD-62951.2	Mm	A-126132.1	8.1	11.8	8.6	14.5
AD-62952.2	Mm	A-126148.1	9.4	23.2	10.1	29.2
AD-62953.2	Mm	A-126164.1	11.3	10.3	13.7	12.1
AD-62956.2	Mm	A-126134.1	2.2	3.9	1.8	1.6
AD-62957.2	Mm	A-126150.1	3.2	22.5	3.1	20.0
AD-62958.2	Mm	A-126166.1	7.5	16.0	5.8	13.2
AD-62961.2	Mm	A-126136.1	4.3	6.9	2.8	5.6
AD-62962.2	Mm	A-126152.1	17.1	42.4	14.2	49.5
AD-62963.2	Mm	A-126168.1	2.3	10.8	0.6	8.3
AD-62966.2	Mm	A-126138.1	5.7	11.6	5.8	5.6
AD-62967.2	Mm	A-126154.1	3.8	21.7	2.0	23.0
AD-62968.2	Mm	A-126170.1	3.5	9.4	0.3	9.0
AD-62971.2	Mm	A-126140.1	4.6	3.1	5.0	2.7
AD-62972.2	Mm	A-126156.1	13.8	22.7	17.0	24.9
AD-62973.2	Mm	A-126172.1	19.3	51.9	19.7	21.9

Example 4. Dose Response Screen in Primary Monkey Hepatocytes.

The IC50s of modified and conjugated HAO1 siRNA duplexes were determined in primary monkey hepatocytes. HAO1 siRNAs were transfected over a range of doses from 10nM to 36fM final duplex concentration over 8, 6-fold dilutions. The results of these assays are shown in Table 5.

Table 5a. HAO1 Dose Response Screen in Primary Mouse Hepatocytes.

DUPLEX ID	Species	IC50 PCH (nM)
AD-62984	Hs	0.017
AD-62994	Hs	0.029
AD-62989	Hs	0.175

AD-62974	Hs	0.288
AD-62975	Hs	0.399
AD-62933	Hs/Mm	0.019
AD-62944	Hs/Mm	0.027
AD-62935	Hs/Mm	0.137
AD-62965	Hs/Mm	0.155
AD-62941	Hs/Mm	0.245
AD-62940	Hs/Mm	0.927

Table 5b. Additional HAO1 Dose Response Screen in Primary Mouse Hepatocytes.

DUPLEX ID	Species	IC50 PCH (nM)
AD-62984.2	Hs	0.017
AD-62994.2	Hs	0.029
AD-62989.2	Hs	0.175
AD-62974.2	Hs	0.288
AD-62975.2	Hs	0.399
AD-62933.2	Hs/Mm	0.019
AD-62944.2	Hs/Mm	0.027
AD-62935.2	Hs/Mm	0.137
AD-62965.2	Hs/Mm	0.155
AD-62941.2	Hs/Mm	0.245
AD-62940.2	Hs/Mm	0.927

Example 5. Dose Response Screen in Primary Mouse Hepatocytes.

The IC50s of modified and conjugated HAO1 siRNA duplexes were determined in primary mouse hepatocytes. HAO1 siRNAs were transfected over a range of doses from 10nM to 36fM final duplex concentration over 8, 6-fold dilutions. The results of these assays are shown in Table 6.

Table 6a. HAO1 Dose Response Screen in Primary Mouse Hepatocytes.

DUPLEX ID	Species	IC50 PMH (nM)
AD-62989	Hs	0.003
AD-62994	Hs	0.006
AD-62975	Hs	0.059
AD-62974	Hs	0.122
AD-62984	Hs	0.264
AD-62944	Hs/Mm	0.002
AD-62935	Hs/Mm	0.007

AD-62965	Hs/Mm	0.008
AD-62933	Hs/Mm	0.008
AD-62941	Hs/Mm	0.087
AD-62940	Hs/Mm	0.090

Table 6b. Additional HAO1 Dose Response Screen in Primary Mouse Hepatocytes.

DUPLEX ID	Species	IC50 PMH (nM)
AD-62989.2	Hs	0.003
AD-62994.2	Hs	0.006
AD-62975.2	Hs	0.059
AD-62974.2	Hs	0.122
AD-62984.2	Hs	0.264
AD-62944.2	Hs/Mm	0.002
AD-62935.2	Hs/Mm	0.007
AD-62965.2	Hs/Mm	0.008
AD-62933.2	Hs/Mm	0.008
AD-62941.2	Hs/Mm	0.087
AD-62940.2	Hs/Mm	0.090

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Table 7. Additional HAO1 Single Dose Screen in Primary Cyno and Mouse Hepatocytes

Duplex ID	10nM PCH	0.1nM PCH	SD 10nM PCH	SD 0.1nM PCH	10nM PMH	0.1nM PMH	SD 10nM PMH	SD 0.1nM PMH
AD-62933.1	26.1	22.8	17.0	6.0	9.0	26.3	6.0	7.6
AD-65584.1	12.9	28.0	5.1	6.0	3.8	12.3	0.7	7.3
AD-65585.1	9.8	21.0	4.1	1.0	6.8	11.6	4.5	5.7
AD-65586.1	24.3	24.2	10.9	2.7	16.7	19.0	5.1	1.8
AD-65587.1	24.7	31.7	10.2	21.9	13.6	27.1	5.7	10.3
AD-65588.1	39.2	33.0	35.6	5.6	27.1	33.5	11.0	8.3
AD-65590.1	5.6	15.4	0.4	6.6	4.2	8.7	1.1	0.5
AD-65591.1	13.9	20.4	5.0	4.9	7.6	18.4	0.1	2.9
AD-65592.1	15.6	24.3	7.4	3.7	10.1	24.5	3.1	1.0
AD-65593.1	30.8	37.5	4.4	8.7	38.4	41.3	5.2	10.4
AD-65594.1	18.0	21.8	5.6	2.6	24.7	25.3	0.5	7.6
AD-65595.1	19.9	31.9	0.1	11.3	9.1	12.2	5.0	5.7
AD-65596.1	12.3	19.2	0.6	1.6	10.0	19.9	1.0	1.9
AD-65597.1	10.2	34.8	2.8	10.1	22.8	32.0	6.2	5.7
AD-65598.1	14.4	21.2	3.2	8.6	10.8	22.0	2.6	8.8
AD-65599.1	15.0	28.3	2.5	21.3	18.0	25.4	1.7	8.3
AD-65600.1	11.8	13.7	5.6	0.3	6.4	14.5	5.7	6.8
AD-65601.1	15.4	20.5	0.5	1.6	5.5	17.2	0.3	3.9

AD-65602.1	12.9	23.3	0.8	12.0	11.0	25.4	2.6	2.6
AD-65603.1	33.8	41.0	2.2	6.8	37.4	58.6	3.0	10.5
AD-65604.1	10.4	18.7	1.3	2.3	12.9	24.5	0.9	9.2
AD-65606.1	14.3	12.3	0.2	3.1	4.8	14.0	2.0	4.2
AD-65607.1	9.2	18.5	2.1	3.6	14.4	32.8	1.9	1.6
AD-65608.1	36.6	31.1	7.9	11.6	27.5	29.8	8.5	4.6
AD-65609.1	14.2	19.8	5.1	0.8	14.6	23.6	5.3	1.5
AD-65610.1	59.1	59.6	15.0	13.3	35.0	70.9	10.0	0.1
AD-65611.1	12.9	14.2	5.4	1.8	4.5	17.3	0.6	2.2
AD-65612.1	19.3	20.5	1.5	9.0	16.2	23.3	3.8	1.7
AD-65613.1	20.0	19.3	5.7	0.7	11.0	23.9	1.0	5.4
AD-65614.1	12.4	27.1	2.2	0.5	14.2	16.7	3.8	11.9
AD-65615.1	53.1	60.3	1.4	7.7	48.2	80.9	9.9	39.4
AD-65616.1	21.7	12.5	17.8	5.5	5.3	13.3	0.5	7.2
AD-65618.1	19.4	67.6	3.4	35.9	16.7	21.6	4.2	4.8
AD-65619.1	17.0	27.2	0.5	12.4	12.5	26.3	3.2	2.3
AD-65620.1	58.0	70.5	21.8	2.8	37.9	54.8	0.4	12.7
AD-65621.1	12.3	17.5	4.6	2.3	3.8	11.3	1.3	0.3
AD-65622.1	17.7	20.4	6.1	0.9	10.8	13.9	6.3	3.1
AD-65623.1	44.4	32.9	7.9	NA	37.7	20.6	28.5	0.9
AD-65624.1	13.0	23.3	5.0	9.8	9.2	7.9	2.8	0.4
AD-65625.1	9.8	13.3	0.6	1.5	10.0	19.2	4.6	1.6
AD-65626.1	7.7	15.0	1.1	4.9	8.6	14.7	3.6	2.4
AD-65627.1	18.8	24.8	7.8	1.8	19.7	18.5	8.1	12.0
AD-65628.1	27.3	31.7	4.9	3.9	29.7	43.4	6.4	19.6
AD-65629.1	12.8	20.8	1.0	8.1	18.9	23.2	3.2	13.9
AD-65630.1	7.2	14.0	0.3	5.3	6.1	8.5	1.3	2.1
AD-65631.1	6.7	17.2	0.7	5.7	12.0	23.1	4.0	0.9
AD-65633.1	13.8	28.6	3.4	5.4	17.0	26.2	1.2	3.9
AD-65634.1	12.2	23.6	6.6	1.2	21.6	35.2	1.4	8.2
AD-65635.1	11.7	27.7	5.7	4.7	18.5	38.4	2.5	6.5
AD-65636.1	13.1	29.4	0.6	12.9	21.3	35.6	3.1	13.1
AD-65637.1	16.0	22.8	5.1	9.6	8.3	18.5	0.6	0.4
AD-65638.1	11.5	15.9	4.3	2.1	20.8	31.8	3.5	3.2
AD-65639.1	14.6	28.3	7.4	5.5	18.6	35.2	0.2	0.3
AD-65641.1	32.3	49.3	3.4	8.9	29.1	34.0	4.8	8.8
AD-65642.1	10.4	23.0	0.1	4.7	10.1	21.3	1.0	6.5
AD-65643.1	12.6	13.7	0.3	2.5	5.3	20.6	1.8	6.8
AD-65644.1	8.1	13.5	0.1	0.3	16.4	24.1	3.4	4.2
AD-65645.1	69.5	88.7	6.3	26.6	81.8	75.5	13.6	5.8
AD-65646.1	8.9	47.0	0.9	15.6	26.5	37.7	3.7	4.7
AD-65647.1	11.0	14.0	2.9	0.3	16.6	23.7	2.6	0.7
AD-65648.1	7.3	25.4	3.3	2.9	5.9	13.9	2.1	0.9
AD-65649.1	11.6	23.0	1.9	3.4	20.7	29.8	2.1	3.6

AD-65650.1	27.9	40.6	13.1	14.0	27.6	30.6	9.7	6.8
AD-65652.1	73.4	72.2	5.2	1.8	47.6	59.7	7.5	21.4
AD-65653.1	9.6	32.4	2.7	4.7	5.9	24.3	0.0	6.7
AD-65654.1	41.6	45.5	10.4	11.7	22.8	35.7	2.9	3.1
AD-65655.1	19.2	18.3	0.1	4.8	17.8	18.8	3.8	3.9
AD-65656.1	10.8	16.1	4.7	3.1	6.2	13.8	1.6	1.8
AD-65657.1	107.8	114.5	8.7	6.7	36.3	51.2	1.6	14.1
AD-65658.1	9.6	13.5	0.7	1.3	4.8	11.7	0.2	3.3
AD-65659.1	17.5	39.8	1.1	1.4	13.0	24.6	3.5	3.3
AD-65660.1	21.5	33.1	5.4	1.6	14.6	29.0	0.5	4.1
AD-65661.1	13.9	40.1	2.2	12.8	13.2	27.3	6.8	7.1
AD-65662.1	111.2	242.2	29.9	179.6	42.5	47.9	4.6	1.6
AD-65663.1	11.5	28.2	3.8	NA	5.5	7.6	1.4	0.1
AD-65665.1	104.8	141.7	13.0	26.9	39.4	44.2	13.1	5.3
AD-65666.1	14.4	28.1	6.9	1.8	3.8	12.7	0.3	4.8

Table 8. Additional Single Dose Screen in Primary Cyno Hepatocytes.

Duplex	10nM PCH	10nM PCH SD	0.1nM PCH	0.1nM {CH SD
AD-65626.5	7.1	0.7	23.5	3.7
AD-68272.1	10.1	1.9	39.5	10.3
AD-68273.1	6.8	2.2	29.7	10.1
AD-68274.1	15.7	4.7	49.4	12.1
AD-68275.1	15.5	2.7	47.4	10.4
AD-68276.1	22.3	8.1	83.0	21.7
AD-68277.1	14.2	1.1	25.2	7.9
AD-68278.1	18.6	3.2	97.5	25.4
AD-68279.1	14.7	3.8	62.5	19.6
AD-68280.1	24.9	2.6	54.7	8.1
AD-68281.1	38.3	18.6	70.7	8.8
AD-68282.1	11.3	3.1	35.9	3.6
AD-68283.1	14.4	3.6	79.9	26.5
AD-68284.1	25.1	4.7	82.3	8.2
AD-68285.1	10.4	1.3	39.3	10.3
AD-68286.1	14.7	4.5	71.9	18.3
AD-68287.1	8.0	2.3	28.4	3.5
AD-68288.1	14.8	3.5	31.7	6.3
AD-68289.1	11.8	2.5	30.8	3.5
AD-68290.1	11.5	4.9	40.3	8.4
AD-68291.1	15.8	6.3	69.9	6.6
AD-68292.1	9.8	3.0	37.3	20.7
AD-68293.1	20.2	6.1	85.2	20.8
AD-68294.1	12.9	5.0	68.7	21.6
AD-68295.1	7.5	1.4	22.6	3.9

AD-68296.1	8.5	1.1	51.3	7.0
AD-68297.1	8.2	2.4	27.4	4.0
AD-68298.1	10.1	2.8	35.6	10.4
AD-68299.1	11.8	2.4	47.7	16.2
AD-68300.1	7.2	1.7	33.8	4.6
AD-68301.1	34.2	14.3	78.3	25.8
AD-68302.1	15.6	5.8	57.1	10.0
AD-68303.1	7.0	2.0	23.9	4.5
AD-68304.1	14.8	2.4	64.2	12.1
AD-68305.1	25.3	3.8	106.5	23.8
AD-68306.1	12.4	2.0	19.8	1.8
AD-68307.1	22.2	8.9	93.1	22.6
AD-68308.1	22.2	4.0	79.6	7.8
AD-68309.1	8.0	2.7	19.9	3.7

Example 6. In vivo evaluation of GO-GalNac conjugates in C57B6 mice

GO-GalNAc conjugates were dosed subcutaneously in C57B6 mice at 10, 5, 2.5, or 1.25 mg/kg and mRNA knockdown in liver was evaluated after 72 hours post dose using qPCR. The single dose ED50s were approximately 1.25 and 2.5 mg/kg for compound A (AD-62994) and compound B (AD-62933) respectively. In repeat dose studies conjugates were dosed subcutaneously weekly (QW) for 4 weeks and liver GO mRNA levels were evaluated at 72 hours post the 4th dose. The repeat dose ED50s were ~0.3mg/kg for both compounds. The results are shown in Figure 4.

Example 7. In vivo evaluation of GO knockdown and impact on oxalate levels in AGXT KO mice.

A GO siRNA (AD-40257) in a lipid nanoparticle (LNP) was dosed intravenously in AGXT KO mice (Salido et al (2006) PNAS 103:18249) at 1 mg/kg. Urinary oxalate or glycolate levels were measured on day 15 using ion chromatography/mass spectroscopy. The results are shown in Figure 5. Data is expressed relative to pre dose values and was normalized to creatinine (Cr) to control for urine diluteness. N=4 mice per group and error bars represent standard deviation.

Example 8. In vivo evaluation of GO-GalNac conjugates in a rat AGXT knockdown model.

To generate a rat PH1 model, an AGXT siRNA (AD-63102) in an LNP (AF-011-63102) was dosed at 1 mg/kg intravenously to female Sprague Dawley rats on day 1 and day 7 to maintain knockdown of AGXT in rat liver and 1% Ethylene Glycol was added to the

drinking water to further stimulate oxalate production. On day 0 and day 7 some rats were also dosed with a GO GalNAc-siRNA (AD-62994) conjugate or PBS control. The results are shown in Figure 6. Figure 6A shows quantitation of liver AGXT mRNA levels 72 hours after a single 1mg/kg dose of AGXT siRNA in an LNP. In Figure 6B, levels of urinary oxalate were quantified from 24 hour urines collected from day -1 to 0, day 3 to 4, day 5 to 6, and day 7 to 8. Data was normalized to creatinine to control for the diluteness of the urine. N=3 for AGXT groups and N=2 for PBS control group. In Figure 6C, these same rats (as in figure 6B) were followed out to 49 days with continued weekly dosing on days 14 and 21 of both AF-011-63102 and AD-62994 and 24 hour urine collections as shown. Ethylene glycol remained in the drinking water until day 28. In Figure 6D, duration of HAO1 knockdown in rats is shown by measuring mRNA levels either one week or four weeks after the last of 4 doses (corresponding to days 28 and 49 in Figure 6C) and expressed relative to levels seen in rats treated with PBS. Error bars represent standard deviation throughout.

duplexName	target	senseWksName
AD-40257.1	HAO1	NM_017545.2_1306-1324_s
AD-40257.2	HAO1	NM_017545.2_1306-1324_s
AD-63102.1	AGXT	NM_016702.3_1109-1127_s
AD-63102.2	AGXT	NM_016702.3_1109-1127_s
AD-63102.3	AGXT	NM_016702.3_1109-1127_s

duplexName	Modified sense strand sequence	Unmodified sense strand sequence	SEQ ID NO:
AD-40257.1	uucAAuGGGuGuccuAGGAdTsdT	UUCAAUGGGUGUCCUAGGA	770 & 771
AD-40257.2	uucAAuGGGuGuccuAGGAdTsdT	UUCAAUGGGUGUCCUAGGA	770 & 771
AD-63102.1	AcAAcuGGAGGGAcAucGudTsdT	ACAACUGGAGGGACAUCGU	772 & 773
AD-63102.2	AcAAcuGGAGGGAcAucGudTsdT	ACAACUGGAGGGACAUCGU	772 & 773
AD-63102.3	AcAAcuGGAGGGAcAucGudTsdT	ACAACUGGAGGGACAUCGU	772 & 773

duplexName	Modified antisense strand sequence	Unmodified antisense strand sequence	SEQ ID NO:
AD-40257.1	UCCuAGGAcACCcAUUGAAdTsdT	UCCUAGGACACCCAUUGAA	774 & 775
AD-40257.2	UCCuAGGAcACCcAUUGAAdTsdT	UCCUAGGACACCCAUUGAA	774 & 775
AD-63102.1	ACGAUGUCCCUCcAGUUGUdTsdT	ACGAUGUCCCUCCAGUUGU	776 & 777
AD-63102.2	ACGAUGUCCCUCcAGUUGUdTsdT	ACGAUGUCCCUCCAGUUGU	776 & 777
AD-63102.3	ACGAUGUCCCUCcAGUUGUdTsdT	ACGAUGUCCCUCCAGUUGU	776 & 777

Example 9: In vivo evaluation of GO-GalNac conjugates

Female C57BL/6 Mice, aged 6-8 weeks, were administered a single subcutaneous dose of the GO siRNA-GalNac conjugates in Table 7. The mice were sacrifices after 72 hours and the liver was assayed for HAO mRNA by bDNA analysis. The results are shown in Figure 13.

Table 7: GO (HAO) siRNA-GalNac conjugates.

duplexName	Modified sense strand sequence	SEQ ID NO:
AD-62989.2	UfscsCfuAfgGfaAfCfCfuUfuUfaGfaAfaUfL96	778
AD-62994.2	GfsasCfuUfuCfaUfCfCfuGfgAfaAfuAfuAfL96	779
AD-62933.2	GfsasAfuGfuGfaAfAfGfuCfaUfcGfaCfaAfL96	780
AD-62935.2	CfsasUfuGfgUfgAfGfGfaAfaAfaUfcCfuUfL96	781
AD-62940.2	AfsusCfgAfcAfaGfAfCfaUfuGfgUfgAfgAfL96	782
AD-62941.2	AfscsAfuUfgGfuGfAfGfgAfaAfaAfuCfcUfL96	783
AD-62944.2	GfsasAfaGfuCfaUfCfCfgGfaCfaAfgAfcAfuUfL96	784
AD-62965.2	AfsasAfgUfcAfuCfGfAfcAfaGfaCfaUfuAfL96	785

duplexName	Modified antisense strand	SEQ ID NO:
AD-62989.2	asUfsuUfcUfaAfaAfgguUfcCfuAfgGfascsa	786
AD-62994.2	usAfsuAfuUfuCfcAfggaUfgAfaAfgUfcscsa	787
AD-62933.2	usUfsgUfcGfaUfgAfcuuUfcAfcAfuUfcsusg	788
AD-62935.2	asAfsgGfaUfuUfuUfccuCfaCfcAfaUfgsusc	789
AD-62940.2	usCfsuCfaCfcAfaUfgucUfuGfuCfgAfusgsa	790
AD-62941.2	asGfsgAfuUfuUfuCfcucAfcCfaAfuGfuscsu	791
AD-62944.2	asAfsuGfuCfuUfgUfcgaUfgAfcUfuUfcsasc	792
AD-62965.2	usAfsaUfgUfcUfuGfucgAfuGfaCfuUfuscsa	793

duplexName	Crossreactivity	Guinea Pig?	MM to mouse	MM to GP
AD-62989.2	Hs	yes	pos8	
AD-62994.2	Hs	no	pos16	pos2,12,16
AD-62933.2	Hs/Mm	yes		
AD-62935.2	Hs/Mm	yes		
AD-62940.2	Hs/Mm	yes		
AD-62941.2	Hs/Mm	yes		
AD-62944.2	Hs/Mm	yes		
AD-62965.2	Hs/Mm	yes		

Example 10: In vivo evaluation of GO-GalNAc conjugates in mice

Female C57 BL/6 mice were administered a single subcutaneous 3 mg/Kg dose of the a number of GO siRNA-GalNAc conjugates described herein or PBS control. Mice were sacrificed after 72 hours and HAO1 mRNA knockdown in liver was evaluated using qPCR. The results are shown in Figure 14, expressed relative to the PBS control.

Example 11: Dose-response evaluation of GO-GalNAc conjugates in mice

Female C57 BL/6 mice were administered a single subcutaneous dose of either 1 or 3 mg/Kg of one of the GO siRNA-GalNAc conjugates compound A (AD-62994), compound B (AD-62933), compound C (AD-65644), compound D (AD-65626), compound E (AD-65590), compound F (AD-65585) or PBS control. Ten days later mice were sacrificed and HAO1 mRNA knockdown in liver was evaluated using qPCR. In repeat dose studies, compounds C, D, F or PBS control were dosed subcutaneously weekly (QW) for 4 weeks and liver HAO1 mRNA levels were evaluated 10 days after the last dose. The results of single-dose are shown in Figure 15 and repeat-dose experiments are shown in Figure 16, expressed relative to the PBS control. These data showed improved potency for compounds AD-65644 and AD-65626 relative to AD-62933 and for compounds AD-65590 and AD-65585 relative to AD-62994.

Example 12: Dose-response evaluation of compound D in mice

Female C57 BL/6 mice were administered a single subcutaneous dose of 0.1, 0.3, 1, 3, or 10 mg/Kg of AD-65626 or PBS control. Ten days later mice were sacrificed and HAO1 mRNA knockdown in liver was evaluated using qPCR with results expressed relative to the PBS control as shown in Figure 17. These results demonstrate a greater than 3-fold improvement in potency compared to compound AD-62933.

Example 13: Relationship of mRNA knockdown to serum glycolate levels in mice

Female C57 BL/6 mice were administered a single subcutaneous dose of 0.1, 0.3, 1, 3, or 10 mg/Kg of AD-65585 or PBS control. Ten days later mice were sacrificed and HAO1 mRNA knockdown in liver was evaluated using qPCR, with results expressed relative to the PBS control. Glycolate levels in serum samples from these same mice were quantified using ion chromatography coupled to mass spectrometry as previously described (Knight et al., Anal. Biochem. 2012 February 1; 421(1): 121–124). The results for these experiments are shown in Figure 18.

These results demonstrate that AD-65585 is as potent as AD-65626, both having a single-dose ED50 of ~0.3 mg/kg in WT mice. Additionally, HAO1 mRNA silencing results in dose-responsive serum glycolate increases of up to 4-fold (approximately 200uM) at the highest two doses.

Example 14: Relationship of mRNA knockdown to serum glycolate levels in rats

Male Sprague Dawley rats were administered a single subcutaneous dose of 1, 3, or 10 mg/Kg of AD-65626 or PBS control. Fourteen days later rats were sacrificed and HAO1 mRNA knockdown in liver was evaluated using qPCR, with results expressed relative to the PBS control. Glycolate levels in serum samples from these same rats collected both prior to dosing and at day 14 were quantified using ion chromatography coupled to mass spectrometry, again as described (Knight et al., Anal. Biochem. 2012 February 1; 421(1): 121–124). The results for these experiments are shown in Figure 19.

As observed in wild-type mice, these results demonstrate that HAO1 mRNA silencing in Sprague Dawley rats results in dose-responsive serum glycolate increases of up to 12-fold (approximately 140 μM) at the highest dose.

Example 15: Pharmacology studies with ALN-65585

HAO1 inhibition in hepatocytes.

Primary cyno hepatocytes were transfected with RNAimax (Invitrogen) with serially diluted AD-65585 (ALN-65585, "ALN-GO1") or a non-targeting mRNA Luciferase control (AD1955) at 10 nM. Relative levels of HAO1 mRNA were determined by normalizing to GAPDH mRNA levels as quantified by real-time RT-PCR. The data was plotted to calculate the IC50 value of 10 pM. The results are shown Figure 20.

In vitro transfection of AD-65585 demonstrates an ED50 of approximately 10pM in primary cynomolgus hepatocytes.

Single Dose Pharmacology in Mouse

ALN-GO1 pharmacology was evaluated in mice by quantifying liver HAO1 mRNA and serum glycolate levels (Figure 21). A single SC dose of ALN-GO1 resulted in a dose dependent suppression of HAO1 mRNA with a dose of 10 mg/kg resulting in ED90 silencing. The ED50 dose for GO1 silencing in the mouse was estimated to be 0.3 mg/kg. Serum glycolate levels increased in a dose-responsive manner with a maximum level approximately 4-fold above baseline levels. The results are shown in Figure 21, illustrating levels of liver HAO1 mRNA and serum glycolate 10 days after a single subcutaneous dose of ALN-65585 in C57BL/6 mice. Bars represent the mean of 3 or 4 animals and error bars depict the standard deviation.

Single Dose Duration in Mouse

GO1 silencing was durable and reversible post a single SC dose (Figure 22). A single SC dose of ALN-GO1 in mice at 3mg/kg resulted in ≥70% mRNA silencing for approximately 6 weeks, after which mRNA levels recovered to baseline levels through 12 weeks post-dose. The results are shown in figure 22: Levels of liver HAO1 mRNA at multiple time points following a single subcutaneous dose of ALN-65585 in C57BL/6 mice. Each data point represents the mean of 3 animals and error bars depict the standard deviation.

Single Dose Pharmacology in Rat

ALN-GO1 pharmacology was also evaluated in rats by quantifying liver HAO1 mRNA levels (Figure 23). A single SC administration of ALN-GO1 to male Sprague Dawley rats resulted in a dose dependent suppression of HAO1 mRNA with a dose of ≥3mg/kg resulting in ED90 silencing. The results are shown in figure 23: Levels of liver HAO1 mRNA 10 days after a single subcutaneous dose of ALN-65585 in Sprague Dawley rats. Bars represent the mean of 3 animals and error bars depict the standard deviation. The ED50 dose for GO1 silencing in the rat was estimated to be 0.3 mg/kg.

Single Dose Pharmacology in AGXT KO Mouse

The impact of ALN-GO1 on oxalate levels was evaluated in an AGXT KO mouse model of PH1. The results are shown in Figure 24: 24hr urinary oxalate (top) and glycolate (bottom) excretion of Agxt KO mice after a single subcutaneous dose of ALN-65585. Different letters means significant difference between the 3 dose groups at each specific week (n=3 per dose). Urinary excretions over time did not change significantly in the PBS control animal (n=1).

Urinary oxalate levels showed dose-dependent reductions after a single dose of ALN-GO1 with a maximum of approximately 50% oxalate lowering at the 3mg/kg dose that lasted for ≥3 weeks before recovery to pre-dose levels. Urinary glycolate levels showed dose-dependent increases after a single dose of ALN-GO1 with a maximum of approximately 5-fold increases at the 3mg/kg dose that lasted for ≥4 weeks.

Single Dose Pharmacology in PH1 Induced Rat Model

ALN-GO1 was evaluated in a second PH1 rodent model where liver AGXT was inhibited in rats using siRNA and oxalate levels were stimulated with ethylene glycol (Figure 25A and Figure 25B). Liver HAO1 mRNA and 24-hour urinary oxalate were quantified to

determine the degree of HAO1 lowering required for maximal oxalate reduction. The results are shown in Figure 25A and Figure 25B: Levels of liver HAO1 mRNA a rat induced model of PH1 14 days after a single subcutaneous dose of ALN-65585 and weekly dosing of AF-011-AGXT siRNA (2 doses, of 1mg/kg). 24hr urinary oxalate normalized to urinary creatinine. Bars represent the mean of 3 animals and error bars depict the standard deviation. mRNA and oxalate lowering correlation plot represents individual animals from multiple experiments.

A single dose of ALN-GO1 in this model demonstrated dose-responsive mRNA and urinary oxalate lowering with approximately 85% maximum mRNA reduction and approximately 90% maximum urinary oxalate reduction observed at the highest dose of ALN-GO1 (Figure 25A and Figure 25B). In this induced rat model of PH1, mRNA and urinary oxalate reductions resulted in a 1:1 correlation.

Multi-Dose Pharmacology in PH1 Induced Rat Model

Potency of ALN-GO1 was evaluated in studies in normal rats with inhibited AGXT activity and ethylene glycol (an induced model of PH1) by quantifying liver HAO1 mRNA and 24-hour urinary oxalate. The results are shown in Figure 26: Levels of liver HAO1 mRNA a rat induced model of PH1 28 days after repeat subcutaneous dosing of ALN-65585 and repeat IV dosing of AF-011-AGXT siRNA (4 doses, of 1mg/kg). 24hr urinary oxalate normalized to urinary creatinine. Bars represent the mean of 2 or 3 animals and error bars depict the standard deviation.

Treatment with ALN-GO1 resulted in sustained urinary oxalate reductions in all treatment groups for approximately 3 weeks. On day 28 after repeat dosing of ALN-GO1 (and four doses of AF-011-AGXT) all groups showed >95%mRNA reduction >85% urinary oxalate lowering.

Multi-Dose Pharmacology in NHP

ALN-GO1 pharmacology was evaluated in cynomolgus monkeys (non-human primate (NHP)) by quantifying HAO1 mRNA in liver biopsy, and serum glycolate levels. The following table shows the NHP Pharmacology study outline detailing dose level and dose regimen.

Group #	Test Article	Dose level (mg/kg)	Dose frequency
1	PBS	Na	QM x 6
2	AD-65585	0.25	QM x 8

3	AD-65585	1	QM x 8
4	AD-65585	1	QM x 6
5	AD-65585	2	QM x 6
6	AD-65585	4	QM x 6
7	AD-65585	2 -> 1	QM x 4 -> QM x 5

The results are shown in Figure 27. NHP serum glycolate levels for all groups out to day 85, data represents group averages of 3 animals per group, lines represent standard deviation. Liver biopsy HAO1 mRNA on Day 29, lines represent group averages, symbols represent individual animal mRNA levels relative to PBS control on Day 29.

After the first month of dosing (day 29), dose-responsive mRNA silencing was observed in all groups, with up to 99% mRNA silencing in groups 6 and 7 dosed with 4mg/kg monthly or 2mg/kg weekly. Maximum elevated serum glycolate levels of approximately 70μM were maintained for at least 3 weeks in group 6 dosed with 4mg/kg monthly.

Intermediate serum glycolate

Example 16: Additional siRNA sequences.

Additional siRNA design was carried out to identify siRNAs targeting HAO1 NM_017545.2.

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUGUAUGUUACUUCUUAGAGA	794	asusguauGfuUfAfCfuucuuagagaL96	1890	sense	21
UCUCUAAGAAGUAACAUACAUCC	795	usCfsucuAfaGfAfaguaAfcAfuacauscsc	1891	antis	23
UGUAUGUUACUUCUUAGAGAG	796	usgsuaugUfuAfCfUfucuuagagagL96	1892	sense	21
CUCUCUAAGAAGUAACAUACAUC	797	csUfscucUfaAfGfaaguAfaCfauacasusc	1893	antis	23
UAGGAUGUAUGUUACUUCUUA	798	usasggauGfuAfUfGfuuacuucuuaL96	1894	sense	21
UAAGAAGUAACAUACAUCCUAAA	799	usAfsagaAfgUfAfacauAfcAfuccuasasa	1895	antis	23
UUAGGAUGUAUGUUACUUCUU	800	ususaggaUfgUfAfUfguuacuucuuL96	1896	sense	21
AAGAAGUAACAUACAUCCUAAAA	801	asAfsgaaGfuAfAfcauaCfaUfccuaasasa	1897	antis	23
AGAAAGGUGUUCAAGAUGUCC	802	asgsaaagGfuGfUfUfcaagauguccL96	1898	sense	21
GGACAUCUUGAACACCUUUCUCC	803	gsGfsacaUfcUfUfgaacAfcCfuuucuscsc	1899	antis	23
GAAAGGUGUUCAAGAUGUCCU	804	gsasaaggUfgUfUfCfaagauguccuL96	1900	sense	21
AGGACAUCUUGAACACCUUUCUC	805	asGfsgacAfuCfUfugaaCfaCfcuuucsusc	1901	antis	23
GGGGAGAAAGGUGUCAAGAU	806	gsgsggagAfaAfGfGfuguucaagauL96	1902	sense	21
AUCUUGAACACCUUUCUCCCCCU	807	asUfscuuGfaAfCfaccuUfuCfucccccscsu	1903	antis	23
GGGGGAGAAAGGUGUUCAAGA	808	gsgsgggaGfaAfAfGfguguucaagaL96	1904	sense	21
UCUUGAACACCUUUCUCCCCCUG	809	usCfsuugAfaCfAfccuuUfcUfcccccsusg	1905	antis	23
AGAAACUUUGGCUGAUAAUAU	810	asgsaaacUfuUfGfGfcugauaauauL96	1906	sense	21
AUAUUAUCAGCCAAAGUUUCUUC	811	asUfsauuAfuCfAfgccaAfaGfuuucususc	1907	antis	23
GAAACUUUGGCUGAUAAUAUU	812	gsasaacuUfuGfGfCfugauaauauuL96	1908	sense	21
AAUAUUAUCAGCCAAAGUUUCUU	813	asAfsuauUfaUfCfagccAfaAfguuucsusu	1909	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUGAAGAAACUUUGGCUGAUA	814	asusgaagAfaAfCfUfuuggcugauaL96	1910	sense	21
UAUCAGCCAAAGUUUCUUCAUCA	815	usAfsucaGfcCfAfaaguUfuCfuucauscsa	1911	antis	23
GAUGAAGAAACUUUGGCUGAU	816	gsasugaaGfaAfAfCfuuuggcugauL96	1912	sense	21
AUCAGCCAAAGUUUCUUCAUCAU	817	asUfscagCfcAfAfaguuUfcUfucaucsasu	1913	antis	23
AAGGCACUGAUGUUCUGAAAG	818	asasggcaCfuGfAfUfguucugaaagL96	1914	sense	21
CUUUCAGAACAUCAGUGCCUUUC	819	csUfsuucAfgAfAfcaucAfgUfgccuususc	1915	antis	23
AGGCACUGAUGUUCUGAAAGC	820	asgsgcacUfgAfUfGfuucugaaagcL96	1916	sense	21
GCUUUCAGAACAUCAGUGCCUUU	821	gsCfsuuuCfaGfAfacauCfaGfugccususu	1917	antis	23
CGGAAAGGCACUGAUGUUCUG	822	csgsgaaaGfgCfAfCfugauguucugL96	1918	sense	21
CAGAACAUCAGUGCCUUUCCGCA	823	csAfsgaaCfaUfCfagugCfcUfuuccgscsa	1919	antis	23
GCGGAAAGGCACUGAUGUUCU	824	gscsggaaAfgGfCfAfcugauguucuL96	1920	sense	21
AGAACAUCAGUGCCUUUCCGCAC	825	asGfsaacAfuCfAfgugcCfuUfuccgcsasc	1921	antis	23
AGAAGACUGACAUCAUUGCCA	826	asgsaagaCfuGfAfCfaucauugccaL96	1922	sense	21
UGGCAAUGAUGUCAGUCUUCUCA	827	usGfsgcaAfuGfAfugucAfgUfcuucuscsa	1923	antis	23
GAAGACUGACAUCAUUGCCAA	828	gsasagacUfgAfCfAfucauugccaaL96	1924	sense	21
UUGGCAAUGAUGUCAGUCUUCUC	829	usUfsggcAfaUfGfauguCfaGfucuucsusc	1925	antis	23
GCUGAGAAGACUGACAUCAUU	830	gscsugagAfaGfAfCfugacaucauuL96	1926	sense	21
AAUGAUGUCAGUCUUCUCAGCCA	831	asAfsugaUfgUfCfagucUfuCfucagcscsa	1927	antis	23
GGCUGAGAAGACUGACAUCAU	832	gsgscugaGfaAfGfAfcugacaucauL96	1928	sense	21
AUGAUGUCAGUCUUCUCAGCCAU	833	asUfsgauGfuCfAfgucuUfcUfcagccsasu	1929	antis	23
UAAUGCCUGAUUCACAACUUU	834	usasaugcCfuGfAfUfucacaacuuuL96	1930	sense	21
AAAGUUGUGAAUCAGGCAUUACC	835	asAfsaguUfgUfGfaaucAfgGfcauuascsc	1931	antis	23
AAUGCCUGAUUCACAACUUUG	836	asasugccUfgAfUfUfcacaacuuugL96	1932	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CAAAGUUGUGAAUC AGGCAUUAC	837	csAfsaagUfuGfUfgaau CfaGfgcauusasc	1933	antis	23
UUGGUAAUGCCUGA UUCACAA	838	ususgguaAfuGfCfCfug auucacaaL96	1934	sense	21
UUGUGAAUCAGGCA UUACCAACA	839	usUfsgugAfaUfCfaggc AfuUfaccaascsa	1935	antis	23
GUUGGUAAUGCCUG AUUCACA	840	gsusugguAfaUfGfCfcu gauucacaL96	1936	sense	21
UGUGAAUCAGGCAU UACCAACAC	841	usGfsugaAfuCfAfggca UfuAfccaacsasc	1937	antis	23
UAUCAAAUGGCUGA GAAGACU	842	usasucaaAfuGfGfCfug agaagacuL96	1938	sense	21
AGUCUUCUCAGCCA UUUGAUAUC	843	asGfsucuUfcUfCfagcc AfuUfugauasusc	1939	antis	23
AUCAAAUGGCUGAG AAGACUG	844	asuscaaaUfgGfCfUfga gaagacugL96	1940	sense	21
CAGUCUUCUCAGCC AUUUGAUAU	845	csAfsgucUfuCfUfcagc CfaUfuugausasu	1941	antis	23
AAGAUAUCAAAUGG CUGAGAA	846	asasgauaUfcAfAfAfug gcugagaaL96	1942	sense	21
UUCUCAGCCAUUUG AUAUCUUCC	847	usUfscucAfgCfCfauuu GfaUfaucuuscsc	1943	antis	23
GAAGAUAUCAAAUG GCUGAGA	848	gsasagauAfuCfAfAfau ggcugagaL96	1944	sense	21
UCUCAGCCAUUUGA UAUCUUCCC	849	usCfsucaGfcCfAfuuug AfuAfucuucscsc	1945	antis	23
UCUGACAGUGCACA AUAUUUU	850	uscsugacAfgUfGfCfac aauauuuuL96	1946	sense	21
AAAAUAUUGUGCAC UGUCAGAUC	851	asAfsaauAfuUfGfugca CfuGfucagasusc	1947	antis	23
CUGACAGUGCACAA UAUUUUC	852	csusgacaGfuGfCfAfca auauuuucL96	1948	sense	21
GAAAAUAUUGUGCA CUGUCAGAU	853	gsAfsaaaUfaUfUfgugc AfcUfgucagsasu	1949	antis	23
AAGAUCUGACAGUG CACAAUA	854	asasgaucUfgAfCfAfgu gcacaauaL96	1950	sense	21
UAUUGUGCACUGUC AGAUCUUGG	855	usAfsuugUfgCfAfcugu CfaGfaucuusgsg	1951	antis	23
CAAGAUCUGACAGU GCACAAU	856	csasagauCfuGfAfCfag ugcacaauL96	1952	sense	21
AUUGUGCACUGUCA GAUCUUGGA	857	asUfsuguGfcAfCfuguc AfgAfucuugsgsa	1953	antis	23
ACUGAUGUUCUGAA AGCUCUG	858	ascsugauGfuUfCfUfga aagcucugL96	1954	sense	21
CAGAGCUUUCAGAA CAUCAGUGC	859	csAfsgagCfuUfUfcaga AfcAfucagusgsc	1955	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CUGAUGUUCUGAAAGCUCUGG	860	csusgaugUfuCfUfGfaaagcucuggL96	1956	sense	21
CCAGAGCUUUCAGAACAUCAGUG	861	csCfsagaGfcUfUfucagAfaCfaucagsusg	1957	antis	23
AGGCACUGAUGUUCUGAAAGC	862	asgsgcacUfgAfUfGfuucugaaagcL96	1958	sense	21
GCUUUCAGAACAUCAGUGCCUUU	863	gsCfsuuuCfaGfAfacauCfaGfugccususu	1959	antis	23
AAGGCACUGAUGUUCUGAAAG	864	asasggcaCfuGfAfUfguucugaaagL96	1960	sense	21
CUUUCAGAACAUCAGUGCCUUUC	865	csUfsuucAfgAfAfcaucAfgUfgccuususc	1961	antis	23
AACAACAUGCUAAAUCAGUAC	866	asascaacAfuGfCfUfaaaucaguacL96	1962	sense	21
GUACUGAUUUAGCAUGUUGUUCA	867	gsUfsacuGfaUfUfuagcAfuGfuuguuscsa	1963	antis	23
ACAACAUGCUAAAUCAGUACU	868	ascsaacaUfgCfUfAfaaucaguacuL96	1964	sense	21
AGUACUGAUUUAGCAUGUUGUUC	869	asGfsuacUfgAfUfuuagCfaUfguugususc	1965	antis	23
UAUGAACAACAUGCUAAAUCA	870	usasugaaCfaAfCfAfugcuaaaucaL96	1966	sense	21
UGAUUUAGCAUGUUGUUCAUAAU	871	usGfsauuUfaGfCfauguUfgUfucauasasu	1967	antis	23
UUAUGAACAACAUGCUAAAUC	872	ususaugaAfcAfAfCfaugcuaaaucL96	1968	sense	21
GAUUUAGCAUGUUGUUCAUAAUC	873	gsAfsuuuAfgCfAfuguuGfuUfcauaasusc	1969	antis	23
UCUUUAGUGUCUGAAUAUAUC	874	uscsuuuaGfuGfUfCfugaauauaucL96	1970	sense	21
GAUAUAUUCAGACACUAAAGAUG	875	gsAfsuauAfuUfCfagacAfcUfaaagasusg	1971	antis	23
CUUUAGUGUCUGAAUAUAUCC	876	csusuuagUfgUfCfUfgaauauauccL96	1972	sense	21
GGAUAUAUUCAGACACUAAAGAU	877	gsGfsauaUfaUfUfcagaCfaCfuaaagsasu	1973	antis	23
CACAUCUUUAGUGUCUGAAUA	878	csascaucUfuUfAfGfugucugaauaL96	1974	sense	21
UAUUCAGACACUAAAGAUGUGAU	879	usAfsuucAfgAfCfacuaAfaGfaugugsasu	1975	antis	23
UCACAUCUUUAGUGUCUGAAU	880	uscsacauCfuUfUfAfgugucugaauL96	1976	sense	21
AUUCAGACACUAAAGAUGUGAUU	881	asUfsucaGfaCfAfcuaaAfgAfugugasusu	1977	antis	23
UGAUACUUCUUUGAAUGUAGA	882	usgsauacUfuCfUfUfugaauguagaL96	1978	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UCUACAUUCAAAGA AGUAUCACC	883	usCfsuacAfuUfCfaaag AfaGfuaucascsc	1979	antis	23
GAUACUUCUUUGAA UGUAGAU	884	gsasuacuUfcUfUfUfga auguagauL96	1980	sense	21
AUCUACAUUCAAAG AAGUAUCAC	885	asUfscuaCfaUfUfcaaa GfaAfguaucsasc	1981	antis	23
UUGGUGAUACUUCU UUGAAUG	886	ususggugAfuAfCfUfuc uuugaaugL96	1982	sense	21
CAUUCAAAGAAGUA UCACCAAUU	887	csAfsuucAfaAfGfaagu AfuCfaccaasusu	1983	antis	23
AUUGGUGAUACUUC UUUGAAU	888	asusugguGfaUfAfCfuu cuuugaauL96	1984	sense	21
AUUCAAAGAAGUAU CACCAAUUA	889	asUfsucaAfaGfAfagua UfcAfccaaususa	1985	antis	23
AAUAACCUGUGAAA AUGCUCC	890	asasuaacCfuGfUfGfaa aaugcuccL96	1986	sense	21
GGAGCAUUUUCACA GGUUAUUGC	891	gsGfsagcAfuUfUfucac AfgGfuuauusgsc	1987	antis	23
AUAACCUGUGAAAA UGCUCCC	892	asusaaccUfgUfGfAfaa augcucccL96	1988	sense	21
GGGAGCAUUUUCAC AGGUUAUUG	893	gsGfsgagCfaUfUfuuca CfaGfguuaususg	1989	antis	23
UAGCAAUAACCUGU GAAAAUG	894	usasgcaaUfaAfCfCfug ugaaaaugL96	1990	sense	21
CAUUUUCACAGGUU AUUGCUAUC	895	csAfsuuuUfcAfCfaggu UfaUfugcuasusc	1991	antis	23
AUAGCAAUAACCUG UGAAAAU	896	asusagcaAfuAfAfCfcu gugaaaauL96	1992	sense	21
AUUUUCACAGGUUA UUGCUAUCC	897	asUfsuuuCfaCfAfgguu AfuUfgcuauscsc	1993	antis	23
AAUCACAUCUUUAG UGUCUGA	898	asasucacAfuCfUfUfua gugucugaL96	1994	sense	21
UCAGACACUAAAGA UGUGAUUGG	899	usCfsagaCfaCfUfaaag AfuGfugauusgsg	1995	antis	23
AUCACAUCUUUAGU GUCUGAA	900	asuscacaUfcUfUfUfag ugucugaaL96	1996	sense	21
UUCAGACACUAAAG AUGUGAUUG	901	usUfscagAfcAfCfuaaa GfaUfgugaususg	1997	antis	23
UUCCAAUCACAUCU UUAGUGU	902	ususccaaUfcAfCfAfuc uuuaguguL96	1998	sense	21
ACACUAAAGAUGUG AUUGGAAAU	903	asCfsacuAfaAfGfaugu GfaUfuggaasasu	1999	antis	23
UUUCCAAUCACAUC UUUAGUG	904	ususuccaAfuCfAfCfau cuuuagugL96	2000	sense	21
CACUAAAGAUGUGA UUGGAAAUC	905	csAfscuaAfaGfAfugug AfuUfggaaasusc	2001	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
ACGGGCAUGAUGUUGAGUUCC	906	ascsgggcAfuGfAfUfgugaguuccL96	2002	sense	21
GGAACUCAACAUCAUGCCCGUUC	907	gsGfsaacUfcAfAfcaucAfuGfcccgususc	2003	antis	23
CGGGCAUGAUGUUGAGUUCCU	908	csgsggcaUfgAfUfGfuugaguuccuL96	2004	sense	21
AGGAACUCAACAUCAUGCCCGUU	909	asGfsgaaCfuCfAfacauCfaUfgcccgsusu	2005	antis	23
GGGAACGGGCAUGAUGUUGAG	910	gsgsgaacGfgGfCfAfugauguugagL96	2006	sense	21
CUCAACAUCAUGCCCGUUCCCAG	911	csUfscaaCfaUfCfaugcCfcGfuucccsasg	2007	antis	23
UGGGAACGGGCAUGAUGUUGA	912	usgsggaaCfgGfGfCfaugauguugaL96	2008	sense	21
UCAACAUCAUGCCCGUUCCCAGG	913	usCfsaacAfuCfAfugccCfgUfucccasgsg	2009	antis	23
ACUAAGGUGAAAAGAUAAUGA	914	ascsuaagGfuGfAfAfaagauaaugaL96	2010	sense	21
UCAUUAUCUUUUCACCUUAGUGU	915	usCfsauuAfuCfUfuuucAfcCfuuagusgsu	2011	antis	23
CUAAGGUGAAAAGAUAAUGAU	916	csusaaggUfgAfAfAfagauaaugauL96	2012	sense	21
AUCAUUAUCUUUUCACCUUAGUG	917	asUfscauUfaUfCfuuuuCfaCfcuuagsusg	2013	antis	23
AAACACUAAGGUGAAAAGAUA	918	asasacacUfaAfGfGfugaaaagauaL96	2014	sense	21
UAUCUUUUCACCUUAGUGUUUGC	919	usAfsucuUfuUfCfaccuUfaGfuguuusgsc	2015	antis	23
CAAACACUAAGGUGAAAAGAU	920	csasaacaCfuAfAfGfgugaaaagauL96	2016	sense	21
AUCUUUUCACCUUAGUGUUUGCU	921	asUfscuuUfuCfAfccuuAfgUfguuugscsu	2017	antis	23
AGGUAGCACUGGAGAGAAUUG	922	asgsguagCfaCfUfGfgagagaauugL96	2018	sense	21
CAAUUCUCUCCAGUGCUACCUUC	923	csAfsauuCfuCfUfccagUfgCfuaccususc	2019	antis	23
GGUAGCACUGGAGAGAAUUGG	924	gsgsuagcAfcUfGfGfagagaauuggL96	2020	sense	21
CCAAUUCUCUCCAGUGCUACCUU	925	csCfsaauUfcUfCfuccaGfuGfcuaccsusu	2021	antis	23
GAGAAGGUAGCACUGGAGAGA	926	gsasgaagGfuAfGfCfacuggagagaL96	2022	sense	21
UCUCUCCAGUGCUACCUUCUCAA	927	usCfsucuCfcAfGfugcuAfcCfuucucsasa	2023	antis	23
UGAGAAGGUAGCACUGGAGAG	928	usgsagaaGfgUfAfGfcacuggagagL96	2024	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CUCUCCAGUGCUAC CUUCUCAAA	929	csUfscucCfaGfUfgcua CfcUfucucasasa	2025	antis	23
AGUGGACUUGCUGC AUAUGUG	930	asgsuggaCfuUfGfCfug cauaugugL96	2026	sense	21
CACAUAUGCAGCAA GUCCACUGU	931	csAfscauAfuGfCfagca AfgUfccacusgsu	2027	antis	23
GUGGACUUGCUGCA UAUGUGG	932	gsusggacUfuGfCfUfgc auauguggL96	2028	sense	21
CCACAUAUGCAGCA AGUCCACUG	933	csCfsacaUfaUfGfcagc AfaGfuccacsusg	2029	antis	23
CGACAGUGGACUUG CUGCAUA	934	csgsacagUfgGfAfCfuu gcugcauaL96	2030	sense	21
UAUGCAGCAAGUCC ACUGUCGUC	935	usAfsugcAfgCfAfaguc CfaCfugucgsusc	2031	antis	23
ACGACAGUGGACUU GCUGCAU	936	ascsgacaGfuGfGfAfcu ugcugcauL96	2032	sense	21
AUGCAGCAAGUCCA CUGUCGUCU	937	asUfsgcaGfcAfAfgucc AfcUfgucguscsu	2033	antis	23
AAGGUGUUCAAGAU GUCCUCG	938	asasggugUfuCfAfAfga uguccucgL96	2034	sense	21
CGAGGACAUCUUGA ACACCUUUC	939	csGfsaggAfcAfUfcuug AfaCfaccuususc	2035	antis	23
AGGUGUUCAAGAUG UCCUCGA	940	asgsguguUfcAfAfGfau guccucgaL96	2036	sense	21
UCGAGGACAUCUUG AACACCUUU	941	usCfsgagGfaCfAfucuu GfaAfcaccususu	2037	antis	23
GAGAAAGGUGUUCA AGAUGUC	942	gsasgaaaGfgUfGfUfuc aagaugucL96	2038	sense	21
GACAUCUUGAACAC CUUUCUCCC	943	gsAfscauCfuUfGfaaca CfcUfuucucscsc	2039	antis	23
GGAGAAAGGUGUUC AAGAUGU	944	gsgsagaaAfgGfUfGfuu caagauguL96	2040	sense	21
ACAUCUUGAACACC UUUCUCCCC	945	asCfsaucUfuGfAfacac CfuUfucuccscsc	2041	antis	23
AACCGUCUGGAUGA UGUGCGU	946	asasccguCfuGfGfAfug augugcguL96	2042	sense	21
ACGCACAUCAUCCA GACGGUUGC	947	asCfsgcaCfaUfCfaucc AfgAfcgguusgsc	2043	antis	23
ACCGUCUGGAUGAU GUGCGUA	948	ascscgucUfgGfAfUfga ugugcguaL96	2044	sense	21
UACGCACAUCAUCC AGACGGUUG	949	usAfscgcAfcAfUfcauc CfaGfacggususg	2045	antis	23
GGGCAACCGUCUGG AUGAUGU	950	gsgsgcaaCfcGfUfCfug gaugauguL96	2046	sense	21
ACAUCAUCCAGACG GUUGCCCAG	951	asCfsaucAfuCfCfagac GfgUfugcccsasg	2047	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UGGGCAACCGUCUGGAUGAUG	952	usgsggcaAfcCfGfUfcuggaugaugL96	2048	sense	21
CAUCAUCCAGACGGUUGCCCAGG	953	csAfsucaUfcCfAfgacgGfuUfgcccasgsg	2049	antis	23
GAAACUUUGGCUGAUAAUAUU	954	gsasaacuUfuGfGfCfugauaauauuuL96	2050	sense	21
AAUAUUAUCAGCCAAAGUUUCUU	955	asAfsuauUfaUfCfagccAfaAfguuucsusu	2051	antis	23
AAACUUUGGCUGAUAAUAUUG	956	asasacuuUfgGfCfUfgauaauauuugL96	2052	sense	21
CAAUAUUAUCAGCCAAAGUUUCU	957	csAfsauaUfuAfUfcagcCfaAfaguuuscsu	2053	antis	23
UGAAGAAACUUUGGCUGAUAA	958	usgsaagaAfaCfUfUfuggcugauaaL96	2054	sense	21
UUAUCAGCCAAAGUUUCUUCAUC	959	usUfsaucAfgCfCfaaagUfuUfcuucasusc	2055	antis	23
AUGAAGAAACUUUGGCUGAUA	960	asusgaagAfaAfCfUfuuggcugauaL96	2056	sense	21
UAUCAGCCAAAGUUUCUUCAUCA	961	usAfsucaGfcCfAfaaguUfuCfuucauscsa	2057	antis	23
AAAGGUGUUCAAGAUGUCCUC	962	asasagguGfuUfCfAfagauguccucL96	2058	sense	21
GAGGACAUCUUGAACACCUUUCU	963	gsAfsggaCfaUfCfuugaAfcAfccuuuscsu	2059	antis	23
AAGGUGUUCAAGAUGUCCUCG	964	asasggugUfuCfAfAfgauguccucgL96	2060	sense	21
CGAGGACAUCUUGAACACCUUUC	965	csGfsaggAfcAfUfcuugAfaCfaccuususc	2061	antis	23
GGAGAAAGGUGUUCAAGAUGU	966	gsgsagaaAfgGfUfGfuucaagauguL96	2062	sense	21
ACAUCUUGAACACCUUUCUCCCC	967	asCfsaucUfuGfAfacacCfuUfucuccscsc	2063	antis	23
GGGAGAAAGGUGUUCAAGAUG	968	gsgsgagaAfaGfGfUfgucaagaugL96	2064	sense	21
CAUCUUGAACACCUUUCUCCCCC	969	csAfsucuUfgAfAfcaccUfuUfcucccscsc	2065	antis	23
AAAUCAGUACUUCCAAAGUCU	970	asasaucaGfuAfCfUfuccaaagucuL96	2066	sense	21
AGACUUUGGAAGUACUGAUUUAG	971	asGfsacuUfuGfGfaaguAfcUfgauuusasg	2067	antis	23
AAUCAGUACUUCCAAAGUCUA	972	asasucagUfaCfUfUfccaaagucuaL96	2068	sense	21
UAGACUUUGGAAGUACUGAUUUA	973	usAfsgacUfuUfGfgaagUfaCfugauususa	2069	antis	23
UGCUAAAUCAGUACUUCCAAA	974	usgscuaaAfuCfAfGfuacuuccaaaL96	2070	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UUUGGAAGUACUGAUUUAGCAUG	975	usUfsuggAfaGfUfacugAfuUfuagcasusg	2071	antis	23
AUGCUAAAUCAGUACUUCCAA	976	asusgcuaAfaUfCfAfguacuuccaaL96	2072	sense	21
UUGGAAGUACUGAUUUAGCAUGU	977	usUfsggaAfgUfAfcugaUfuUfagcausgsu	2073	antis	23
ACAUCUUUAGUGUCUGAAUAU	978	ascsaucuUfuAfGfUfgucugaauauL96	2074	sense	21
AUAUUCAGACACUAAAGAUGUGA	979	asUfsauuCfaGfAfcacuAfaAfgaugusgsa	2075	antis	23
CAUCUUUAGUGUCUGAAUAUA	980	csasucuuUfaGfUfGfucugaauauaL96	2076	sense	21
UAUAUUCAGACACUAAAGAUGUG	981	usAfsuauUfcAfGfacacUfaAfagaugsusg	2077	antis	23
AAUCACAUCUUUAGUGUCUGA	982	asasucacAfuCfUfUfuagugucugaL96	2078	sense	21
UCAGACACUAAAGAUGUGAUUGG	983	usCfsagaCfaCfUfaaagAfuGfugauusgsg	2079	antis	23
CAAUCACAUCUUUAGUGUCUG	984	csasaucaCfaUfCfUfuuagugucugL96	2080	sense	21
CAGACACUAAAGAUGUGAUUGGA	985	csAfsgacAfcUfAfaagaUfgUfgauugsgsa	2081	antis	23
GCAUGUAUUACUUGACAAAGA	986	gscsauguAfuUfAfCfuugacaaagaL96	2082	sense	21
UCUUUGUCAAGUAAUACAUGCUG	987	usCfsuuuGfuCfAfaguaAfuAfcaugcsusg	2083	antis	23
CAUGUAUUACUUGACAAAGAG	988	csasuguaUfuAfCfUfugacaaagagL96	2084	sense	21
CUCUUUGUCAAGUAAUACAUGCU	989	csUfscuuUfgUfCfaaguAfaUfacaugscsu	2085	antis	23
UUCAGCAUGUAUUACUUGACA	990	ususcagcAfuGfUfAfuuacuugacaL96	2086	sense	21
UGUCAAGUAAUACAUGCUGAAAA	991	usGfsucaAfgUfAfauacAfuGfcugaasasa	2087	antis	23
UUUCAGCAUGUAUUACUUGAC	992	ususucagCfaUfGfUfauuacuugacL96	2088	sense	21
GUCAAGUAAUACAUGCUGAAAAA	993	gsUfscaaGfuAfAfuacaUfgCfugaaasasa	2089	antis	23
AUGUUACUUCUUAGAGAGAAA	994	asusguuaCfuUfCfUfuagagagaaaL96	2090	sense	21
UUUCUCUCUAAGAAGUAACAUAC	995	usUfsucuCfuCfUfaagaAfgUfaacausasc	2091	antis	23
UGUUACUUCUUAGAGAGAAAU	996	usgsuuacUfuCfUfUfagagagaaauL96	2092	sense	21
AUUUCUCUCUAAGAAGUAACAUA	997	asUfsuucUfcUfCfuaagAfaGfuaacasusa	2093	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUGUAUGUUACUUCUUAGAGA	998	asusguauGfuUfAfCfuucuuagagaL96	2094	sense	21
UCUCUAAGAAGUAACAUACAUCC	999	usCfsucuAfaGfAfaguaAfcAfuacauscsc	2095	antis	23
GAUGUAUGUUACUUCUUAGAG	1000	gsasuguaUfgUfUfAfcuucuuagagL96	2096	sense	21
CUCUAAGAAGUAACAUACAUCCU	1001	csUfscuaAfgAfAfguaaCfaUfacaucscsu	2097	antis	23
ACAACUUUGAGAAGGUAGCAC	1002	ascsaacuUfuGfAfGfaagguagcacL96	2098	sense	21
GUGCUACCUUCUCAAAGUUGUGA	1003	gsUfsgcuAfcCfUfucucAfaAfguugusgsa	2099	antis	23
CAACUUUGAGAAGGUAGCACU	1004	csasacuuUfgAfGfAfagguagcacuL96	2100	sense	21
AGUGCUACCUUCUCAAAGUUGUG	1005	asGfsugcUfaCfCfuucuCfaAfaguugsusg	2101	antis	23
AUUCACAACUUUGAGAAGGUA	1006	asusucacAfaCfUfUfugagaagguaL96	2102	sense	21
UACCUUCUCAAAGUUGUGAAUCA	1007	usAfsccuUfcUfCfaaagUfuGfugaauscsa	2103	antis	23
GAUUCACAACUUUGAGAAGGU	1008	gsasuucaCfaAfCfUfuugagaagguL96	2104	sense	21
ACCUUCUCAAAGUUGUGAAUCAG	1009	asCfscuuCfuCfAfaaguUfgUfgaaucsasg	2105	antis	23
AACAUGCUAAAUCAGUACUUC	1010	asascaugCfuAfAfAfucaguacuucL96	2106	sense	21
GAAGUACUGAUUUAGCAUGUUGU	1011	gsAfsaguAfcUfGfauuuAfgCfauguusgsu	2107	antis	23
ACAUGCUAAAUCAGUACUUCC	1012	ascsaugcUfaAfAfUfcaguacuuccL96	2108	sense	21
GGAAGUACUGAUUUAGCAUGUUG	1013	gsGfsaagUfaCfUfgauuUfaGfcaugususg	2109	antis	23
GAACAACAUGCUAAAUCAGUA	1014	gsasacaaCfaUfGfCfuaaaucaguaL96	2110	sense	21
UACUGAUUUAGCAUGUUGUUCAU	1015	usAfscugAfuUfUfagcaUfgUfuguucsasu	2111	antis	23
UGAACAACAUGCUAAAUCAGU	1016	usgsaacaAfcAfUfGfcuaaaucaguL96	2112	sense	21
ACUGAUUUAGCAUGUUGUUCAUA	1017	asCfsugaUfuUfAfgcauGfuUfguucasusa	2113	antis	23
AAACCAGUACUUUAUCAUUUU	1018	asasaccaGfuAfCfUfuuaucauuuuL96	2114	sense	21
AAAAUGAUAAAGUACUGGUUUCA	1019	asAfsaauGfaUfAfaaguAfcUfgguuuscsa	2115	antis	23
AACCAGUACUUUAUCAUUUUC	1020	asasccagUfaCfUfUfuaucauuuucL96	2116	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GAAAAUGAUAAAGU ACUGGUUUC	1021	gsAfsaaaUfgAfUfaaag UfaCfugguususc	2117	antis	23
UUUGAAACCAGUAC UUUAUCA	1022	ususugaaAfcCfAfGfua cuuuaucaL96	2118	sense	21
UGAUAAAGUACUGG UUUCAAAAU	1023	usGfsauaAfaGfUfacug GfuUfucaaasasu	2119	antis	23
UUUUGAAACCAGUA CUUUAUC	1024	ususuugaAfaCfCfAfgu acuuuaucL96	2120	sense	21
GAUAAAGUACUGGU UUCAAAAUU	1025	gsAfsuaaAfgUfAfcugg UfuUfcaaaasusu	2121	antis	23
GAGAAGAUGGGCUA CAAGGCC	1026	gsasgaagAfuGfGfGfcu acaaggccL96	2122	sense	21
GGCCUUGUAGCCCA UCUUCUCUG	1027	gsGfsccuUfgUfAfgccc AfuCfuucucsusg	2123	antis	23
AGAAGAUGGGCUAC AAGGCCA	1028	asgsaagaUfgGfGfCfua caaggccaL96	2124	sense	21
UGGCCUUGUAGCCC AUCUUCUCU	1029	usGfsgccUfuGfUfagcc CfaUfcuucuscsu	2125	antis	23
GGCAGAGAAGAUGG GCUACAA	1030	gsgscagaGfaAfGfAfug ggcuacaaL96	2126	sense	21
UUGUAGCCCAUCUU CUCUGCCUG	1031	usUfsguaGfcCfCfaucu UfcUfcugccsusg	2127	antis	23
AGGCAGAGAAGAUG GGCUACA	1032	asgsgcagAfgAfAfGfau gggcuacaL96	2128	sense	21
UGUAGCCCAUCUUC UCUGCCUGC	1033	usGfsuagCfcCfAfucuu CfuCfugccusgsc	2129	antis	23
AACGGGCAUGAUGU UGAGUUC	1034	asascgggCfaUfGfAfug uugaguucL96	2130	sense	21
GAACUCAACAUCAU GCCCGUUCC	1035	gsAfsacuCfaAfCfauca UfgCfccguuscsc	2131	antis	23
ACGGGCAUGAUGUU GAGUUCC	1036	ascsgggcAfuGfAfUfgu ugaguuccL96	2132	sense	21
GGAACUCAACAUCA UGCCCGUUC	1037	gsGfsaacUfcAfAfcauc AfuGfcccgususc	2133	antis	23
UGGGAACGGGCAUG AUGUUGA	1038	usgsggaaCfgGfGfCfau gauguugaL96	2134	sense	21
UCAACAUCAUGCCC GUUCCCAGG	1039	usCfsaacAfuCfAfugcc CfgUfucccasgsg	2135	antis	23
CUGGGAACGGGCAU GAUGUUG	1040	csusgggaAfcGfGfGfca ugauguugL96	2136	sense	21
CAACAUCAUGCCCG UUCCCAGGG	1041	csAfsacaUfcAfUfgccc GfuUfcccagsgsg	2137	antis	23
AUGUGGCUAAAGCA AUAGACC	1042	asusguggCfuAfAfAfgc aauagaccL96	2138	sense	21
GGUCUAUUGCUUUA GCCACAUAU	1043	gsGfsucuAfuUfGfcuuu AfgCfcacausasu	2139	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UGUGGCUAAAGCAA UAGACCC	1044	usgsuggcUfaAfAfGfca auagacccL96	2140	sense	21
GGGUCUAUUGCUUU AGCCACAUA	1045	gsGfsgucUfaUfUfgcuu UfaGfccacasusa	2141	antis	23
GCAUAUGUGGCUAA AGCAAUA	1046	gscsauauGfuGfGfCfua aagcaauaL96	2142	sense	21
UAUUGCUUUAGCCA CAUAUGCAG	1047	usAfsuugCfuUfUfagcc AfcAfuaugcsasg	2143	antis	23
UGCAUAUGUGGCUA AAGCAAU	1048	usgscauaUfgUfGfGfcu aaagcaauL96	2144	sense	21
AUUGCUUUAGCCAC AUAUGCAGC	1049	asUfsugcUfuUfAfgcca CfaUfaugcasgsc	2145	antis	23
AGGAUGCUCCGGAA UGUUGCU	1050	asgsgaugCfuCfCfGfga auguugcuL96	2146	sense	21
AGCAACAUUCCGGA GCAUCCUUG	1051	asGfscaaCfaUfUfccgg AfgCfauccususg	2147	antis	23
GGAUGCUCCGGAAU GUUGCUG	1052	gsgsaugcUfcCfGfGfaa uguugcugL96	2148	sense	21
CAGCAACAUUCCGG AGCAUCCUU	1053	csAfsgcaAfcAfUfuccg GfaGfcauccsusu	2149	antis	23
UCCAAGGAUGCUCC GGAAUGU	1054	uscscaagGfaUfGfCfuc cggaauguL96	2150	sense	21
ACAUUCCGGAGCAU CCUUGGAUA	1055	asCfsauuCfcGfGfagca UfcCfuuggasusa	2151	antis	23
AUCCAAGGAUGCUC CGGAAUG	1056	asusccaaGfgAfUfGfcu ccggaaugL96	2152	sense	21
CAUUCCGGAGCAUC CUUGGAUAC	1057	csAfsuucCfgGfAfgcau CfcUfuggausasc	2153	antis	23
UCACAUCUUUAGUG UCUGAAU	1058	uscsacauCfuUfUfAfgu gucugaauL96	2154	sense	21
AUUCAGACACUAAA GAUGUGAUU	1059	asUfsucaGfaCfAfcuaa AfgAfugugasusu	2155	antis	23
CACAUCUUUAGUGU CUGAAUA	1060	csascaucUfuUfAfGfug ucugaauaL96	2156	sense	21
UAUUCAGACACUAA AGAUGUGAU	1061	usAfsuucAfgAfCfacua AfaGfaugugsasu	2157	antis	23
CCAAUCACAUCUUU AGUGUCU	1062	cscsaaucAfcAfUfCfuu uagugucuL96	2158	sense	21
AGACACUAAAGAUG UGAUUGGAA	1063	asGfsacaCfuAfAfagau GfuGfauuggsasa	2159	antis	23
UCCAAUCACAUCUU UAGUGUC	1064	uscscaauCfaCfAfUfcu uuagugucL96	2160	sense	21
GACACUAAAGAUGU GAUUGGAAA	1065	gsAfscacUfaAfAfgaug UfgAfuuggasasa	2161	antis	23
AAAUGUGUUUAGAC AACGUCA	1066	asasauguGfuUfUfAfga caacgucaL96	2162	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UGACGUUGUCUAAACACAUUUUC	1067	usGfsacgUfuGfUfcuaaAfcAfcauuususc	2163	antis	23
AAUGUGUUUAGACAACGUCAU	1068	asasugugUfuUfAfGfacaacgucauL96	2164	sense	21
AUGACGUUGUCUAAACACAUUUU	1069	asUfsgacGfuUfGfucuaAfaCfacauususu	2165	antis	23
UUGAAAAUGUGUUUAGACAAC	1070	ususgaaaAfuGfUfGfuuuagacaacL96	2166	sense	21
GUUGUCUAAACACAUUUUCAAUG	1071	gsUfsuguCfuAfAfacacAfuUfuucaasusg	2167	antis	23
AUUGAAAAUGUGUUUAGACAA	1072	asusugaaAfaUfGfUfguuuagacaaL96	2168	sense	21
UUGUCUAAACACAUUUUCAAUGU	1073	usUfsgucUfaAfAfcacaUfuUfucaausgsu	2169	antis	23
UACUAAAGGAAGAAUUCCGGU	1074	usascuaaAfgGfAfAfgaauuccgguL96	2170	sense	21
ACCGGAAUUCUUCCUUUAGUAUC	1075	asCfscggAfaUfUfcuucCfuUfuaguasusc	2171	antis	23
ACUAAAGGAAGAAUUCCGGUU	1076	ascsuaaaGfgAfAfGfaauuccgguuL96	2172	sense	21
AACCGGAAUUCUUCCUUUAGUAU	1077	asAfsccgGfaAfUfucuuCfcUfuuagusasu	2173	antis	23
GAGAUACUAAAGGAAGAAUUC	1078	gsasgauaCfuAfAfAfggaagaauucL96	2174	sense	21
GAAUUCUUCCUUUAGUAUCUCGA	1079	gsAfsauuCfuUfCfcuuuAfgUfaucucsgsa	2175	antis	23
CGAGAUACUAAAGGAAGAAUU	1080	csgsagauAfcUfAfAfaggaagaauuL96	2176	sense	21
AAUUCUUCCUUUAGUAUCUCGAG	1081	asAfsuucUfuCfCfuuuaGfuAfucucgsasg	2177	antis	23
AACUUUGGCUGAUAAUAUUGC	1082	asascuuuGfgCfUfGfauaauauugcL96	2178	sense	21
GCAAUAUUAUCAGCCAAAGUUUC	1083	gsCfsaauAfuUfAfucagCfcAfaaguususc	2179	antis	23
ACUUUGGCUGAUAAUAUUGCA	1084	ascsuuugGfcUfGfAfuaauauugcaL96	2180	sense	21
UGCAAUAUUAUCAGCCAAAGUUU	1085	usGfscaaUfaUfUfaucaGfcCfaaagususu	2181	antis	23
AAGAAACUUUGGCUGAUAAUA	1086	asasgaaaCfuUfUfGfgcugauaauaL96	2182	sense	21
UAUUAUCAGCCAAAGUUUCUUCA	1087	usAfsuuaUfcAfGfccaaAfgUfuucuuscsa	2183	antis	23
GAAGAAACUUUGGCUGAUAAU	1088	gsasagaaAfcUfUfUfggcugauaauL96	2184	sense	21
AUUAUCAGCCAAAGUUUCUUCAU	1089	asUfsuauCfaGfCfcaaaGfuUfucuucsasu	2185	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AAAUGGCUGAGAAG ACUGACA	1090	asasauggCfuGfAfGfaa gacugacaL96	2186	sense	21
UGUCAGUCUUCUCA GCCAUUUGA	1091	usGfsucaGfuCfUfucuc AfgCfcauuusgsa	2187	antis	23
AAUGGCUGAGAAGA CUGACAU	1092	asasuggcUfgAfGfAfag acugacauL96	2188	sense	21
AUGUCAGUCUUCUC AGCCAUUUG	1093	asUfsgucAfgUfCfuucu CfaGfccauususg	2189	antis	23
UAUCAAAUGGCUGA GAAGACU	1094	usasucaaAfuGfGfCfug agaagacuL96	2190	sense	21
AGUCUUCUCAGCCA UUUGAUAUC	1095	asGfsucuUfcUfCfagcc AfuUfugauasusc	2191	antis	23
AUAUCAAAUGGCUG AGAAGAC	1096	asusaucaAfaUfGfGfcu gagaagacL96	2192	sense	21
GUCUUCUCAGCCAU UUGAUAUCU	1097	gsUfscuuCfuCfAfgcca UfuUfgauauscsu	2193	antis	23
GUGGUUCUUAAAUU GUAAGCU	1098	gsusgguuCfuUfAfAfau uguaagcuL96	2194	sense	21
AGCUUACAAUUUAA GAACCACUG	1099	asGfscuuAfcAfAfuuua AfgAfaccacsusg	2195	antis	23
UGGUUCUUAAAUUG UAAGCUC	1100	usgsguucUfuAfAfAfuu guaagcucL96	2196	sense	21
GAGCUUACAAUUUA AGAACCACU	1101	gsAfsgcuUfaCfAfauuu AfaGfaaccascsu	2197	antis	23
AACAGUGGUUCUUA AAUUGUA	1102	asascaguGfgUfUfCfuu aaauuguaL96	2198	sense	21
UACAAUUUAAGAAC CACUGUUUU	1103	usAfscaaUfuUfAfagaa CfcAfcuguususu	2199	antis	23
AAACAGUGGUUCUU AAAUUGU	1104	asasacagUfgGfUfUfcu uaaauuguL96	2200	sense	21
ACAAUUUAAGAACC ACUGUUUUA	1105	asCfsaauUfuAfAfgaac CfaCfuguuususa	2201	antis	23
AAGUCAUCGACAAG ACAUUGG	1106	asasgucaUfcGfAfCfaa gacauuggL96	2202	sense	21
CCAAUGUCUUGUCG AUGACUUUC	1107	csCfsaauGfuCfUfuguc GfaUfgacuususc	2203	antis	23
AGUCAUCGACAAGA CAUUGGU	1108	asgsucauCfgAfCfAfag acauugguL96	2204	sense	21
ACCAAUGUCUUGUC GAUGACUUU	1109	asCfscaaUfgUfCfuugu CfgAfugacususu	2205	antis	23
GUGAAAGUCAUCGA CAAGACA	1110	gsusgaaaGfuCfAfUfcg acaagacaL96	2206	sense	21
UGUCUUGUCGAUGA CUUUCACAU	1111	usGfsucuUfgUfCfgaug AfcUfuucacsasu	2207	antis	23
UGUGAAAGUCAUCG ACAAGAC	1112	usgsugaaAfgUfCfAfuc gacaagacL96	2208	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GUCUUGUCGAUGAC UUUCACAUU	1113	gsUfscuuGfuCfGfauga CfuUfucacasusu	2209	antis	23
GAUAAUAUUGCAGC AUUUUCC	1114	gsasuaauAfuUfGfCfag cauuuuccL96	2210	sense	21
GGAAAAUGCUGCAA UAUUAUCAG	1115	gsGfsaaaAfuGfCfugca AfuAfuuaucsasg	2211	antis	23
AUAAUAUUGCAGCA UUUUCCA	1116	asusaauaUfuGfCfAfgc auuuuccaL96	2212	sense	21
UGGAAAAUGCUGCA AUAUUAUCA	1117	usGfsgaaAfaUfGfcugc AfaUfauuauscsa	2213	antis	23
GGCUGAUAAUAUUG CAGCAUU	1118	gsgscugaUfaAfUfAfuu gcagcauuL96	2214	sense	21
AAUGCUGCAAUAUU AUCAGCCAA	1119	asAfsugcUfgCfAfauau UfaUfcagccsasa	2215	antis	23
UGGCUGAUAAUAUU GCAGCAU	1120	usgsgcugAfuAfAfUfau ugcagcauL96	2216	sense	21
AUGCUGCAAUAUUA UCAGCCAAA	1121	asUfsgcuGfcAfAfuauu AfuCfagccasasa	2217	antis	23
GCUAAUUUGUAUCA AUGAUUA	1122	gscsuaauUfuGfUfAfuc aaugauuaL96	2218	sense	21
UAAUCAUUGAUACA AAUUAGCCG	1123	usAfsaucAfuUfGfauac AfaAfuuagcscsg	2219	antis	23
CUAAUUUGUAUCAA UGAUUAU	1124	csusaauuUfgUfAfUfca augauuauL96	2220	sense	21
AUAAUCAUUGAUAC AAAUUAGCC	1125	asUfsaauCfaUfUfgaua CfaAfauuagscsc	2221	antis	23
CCCGGCUAAUUUGU AUCAAUG	1126	cscscggcUfaAfUfUfug uaucaaugL96	2222	sense	21
CAUUGAUACAAAUU AGCCGGGGG	1127	csAfsuugAfuAfCfaaau UfaGfccgggsgsg	2223	antis	23
CCCCGGCUAAUUUG UAUCAAU	1128	cscsccggCfuAfAfUfuu guaucaauL96	2224	sense	21
AUUGAUACAAAUUA GCCGGGGGA	1129	asUfsugaUfaCfAfaauu AfgCfcggggsgsa	2225	antis	23
UAAUUGGUGAUACU UCUUUGA	1130	usasauugGfuGfAfUfac uucuuugaL96	2226	sense	21
UCAAAGAAGUAUCA CCAAUUACC	1131	usCfsaaaGfaAfGfuauc AfcCfaauuascsc	2227	antis	23
AAUUGGUGAUACUU CUUUGAA	1132	asasuuggUfgAfUfAfcu ucuuugaaL96	2228	sense	21
UUCAAAGAAGUAUC ACCAAUUAC	1133	usUfscaaAfgAfAfguau CfaCfcaauusasc	2229	antis	23
GCGGUAAUUGGUGA UACUUCU	1134	gscsgguaAfuUfGfGfug auacuucuL96	2230	sense	21
AGAAGUAUCACCAA UUACCGCCA	1135	asGfsaagUfaUfCfacca AfuUfaccgcscsa	2231	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GGCGGUAAUUGGUGAUACUUC	1136	gsgscgguAfaUfUfGfgugauacuucL96	2232	sense	21
GAAGUAUCACCAAUUACCGCCAC	1137	gsAfsaguAfuCfAfccaaUfuAfccgccsasc	2233	antis	23
CAGUGGUUCUUAAAUUGUAAG	1138	csasguggUfuCfUfUfaaauuguaagL96	2234	sense	21
CUUACAAUUUAAGAACCACUGUU	1139	csUfsuacAfaUfUfuaagAfaCfcacugsusu	2235	antis	23
AGUGGUUCUUAAAUUGUAAGC	1140	asgsugguUfcUfUfAfaauuguaagcL96	2236	sense	21
GCUUACAAUUUAAGAACCACUGU	1141	gsCfsuuaCfaAfUfuuaaGfaAfccacusgsu	2237	antis	23
AAAACAGUGGUUCUUAAAUUG	1142	asasaacaGfuGfGfUfcuuaaaauugL96	2238	sense	21
CAAUUUAAGAACCACUGUUUUAA	1143	csAfsauuUfaAfGfaaccAfcUfguuuusasa	2239	antis	23
UAAAACAGUGGUUCUUAAAUU	1144	usasaaacAfgUfGfGfuucuuaaauuL96	2240	sense	21
AAUUUAAGAACCACUGUUUUAAA	1145	asAfsuuuAfaGfAfaccaCfuGfuuuuasasa	2241	antis	23
ACCUGUAUUCUGUUUACAUGU	1146	ascscuguAfuUfCfUfguuuacauguL96	2242	sense	21
ACAUGUAAACAGAAUACAGGUUA	1147	asCfsaugUfaAfAfcagaAfuAfcaggususa	2243	antis	23
CCUGUAUUCUGUUUACAUGUC	1148	cscsuguaUfuCfUfGfuuuacaugucL96	2244	sense	21
GACAUGUAAACAGAAUACAGGUU	1149	gsAfscauGfuAfAfacagAfaUfacaggsusu	2245	antis	23
AUUAACCUGUAUUCUGUUUAC	1150	asusuaacCfuGfUfAfuucuguuuacL96	2246	sense	21
GUAAACAGAAUACAGGUUAAUAA	1151	gsUfsaaaCfaGfAfauacAfgGfuuaausasa	2247	antis	23
UAUUAACCUGUAUUCUGUUUA	1152	usasuuaaCfcUfGfUfaucuguuuaL96	2248	sense	21
UAAACAGAAUACAGGUUAAUAAA	1153	usAfsaacAfgAfAfuacaGfgUfuaauasasa	2249	antis	23
AAGAAACUUUGGCUGAUAAUA	1154	asasgaaaCfuUfUfGfgcugauaauaL96	2250	sense	21
UAUUAUCAGCCAAAGUUUCUUCA	1155	usAfsuuaUfcAfGfccaaAfgUfuucuuscsa	2251	antis	23
AGAAACUUUGGCUGAUAAUAU	1156	asgsaaacUfuUfGfGfcugauaauauL96	2252	sense	21
AUAUUAUCAGCCAAAGUUUCUUC	1157	asUfsauuAfuCfAfgccaAfaGfuuucususc	2253	antis	23
GAUGAAGAAACUUUGGCUGAU	1158	gsasugaaGfaAfAfCfuuuggcugauL96	2254	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUCAGCCAAAGUUU CUUCAUCAU	1159	asUfscagCfcAfAfaguu UfcUfucaucsasu	2255	antis	23
UGAUGAAGAAACUU UGGCUGA	1160	usgsaugaAfgAfAfAfcu uuggcugaL96	2256	sense	21
UCAGCCAAAGUUUC UUCAUCAUU	1161	usCfsagcCfaAfAfguuu CfuUfcaucasusu	2257	antis	23
GAAAGGUGUUCAAG AUGUCCU	1162	gsasaaggUfgUfUfCfaa gauguccuL96	2258	sense	21
AGGACAUCUUGAAC ACCUUUCUC	1163	asGfsgacAfuCfUfugaa CfaCfcuuucsusc	2259	antis	23
AAAGGUGUUCAAGA UGUCCUC	1164	asasagguGfuUfCfAfag auguccucL96	2260	sense	21
GAGGACAUCUUGAA CACCUUUCU	1165	gsAfsggaCfaUfCfuuga AfcAfccuuuscsu	2261	antis	23
GGGAGAAAGGUGUU CAAGAUG	1166	gsgsgagaAfaGfGfUfgu ucaagaugL96	2262	sense	21
CAUCUUGAACACCU UUCUCCCCC	1167	csAfsucuUfgAfAfcacc UfuUfcucccscsc	2263	antis	23
GGGGAGAAAGGUGU UCAAGAU	1168	gsgsggagAfaAfGfGfug uucaagauL96	2264	sense	21
AUCUUGAACACCUU UCUCCCCCU	1169	asUfscuuGfaAfCfaccu UfuCfucccscscsu	2265	antis	23
AUCUUGGUGUCGAA UCAUGGG	1170	asuscuugGfuGfUfCfga aucaugggL96	2266	sense	21
CCCAUGAUUCGACA CCAAGAUCC	1171	csCfscauGfaUfUfcgac AfcCfaagauscsc	2267	antis	23
UCUUGGUGUCGAAU CAUGGGG	1172	uscsuuggUfgUfCfGfaa ucauggggL96	2268	sense	21
CCCCAUGAUUCGAC ACCAAGAUC	1173	csCfsccaUfgAfUfucga CfaCfcaagasusc	2269	antis	23
UGGGAUCUUGGUGU CGAAUCA	1174	usgsggauCfuUfGfGfug ucgaaucaL96	2270	sense	21
UGAUUCGACACCAA GAUCCCAUU	1175	usGfsauuCfgAfCfacca AfgAfucccasusu	2271	antis	23
AUGGGAUCUUGGUG UCGAAUC	1176	asusgggaUfcUfUfGfgu gucgaaucL96	2272	sense	21
GAUUCGACACCAAG AUCCCAUUC	1177	gsAfsuucGfaCfAfccaa GfaUfcccaususc	2273	antis	23
GCUACAAGGCCAUA UUUGUGA	1178	gscsuacaAfgGfCfCfau auuugugaL96	2274	sense	21
UCACAAAUAUGGCC UUGUAGCCC	1179	usCfsacaAfaUfAfuggc CfuUfguagcscsc	2275	antis	23
CUACAAGGCCAUAU UUGUGAC	1180	csusacaaGfgCfCfAfua uuugugacL96	2276	sense	21
GUCACAAAUAUGGC CUUGUAGCC	1181	gsUfscacAfaAfUfaugg CfcUfuguagscsc	2277	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUGGGCUACAAGGC CAUAUUU	1182	asusgggcUfaCfAfAfgg ccauauuuL96	2278	sense	21
AAAUAUGGCCUUGU AGCCCAUCU	1183	asAfsauaUfgGfCfcuug UfaGfcccauscsu	2279	antis	23
GAUGGGCUACAAGG CCAUAUU	1184	gsasugggCfuAfCfAfag gccauauuL96	2280	sense	21
AAUAUGGCCUUGUA GCCCAUCUU	1185	asAfsuauGfgCfCfuugu AfgCfccaucsusu	2281	antis	23
ACUGGAGAGAAUUG GAAUGGG	1186	ascsuggaGfaGfAfAfuu ggaaugggL96	2282	sense	21
CCCAUUCCAAUUCU CUCCAGUGC	1187	csCfscauUfcCfAfauuc UfcUfccagusgsc	2283	antis	23
CUGGAGAGAAUUGG AAUGGGU	1188	csusggagAfgAfAfUfug gaaugggL96	2284	sense	21
ACCCAUUCCAAUUC UCUCCAGUG	1189	asCfsccaUfuCfCfaauu CfuCfuccagsusg	2285	antis	23
UAGCACUGGAGAGA AUUGGAA	1190	usasgcacUfgGfAfGfag aauuggaaL96	2286	sense	21
UUCCAAUUCUCUCC AGUGCUACC	1191	usUfsccaAfuUfCfucuc CfaGfugcuascsc	2287	antis	23
GUAGCACUGGAGAG AAUUGGA	1192	gsusagcaCfuGfGfAfga gaauuggaL96	2288	sense	21
UCCAAUUCUCUCCA GUGCUACCU	1193	usCfscaaUfuCfUfcucc AfgUfgcuacscsu	2289	antis	23
ACAGUGGACACACC UUACCUG	1194	ascsagugGfaCfAfCfac cuuaccugL96	2290	sense	21
CAGGUAAGGUGUGU CCACUGUCA	1195	csAfsgguAfaGfGfugug UfcCfacuguscsa	2291	antis	23
CAGUGGACACACCU UACCUGG	1196	csasguggAfcAfCfAfcc uuaccuggL96	2292	sense	21
CCAGGUAAGGUGUG UCCACUGUC	1197	csCfsaggUfaAfGfgugu GfuCfcacugsusc	2293	antis	23
UGUGACAGUGGACA CACCUUA	1198	usgsugacAfgUfGfGfac acaccuuaL96	2294	sense	21
UAAGGUGUGUCCAC UGUCACAAA	1199	usAfsaggUfgUfGfucca CfuGfucacasasa	2295	antis	23
UUGUGACAGUGGAC ACACCUU	1200	ususgugaCfaGfUfGfga cacaccuuL96	2296	sense	21
AAGGUGUGUCCACU GUCACAAAU	1201	asAfsgguGfuGfUfccac UfgUfcacaasasu	2297	antis	23
GAAGACUGACAUCA UUGCCAA	1202	gsasagacUfgAfCfAfuc auugccaaL96	2298	sense	21
UUGGCAAUGAUGUC AGUCUUCUC	1203	usUfsggcAfaUfGfaugu CfaGfucuucsusc	2299	antis	23
AAGACUGACAUCAU UGCCAAU	1204	asasgacuGfaCfAfUfca uugccaauL96	2300	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUUGGCAAUGAUGUCAGUCUUCU	1205	asUfsuggCfaAfUfgaugUfcAfgucuuscsu	2301	antis	23
CUGAGAAGACUGACAUCAUUG	1206	csusgagaAfgAfCfUfgacaucauugL96	2302	sense	21
CAAUGAUGUCAGUCUUCUCAGCC	1207	csAfsaugAfuGfUfcaguCfuUfcucagscsc	2303	antis	23
GCUGAGAAGACUGACAUCAUU	1208	gscsugagAfaGfAfCfugacaucauuL96	2304	sense	21
AAUGAUGUCAGUCUUCUCAGCCA	1209	asAfsugaUfgUfCfagucUfuCfucagcscsa	2305	antis	23
GCUCAGGUUCAAAGUGUUGGU	1210	gscsucagGfuUfCfAfaaguguugguL96	2306	sense	21
ACCAACACUUUGAACCUGAGCUU	1211	asCfscaaCfaCfUfuugaAfcCfugagcsusu	2307	antis	23
CUCAGGUUCAAAGUGUUGGUA	1212	csuscaggUfuCfAfAfaguguugguaL96	2308	sense	21
UACCAACACUUUGAACCUGAGCU	1213	usAfsccaAfcAfCfuuugAfaCfcugagscsu	2309	antis	23
GUAAGCUCAGGUUCAAAGUGU	1214	gsusaagcUfcAfGfGfuucaaaguguL96	2310	sense	21
ACACUUUGAACCUGAGCUUACAA	1215	asCfsacuUfuGfAfaccuGfaGfcuuacsasa	2311	antis	23
UGUAAGCUCAGGUUCAAAGUG	1216	usgsuaagCfuCfAfGfgucaaagugL96	2312	sense	21
CACUUUGAACCUGAGCUUACAAU	1217	csAfscuuUfgAfAfccugAfgCfuuacasasu	2313	antis	23
AUGUAUUACUUGACAAAGAGA	1218	asusguauUfaCfUfUfgacaaagagaL96	2314	sense	21
UCUCUUUGUCAAGUAAUACAUGC	1219	usCfsucuUfuGfUfcaagUfaAfuacausgsc	2315	antis	23
UGUAUUACUUGACAAAGAGAC	1220	usgsuauuAfcUfUfUfGfacaaagagacL96	2316	sense	21
GUCUCUUUGUCAAGUAAUACAUG	1221	gsUfscucUfuUfGfucaaGfuAfauacasusg	2317	antis	23
CAGCAUGUAUUACUUGACAAA	1222	csasgcauGfuAfUfUfacuugacaaaL96	2318	sense	21
UUUGUCAAGUAAUACAUGCUGAA	1223	usUfsuguCfaAfGfuaauAfcAfugcugsasa	2319	antis	23
UCAGCAUGUAUUACUUGACAA	1224	uscsagcaUfgUfAfUfuacuugacaaL96	2320	sense	21
UUGUCAAGUAAUACAUGCUGAAA	1225	usUfsgucAfaGfUfaauaCfaUfgcugasasa	2321	antis	23
CUGCAACUGUAUAUCUACAAG	1226	csusgcaaCfuGfUfAfuaucuacaagL96	2322	sense	21
CUUGUAGAUAUACAGUUGCAGCC	1227	csUfsuguAfgAfUfauacAfgUfugcagscsc	2323	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UGCAACUGUAUAUC UACAAGG	1228	usgscaacUfgUfAfUfau cuacaaggL96	2324	sense	21
CCUUGUAGAUAUAC AGUUGCAGC	1229	csCfsuugUfaGfAfuaua CfaGfuugcasgsc	2325	antis	23
UUGGCUGCAACUGU AUAUCUA	1230	ususggcuGfcAfAfCfug uauaucuaL96	2326	sense	21
UAGAUAUACAGUUG CAGCCAACG	1231	usAfsgauAfuAfCfaguu GfcAfgccaascsg	2327	antis	23
GUUGGCUGCAACUG UAUAUCU	1232	gsusuggcUfgCfAfAfcu guauaucuL96	2328	sense	21
AGAUAUACAGUUGC AGCCAACGA	1233	asGfsauaUfaCfAfguug CfaGfccaacsgsa	2329	antis	23
CAAAUGAUGAAGAA ACUUUGG	1234	csasaaugAfuGfAfAfga aacuuuggL96	2330	sense	21
CCAAAGUUUCUUCA UCAUUUGCC	1235	csCfsaaaGfuUfUfcuuc AfuCfauuugscsc	2331	antis	23
AAAUGAUGAAGAAA CUUUGGC	1236	asasaugaUfgAfAfGfaa acuuuggcL96	2332	sense	21
GCCAAAGUUUCUUC AUCAUUUGC	1237	gsCfscaaAfgUfUfucuu CfaUfcauuusgsc	2333	antis	23
GGGGCAAAUGAUGA AGAAACU	1238	gsgsggcaAfaUfGfAfug aagaaacuL96	2334	sense	21
AGUUUCUUCAUCAU UUGCCCCAG	1239	asGfsuuuCfuUfCfauca UfuUfgccccsasg	2335	antis	23
UGGGGCAAAUGAUG AAGAAAC	1240	usgsgggcAfaAfUfGfau gaagaaacL96	2336	sense	21
GUUUCUUCAUCAUU UGCCCCAGA	1241	gsUfsuucUfuCfAfucau UfuGfccccasgsa	2337	antis	23
CAAAGGGUGUCGUU CUUUUCC	1242	csasaaggGfuGfUfCfgu ucuuuuccL96	2338	sense	21
GGAAAAGAACGACA CCCUUUGUA	1243	gsGfsaaaAfgAfAfcgac AfcCfcuuugsusa	2339	antis	23
AAAGGGUGUCGUUC UUUUCCA	1244	asasagggUfgUfCfGfuu cuuuuccaL96	2340	sense	21
UGGAAAAGAACGAC ACCCUUUGU	1245	usGfsgaaAfaGfAfacga CfaCfccuuusgsu	2341	antis	23
AAUACAAAGGGUGU CGUUCUU	1246	asasuacaAfaGfGfGfug ucguucuuL96	2342	sense	21
AAGAACGACACCCU UUGUAUUGA	1247	asAfsgaaCfgAfCfaccc UfuUfguauusgsa	2343	antis	23
CAAUACAAAGGGUG UCGUUCU	1248	csasauacAfaAfGfGfgu gucguucuL96	2344	sense	21
AGAACGACACCCUU UGUAUUGAA	1249	asGfsaacGfaCfAfcccu UfuGfuauugsasa	2345	antis	23
AAAGGCACUGAUGU UCUGAAA	1250	asasaggcAfcUfGfAfug uucugaaaL96	2346	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UUUCAGAACAUCAG UGCCUUUCC	1251	usUfsucaGfaAfCfauca GfuGfccuuuscsc	2347	antis	23
AAGGCACUGAUGUU CUGAAAG	1252	asasggcaCfuGfAfUfgu ucugaaagL96	2348	sense	21
CUUUCAGAACAUCA GUGCCUUUC	1253	csUfsuucAfgAfAfcauc AfgUfgccuususc	2349	antis	23
GCGGAAAGGCACUG AUGUUCU	1254	gscsggaaAfgGfCfAfcu gauguucuL96	2350	sense	21
AGAACAUCAGUGCC UUUCCGCAC	1255	asGfsaacAfuCfAfgugc CfuUfuccgcsasc	2351	antis	23
UGCGGAAAGGCACU GAUGUUC	1256	usgscggaAfaGfGfCfac ugauguucL96	2352	sense	21
GAACAUCAGUGCCU UUCCGCACA	1257	gsAfsacaUfcAfGfugcc UfuUfccgcascsa	2353	antis	23
AAGGAUGCUCCGGA AUGUUGC	1258	asasggauGfcUfCfCfgg aauguugcL96	2354	sense	21
GCAACAUUCCGGAG CAUCCUUGG	1259	gsCfsaacAfuUfCfcgga GfcAfuccuusgsg	2355	antis	23
AGGAUGCUCCGGAA UGUUGCU	1260	asgsgaugCfuCfCfGfga auguugcuL96	2356	sense	21
AGCAACAUUCCGGA GCAUCCUUG	1261	asGfscaaCfaUfUfccgg AfgCfauccususg	2357	antis	23
AUCCAAGGAUGCUC CGGAAUG	1262	asusccaaGfgAfUfGfcu ccggaaugL96	2358	sense	21
CAUUCCGGAGCAUC CUUGGAUAC	1263	csAfsuucCfgGfAfgcau CfcUfuggausasc	2359	antis	23
UAUCCAAGGAUGCU CCGGAAU	1264	usasuccaAfgGfAfUfgc uccggaauL96	2360	sense	21
AUUCCGGAGCAUCC UUGGAUACA	1265	asUfsuccGfgAfGfcauc CfuUfggauascsa	2361	antis	23
AAUGGGUGGCGGUA AUUGGUG	1266	asasugggUfgGfCfGfgu aauuggugL96	2362	sense	21
CACCAAUUACCGCC ACCCAUUCC	1267	csAfsccaAfuUfAfccgc CfaCfccauuscsc	2363	antis	23
AUGGGUGGCGGUAA UUGGUGA	1268	asusggguGfgCfGfGfua auuggugaL96	2364	sense	21
UCACCAAUUACCGC CACCCAUUC	1269	usCfsaccAfaUfUfaccg CfcAfcccaususc	2365	antis	23
UUGGAAUGGGUGGC GGUAAUU	1270	ususggaaUfgGfGfUfgg cgguaauuL96	2366	sense	21
AAUUACCGCCACCC AUUCCAAUU	1271	asAfsuuaCfcGfCfcacc CfaUfuccaasusu	2367	antis	23
AUUGGAAUGGGUGG CGGUAAU	1272	asusuggaAfuGfGfGfug gcgguaauL96	2368	sense	21
AUUACCGCCACCCA UUCCAAUUC	1273	asUfsuacCfgCfCfaccc AfuUfccaaususc	2369	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GGAAAGGCACUGAUGUUCUGA	1274	gsgsaaagGfcAfCfUfgauguucugaL96	2370	sense	21
UCAGAACAUCAGUGCCUUUCCGC	1275	usCfsagaAfcAfUfcaguGfcCfuuuccsgsc	2371	antis	23
GAAAGGCACUGAUGUUCUGAA	1276	gsasaaggCfaCfUfGfauguucugaaL96	2372	sense	21
UUCAGAACAUCAGUGCCUUUCCG	1277	usUfscagAfaCfAfucagUfgCfcuuucscsg	2373	antis	23
GUGCGGAAAGGCACUGAUGUU	1278	gsusgcggAfaAfGfGfcacugauguuL96	2374	sense	21
AACAUCAGUGCCUUUCCGCACAC	1279	asAfscauCfaGfUfgccuUfuCfcgcacsasc	2375	antis	23
UGUGCGGAAAGGCACUGAUGU	1280	usgsugcgGfaAfAfGfgcacugauguL96	2376	sense	21
ACAUCAGUGCCUUUCCGCACACC	1281	asCfsaucAfgUfGfccuuUfcCfgcacascsc	2377	antis	23
AAUUGUAAGCUCAGGUUCAAA	1282	asasuuguAfaGfCfUfcagguucaaaL96	2378	sense	21
UUUGAACCUGAGCUUACAAUUUA	1283	usUfsugaAfcCfUfgagcUfuAfcaauususa	2379	antis	23
AUUGUAAGCUCAGGUUCAAAG	1284	asusuguaAfgCfUfCfagguucaaagL96	2380	sense	21
CUUUGAACCUGAGCUUACAAUUU	1285	csUfsuugAfaCfCfugagCfuUfacaaususu	2381	antis	23
CUUAAAUUGUAAGCUCAGGUU	1286	csusuaaaUfuGfUfAfagcucagguuL96	2382	sense	21
AACCUGAGCUUACAAUUUAAGAA	1287	asAfsccuGfaGfCfuuacAfaUfuuaagsasa	2383	antis	23
UCUUAAAUUGUAAGCUCAGGU	1288	uscsuuaaAfuUfGfUfaagcucagguL96	2384	sense	21
ACCUGAGCUUACAAUUUAAGAAC	1289	asCfscugAfgCfUfuacaAfuUfuaagasasc	2385	antis	23
GCAAACACUAAGGUGAAAAGA	1290	gscsaaacAfcUfAfAfggugaaaagaL96	2386	sense	21
UCUUUUCACCUUAGUGUUUGCUA	1291	usCfsuuuUfcAfCfcuuaGfuGfuuugcsusa	2387	antis	23
CAAACACUAAGGUGAAAAGAU	1292	csasaacaCfuAfAfGfgugaaaagauL96	2388	sense	21
AUCUUUUCACCUUAGUGUUUGCU	1293	asUfscuuUfuCfAfccuuAfgUfguuugscsu	2389	antis	23
GGUAGCAAACACUAAGGUGAA	1294	gsgsuagcAfaAfCfAfcuaaggugaaL96	2390	sense	21
UUCACCUUAGUGUUUGCUACCUC	1295	usUfscacCfuUfAfguguUfuGfcuaccsusc	2391	antis	23
AGGUAGCAAACACUAAGGUGA	1296	asgsguagCfaAfAfCfacuaaggugaL96	2392	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UCACCUUAGUGUUU GCUACCUCC	1297	usCfsaccUfuAfGfuguu UfgCfuaccuscsc	2393	antis	23
AGGUAGCAAACACU AAGGUGA	1298	asgsguagCfaAfAfCfac uaaggugaL96	2394	sense	21
UCACCUUAGUGUUU GCUACCUCC	1299	usCfsaccUfuAfGfuguu UfgCfuaccuscsc	2395	antis	23
GGUAGCAAACACUA AGGUGAA	1300	gsgsuagcAfaAfCfAfcu aaggugaaL96	2396	sense	21
UUCACCUUAGUGUU UGCUACCUC	1301	usUfscacCfuUfAfgugu UfuGfcuaccsusc	2397	antis	23
UUGGAGGUAGCAAA CACUAAG	1302	ususggagGfuAfGfCfaa acacuaagL96	2398	sense	21
CUUAGUGUUUGCUA CCUCCAAUU	1303	csUfsuagUfgUfUfugcu AfcCfuccaasusu	2399	antis	23
AUUGGAGGUAGCAA ACACUAA	1304	asusuggaGfgUfAfGfca aacacuaaL96	2400	sense	21
UUAGUGUUUGCUAC CUCCAAUUU	1305	usUfsaguGfuUfUfgcua CfcUfccaaususu	2401	antis	23
UAAAGUGCUGUAUC CUUUAGU	1306	usasaaguGfcUfGfUfau ccuuuaguL96	2402	sense	21
ACUAAAGGAUACAG CACUUUAGC	1307	asCfsuaaAfgGfAfuaca GfcAfcuuuasgsc	2403	antis	23
AAAGUGCUGUAUCC UUUAGUA	1308	asasagugCfuGfUfAfuc cuuuaguaL96	2404	sense	21
UACUAAAGGAUACA GCACUUUAG	1309	usAfscuaAfaGfGfauac AfgCfacuuusasg	2405	antis	23
AGGCUAAAGUGCUG UAUCCUU	1310	asgsgcuaAfaGfUfGfcu guauccuuL96	2406	sense	21
AAGGAUACAGCACU UUAGCCUGC	1311	asAfsggaUfaCfAfgcac UfuUfagccusgsc	2407	antis	23
CAGGCUAAAGUGCU GUAUCCU	1312	csasggcuAfaAfGfUfgc uguauccuL96	2408	sense	21
AGGAUACAGCACUU UAGCCUGCC	1313	asGfsgauAfcAfGfcacu UfuAfgccugscsc	2409	antis	23
AAGACAUUGGUGAG GAAAAAU	1314	asasgacaUfuGfGfUfga ggaaaaauL96	2410	sense	21
AUUUUUCCUCACCA AUGUCUUGU	1315	asUfsuuuUfcCfUfcacc AfaUfgucuusgsu	2411	antis	23
AGACAUUGGUGAGG AAAAAUC	1316	asgsacauUfgGfUfGfag gaaaaaucL96	2412	sense	21
GAUUUUUCCUCACC AAUGUCUUG	1317	gsAfsuuuUfuCfCfucac CfaAfugucususg	2413	antis	23
CGACAAGACAUUGG UGAGGAA	1318	csgsacaaGfaCfAfUfug gugaggaaL96	2414	sense	21
UUCCUCACCAAUGU CUUGUCGAU	1319	usUfsccuCfaCfCfaaug UfcUfugucgsasu	2415	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UCGACAAGACAUUGGUGAGGA	1320	uscsgacaAfgAfCfAfuuggugaggaL96	2416	sense	21
UCCUCACCAAUGUCUUGUCGAUG	1321	usCfscucAfcCfAfauguCfuUfgucgasusg	2417	antis	23
AAGAUGUCCUCGAGAUACUAA	1322	asasgaugUfcCfUfCfgagauacuaaL96	2418	sense	21
UUAGUAUCUCGAGGACAUCUUGA	1323	usUfsaguAfuCfUfcgagGfaCfaucuusgsa	2419	antis	23
AGAUGUCCUCGAGAUACUAAA	1324	asgsauguCfcUfCfGfagauacuaaaL96	2420	sense	21
UUUAGUAUCUCGAGGACAUCUUG	1325	usUfsuagUfaUfCfucgaGfgAfcaucususg	2421	antis	23
GUUCAAGAUGUCCUCGAGAUA	1326	gsusucaaGfaUfGfUfccucgagauaL96	2422	sense	21
UAUCUCGAGGACAUCUUGAACAC	1327	usAfsucuCfgAfGfgacaUfcUfugaacsasc	2423	antis	23
UGUUCAAGAUGUCCUCGAGAU	1328	usgsuucaAfgAfUfGfuccucgagauL96	2424	sense	21
AUCUCGAGGACAUCUUGAACACC	1329	asUfscucGfaGfGfacauCfuUfgaacascsc	2425	antis	23
GAGAAAGGUGUUCAAGAUGUC	1330	gsasgaaaGfgUfGfUfucaagaugucL96	2426	sense	21
GACAUCUUGAACACCUUUCUCCC	1331	gsAfscauCfuUfGfaacaCfcUfuucucscsc	2427	antis	23
AGAAAGGUGUUCAAGAUGUCC	1332	asgsaaagGfuGfUfUfcaagauguccL96	2428	sense	21
GGACAUCUUGAACACCUUUCUCC	1333	gsGfsacaUfcUfUfgaacAfcCfuuucuscsc	2429	antis	23
GGGGGAGAAAGGUGUUCAAGA	1334	gsgsgggaGfaAfAfGfguguucaagaL96	2430	sense	21
UCUUGAACACCUUUCUCCCCCUG	1335	usCfsuugAfaCfAfccuuUfcUfcccccsusg	2431	antis	23
AGGGGGAGAAAGGUGUUCAAG	1336	asgsggggAfgAfAfAfgguguucaagL96	2432	sense	21
CUUGAACACCUUUCUCCCCCUGG	1337	csUfsugaAfcAfCfcuuuCfuCfccccusgsg	2433	antis	23
GCUGGGAAGAUAUCAAAUGGC	1338	gscsugggAfaGfAfUfaucaaauggcL96	2434	sense	21
GCCAUUUGAUAUCUUCCCAGCUG	1339	gsCfscauUfuGfAfuaucUfuCfccagcsusg	2435	antis	23
CUGGGAAGAUAUCAAAUGGCU	1340	csusgggaAfgAfUfAfucaaauggcuL96	2436	sense	21
AGCCAUUUGAUAUCUUCCCAGCU	1341	asGfsccaUfuUfGfauauCfuUfcccagscsu	2437	antis	23
AUCAGCUGGGAAGAUAUCAAA	1342	asuscagcUfgGfGfAfagauaucaaaL96	2438	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UUUGAUAUCUUCCCAGCUGAUAG	1343	usUfsugaUfaUfCfuuccCfaGfcugausasg	2439	antis	23
UAUCAGCUGGGAAGAUAUCAA	1344	usasucagCfuGfGfGfaagauaucaaL96	2440	sense	21
UUGAUAUCUUCCCAGCUGAUAGA	1345	usUfsgauAfuCfUfucccAfgCfugauasgsa	2441	antis	23
UCUGUCGACUUCUGUUUUAGG	1346	uscsugucGfaCfUfUfcuguuuuaggL96	2442	sense	21
CCUAAAACAGAAGUCGACAGAUC	1347	csCfsuaaAfaCfAfgaagUfcGfacagasusc	2443	antis	23
CUGUCGACUUCUGUUUUAGGA	1348	csusgucgAfcUfUfCfuguuuuaggaL96	2444	sense	21
UCCUAAAACAGAAGUCGACAGAU	1349	usCfscuaAfaAfCfagaaGfuCfgacagsasu	2445	antis	23
CAGAUCUGUCGACUUCUGUUU	1350	csasgaucUfgUfCfGfacuucuguuuL96	2446	sense	21
AAACAGAAGUCGACAGAUCUGUU	1351	asAfsacaGfaAfGfucgaCfaGfaucugsusu	2447	antis	23
ACAGAUCUGUCGACUUCUGUU	1352	ascsagauCfuGfUfCfgacuucuguuL96	2448	sense	21
AACAGAAGUCGACAGAUCUGUUU	1353	asAfscagAfaGfUfcgacAfgAfucugususu	2449	antis	23
UACUUCUUUGAAUGUAGAUUU	1354	usascuucUfuUfGfAfauguagauuuL96	2450	sense	21
AAAUCUACAUUCAAAGAAGUAUC	1355	asAfsaucUfaCfAfuucaAfaGfaaguasusc	2451	antis	23
ACUUCUUUGAAUGUAGAUUUC	1356	ascsuucuUfuGfAfAfuguagauuucL96	2452	sense	21
GAAAUCUACAUUCAAAGAAGUAU	1357	gsAfsaauCfuAfCfauucAfaAfgaagusasu	2453	antis	23
GUGAUACUUCUUUGAAUGUAG	1358	gsusgauaCfuUfCfUfuugaauguagL96	2454	sense	21
CUACAUUCAAAGAAGUAUCACCA	1359	csUfsacaUfuCfAfaagaAfgUfaucacscsa	2455	antis	23
GGUGAUACUUCUUUGAAUGUA	1360	gsgsugauAfcUfUfCfuugaauguaL96	2456	sense	21
UACAUUCAAAGAAGUAUCACCAA	1361	usAfscauUfcAfAfagaaGfuAfucaccsasa	2457	antis	23
UGGGAAGAUAUCAAAUGGCUG	1362	usgsggaaGfaUfAfUfcaaauggcugL96	2458	sense	21
CAGCCAUUUGAUAUCUUCCCAGC	1363	csAfsgccAfuUfUfgauaUfcUfucccasgsc	2459	antis	23
GGGAAGAUAUCAAAUGGCUGA	1364	gsgsgaagAfuAfUfCfaaauggcugaL96	2460	sense	21
UCAGCCAUUUGAUAUCUUCCCAG	1365	usCfsagcCfaUfUfugauAfuCfuucccsasg	2461	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CAGCUGGGAAGAUAUCAAAUG	1366	csasgcugGfgAfAfGfauaucaaaugL96	2462	sense	21
CAUUUGAUAUCUUCCCAGCUGAU	1367	csAfsuuuGfaUfAfucuuCfcCfagcugsasu	2463	antis	23
UCAGCUGGGAAGAUAUCAAAU	1368	uscsagcuGfgGfAfAfgauaucaaauL96	2464	sense	21
AUUUGAUAUCUUCCCAGCUGAUA	1369	asUfsuugAfuAfUfcuucCfcAfgcugasusa	2465	antis	23
UCCAAAGUCUAUAUAUGACUA	1370	uscscaaaGfuCfUfAfuauaugacuaL96	2466	sense	21
UAGUCAUAUAUAGACUUUGGAAG	1371	usAfsgucAfuAfUfauagAfcUfuuggasasg	2467	antis	23
CCAAAGUCUAUAUAUGACUAU	1372	cscsaaagUfcUfAfUfaugacuauL96	2468	sense	21
AUAGUCAUAUAUAGACUUUGGAA	1373	asUfsaguCfaUfAfuauaGfaCfuuuggsasa	2469	antis	23
UACUUCCAAAGUCUAUAUAUG	1374	usascuucCfaAfAfGfucuauauaugL96	2470	sense	21
CAUAUAUAGACUUUGGAAGUACU	1375	csAfsuauAfuAfGfacuuUfgGfaaguascsu	2471	antis	23
GUACUUCCAAAGUCUAUAUAU	1376	gsusacuuCfcAfAfAfgucuauauauL96	2472	sense	21
AUAUAUAGACUUUGGAAGUACUG	1377	asUfsauaUfaGfAfcuuuGfgAfaguacsusg	2473	antis	23
UUAUGAACAACAUGCUAAAUC	1378	ususaugaAfcAfAfCfaugcuaaaucL96	2474	sense	21
GAUUUAGCAUGUUGUUCAUAAUC	1379	gsAfsuuuAfgCfAfuguuGfuUfcauaasusc	2475	antis	23
UAUGAACAACAUGCUAAAUCA	1380	usasugaaCfaAfCfAfugcuaaaucaL96	2476	sense	21
UGAUUUAGCAUGUUGUUCAUAAU	1381	usGfsauuUfaGfCfauguUfgUfucauasasu	2477	antis	23
AUGAUUAUGAACAACAUGCUA	1382	asusgauuAfuGfAfAfcaacaugcuaL96	2478	sense	21
UAGCAUGUUGUUCAUAAUCAUUG	1383	usAfsgcaUfgUfUfguucAfuAfaucaususg	2479	antis	23
AAUGAUUAUGAACAACAUGCU	1384	asasugauUfaUfGfAfacaacaugcuL96	2480	sense	21
AGCAUGUUGUUCAUAAUCAUUGA	1385	asGfscauGfuUfGfuucaUfaAfucauusgsa	2481	antis	23
AAUUCCCCACUUCAAUACAAA	1386	asasuuccCfcAfCfUfucaauacaaaL96	2482	sense	21
UUUGUAUUGAAGUGGGGAAUUAC	1387	usUfsuguAfuUfGfaaguGfgGfgaauusasc	2483	antis	23
AUUCCCCACUUCAAUACAAAG	1388	asusucccCfaCfUfUfcaauacaaagL96	2484	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CUUUGUAUUGAAGUGGGGAAUUA	1389	csUfsuugUfaUfUfgaagUfgGfggaaususa	2485	antis	23
CUGUAAUUCCCCACUUCAAUA	1390	csusguaaUfuCfCfCfcacuucaauaL96	2486	sense	21
UAUUGAAGUGGGGAAUUACAGAC	1391	usAfsuugAfaGfUfggggAfaUfuacagsasc	2487	antis	23
UCUGUAAUUCCCCACUUCAAU	1392	uscsuguaAfuUfCfCfccacuucaauL96	2488	sense	21
AUUGAAGUGGGGAAUUACAGACU	1393	asUfsugaAfgUfGfggaAfuUfacagascsu	2489	antis	23
UGAUGUGCGUAACAGAUUCAA	1394	usgsauguGfcGfUfAfacagauucaaL96	2490	sense	21
UUGAAUCUGUUACGCACAUCAUC	1395	usUfsgaaUfcUfGfuuacGfcAfcaucasusc	2491	antis	23
GAUGUGCGUAACAGAUUCAAA	1396	gsasugugCfgUfAfAfcagauucaaaL96	2492	sense	21
UUUGAAUCUGUUACGCACAUCAU	1397	usUfsugaAfuCfUfguuaCfgCfacaucsasu	2493	antis	23
UGGAUGAUGUGCGUAACAGAU	1398	usgsgaugAfuGfUfGfcguaacagauL96	2494	sense	21
AUCUGUUACGCACAUCAUCCAGA	1399	asUfscugUfuAfCfgcacAfuCfauccasgsa	2495	antis	23
CUGGAUGAUGUGCGUAACAGA	1400	csusggauGfaUfGfUfgcguaacagaL96	2496	sense	21
UCUGUUACGCACAUCAUCCAGAC	1401	usCfsuguUfaCfGfcacaUfcAfuccagsasc	2497	antis	23
GAAUGGGUGGCGGUAAUUGGU	1402	gsasauggGfuGfGfCfgguaauugguL96	2498	sense	21
ACCAAUUACCGCCACCCAUUCCA	1403	asCfscaaUfuAfCfcgccAfcCfcauucscsa	2499	antis	23
AAUGGGUGGCGGUAAUUGGUG	1404	asasugggUfgGfCfGfguaauuggugL96	2500	sense	21
CACCAAUUACCGCCACCCAUUCC	1405	csAfsccaAfuUfAfccgcCfaCfccauuscsc	2501	antis	23
AUUGGAAUGGGUGGCGGUAAU	1406	asusuggaAfuGfGfGfuggcgguaauL96	2502	sense	21
AUUACCGCCACCCAUUCCAAUUC	1407	asUfsuacCfgCfCfacccAfuUfccaaususc	2503	antis	23
AAUUGGAAUGGGUGGCGGUAA	1408	asasuuggAfaUfGfGfguggcgguaaL96	2504	sense	21
UUACCGCCACCCAUUCCAAUUCU	1409	usUfsaccGfcCfAfcccaUfuCfcaauuscsu	2505	antis	23
UCCGGAAUGUUGCUGAAACAG	1410	uscscggaAfuGfUfUfgcugaaacagL96	2506	sense	21
CUGUUUCAGCAACAUUCCGGAGC	1411	csUfsguuUfcAfGfcaacAfuUfccggasgsc	2507	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CCGGAAUGUUGCUGAAACAGA	1412	cscsggaaUfgUfUfGfcugaaacagaL96	2508	sense	21
UCUGUUUCAGCAACAUUCCGGAG	1413	usCfsuguUfuCfAfgcaaCfaUfuccggsasg	2509	antis	23
AUGCUCCGGAAUGUUGCUGAA	1414	asusgcucCfgGfAfAfuguugcugaaL96	2510	sense	21
UUCAGCAACAUUCCGGAGCAUCC	1415	usUfscagCfaAfCfauucCfgGfagcauscsc	2511	antis	23
GAUGCUCCGGAAUGUUGCUGA	1416	gsasugcuCfcGfGfAfauguugcugaL96	2512	sense	21
UCAGCAACAUUCCGGAGCAUCCU	1417	usCfsagcAfaCfAfuuccGfgAfgcaucscsu	2513	antis	23
UGUCCUCGAGAUACUAAAGGA	1418	usgsuccuCfgAfGfAfuacuaaaggaL96	2514	sense	21
UCCUUUAGUAUCUCGAGGACAUC	1419	usCfscuuUfaGfUfaucuCfgAfggacasusc	2515	antis	23
GUCCUCGAGAUACUAAAGGAA	1420	gsusccucGfaGfAfUfacuaaaggaaL96	2516	sense	21
UUCCUUUAGUAUCUCGAGGACAU	1421	usUfsccuUfuAfGfuaucUfcGfaggacsasu	2517	antis	23
AAGAUGUCCUCGAGAUACUAA	1422	asasgaugUfcCfUfCfgagauacuaaL96	2518	sense	21
UUAGUAUCUCGAGGACAUCUUGA	1423	usUfsaguAfuCfUfcgagGfaCfaucuusgsa	2519	antis	23
CAAGAUGUCCUCGAGAUACUA	1424	csasagauGfuCfCfUfcgagauacuaL96	2520	sense	21
UAGUAUCUCGAGGACAUCUUGAA	1425	usAfsguaUfcUfCfgaggAfcAfucuugsasa	2521	antis	23
ACAACAUGCUAAAUCAGUACU	1426	ascsaacaUfgCfUfAfaaucaguacuL96	2522	sense	21
AGUACUGAUUUAGCAUGUUGUUC	1427	asGfsuacUfgAfUfuuagCfaUfguugususc	2523	antis	23
CAACAUGCUAAAUCAGUACUU	1428	csasacauGfcUfAfAfaucaguacuuL96	2524	sense	21
AAGUACUGAUUUAGCAUGUUGUU	1429	asAfsguaCfuGfAfuuuaGfcAfuguugsusu	2525	antis	23
AUGAACAACAUGCUAAAUCAG	1430	asusgaacAfaCfAfUfgcuaaaucagL96	2526	sense	21
CUGAUUUAGCAUGUGUUCAUAA	1431	csUfsgauUfuAfGfcaugUfuGfuucausasa	2527	antis	23
UAUGAACAACAUGCUAAAUCA	1432	usasugaaCfaAfCfAfugcuaaaucaL96	2528	sense	21
UGAUUUAGCAUGUUGUUCAUAAU	1433	usGfsauuUfaGfCfauguUfgUfucauasasu	2529	antis	23
GCCAAGGCUGUGUUUGUGGGG	1434	gscscaagGfcUfGfUfguuugugggL96	2530	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CCCCACAAACACAG CCUUGGCGC	1435	csCfsccaCfaAfAfcaca GfcCfuuggcsgsc	2531	antis	23
CCAAGGCUGUGUUU GUGGGGA	1436	cscsaaggCfuGfUfGfuu ugugggaL96	2532	sense	21
UCCCCACAAACACA GCCUUGGCG	1437	usCfscccAfcAfAfacac AfgCfcuuggscsg	2533	antis	23
UGGCGCCAAGGCUG UGUUUGU	1438	usgsgcgcCfaAfGfGfcu guguuuguL96	2534	sense	21
ACAAACACAGCCUU GGCGCCAAG	1439	asCfsaaaCfaCfAfgccu UfgGfcgccasasg	2535	antis	23
UUGGCGCCAAGGCU GUGUUUG	1440	ususggcgCfcAfAfGfgc uguguuugL96	2536	sense	21
CAAACACAGCCUUG GCGCCAAGA	1441	csAfsaacAfcAfGfccuu GfgCfgccaasgsa	2537	antis	23
UGAAAGCUCUGGCU CUUGGCG	1442	usgsaaagCfuCfUfGfgc ucuuggcgL96	2538	sense	21
CGCCAAGAGCCAGA GCUUUCAGA	1443	csGfsccaAfgAfGfccag AfgCfuuucasgsa	2539	antis	23
GAAAGCUCUGGCUC UUGGCGC	1444	gsasaagcUfcUfGfGfcu cuuggcgcL96	2540	sense	21
GCGCCAAGAGCCAG AGCUUUCAG	1445	gsCfsgccAfaGfAfgcca GfaGfcuuucsasg	2541	antis	23
GUUCUGAAAGCUCU GGCUCUU	1446	gsusucugAfaAfGfCfuc uggcucuuL96	2542	sense	21
AAGAGCCAGAGCUU UCAGAACAU	1447	asAfsgagCfcAfGfagcu UfuCfagaacsasu	2543	antis	23
UGUUCUGAAAGCUC UGGCUCU	1448	usgsuucuGfaAfAfGfcu cuggcucuL96	2544	sense	21
AGAGCCAGAGCUUU CAGAACAUC	1449	asGfsagcCfaGfAfgcuu UfcAfgaacasusc	2545	antis	23
CAGCCACUAUUGAU GUUCUGC	1450	csasgccaCfuAfUfUfga uguucugcL96	2546	sense	21
GCAGAACAUCAAUA GUGGCUGGC	1451	gsCfsagaAfcAfUfcaau AfgUfggcugsgsc	2547	antis	23
AGCCACUAUUGAUG UUCUGCC	1452	asgsccacUfaUfUfGfau guucugccL96	2548	sense	21
GGCAGAACAUCAAU AGUGGCUGG	1453	gsGfscagAfaCfAfucaa UfaGfuggcusgsg	2549	antis	23
GUGCCAGCCACUAU UGAUGUU	1454	gsusgccaGfcCfAfCfua uugauguuL96	2550	sense	21
AACAUCAAUAGUGG CUGGCACCC	1455	asAfscauCfaAfUfagug GfcUfggcacscsc	2551	antis	23
GGUGCCAGCCACUA UUGAUGU	1456	gsgsugccAfgCfCfAfcu auugauguL96	2552	sense	21
ACAUCAAUAGUGGC UGGCACCCC	1457	asCfsaucAfaUfAfgugg CfuGfgcaccscsc	2553	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
ACAAGGACCGAGAAGUCACCA	1458	ascsaaggAfcCfGfAfgaagucaccaL96	2554	sense	21
UGGUGACUUCUCGGUCCUUGUAG	1459	usGfsgugAfcUfUfcucgGfuCfcuugusasg	2555	antis	23
CAAGGACCGAGAAGUCACCAA	1460	csasaggaCfcGfAfGfaagucaccaaL96	2556	sense	21
UUGGUGACUUCUCGGUCCUUGUA	1461	usUfsgguGfaCfUfucucGfgUfccuugsusa	2557	antis	23
AUCUACAAGGACCGAGAAGUC	1462	asuscuacAfaGfGfAfccgagaagucL96	2558	sense	21
GACUUCUCGGUCCUUGUAGAUAU	1463	gsAfscuuCfuCfGfgucc UfuGfuagausasu	2559	antis	23
UAUCUACAAGGACCGAGAAGU	1464	usasucuaCfaAfGfGfaccgagaaguL96	2560	sense	21
ACUUCUCGGUCCUUGUAGAUAUA	1465	asCfsuucUfcGfGfuccuUfgUfagauasusa	2561	antis	23
CAGAAUGUGAAAGUCAUCGAC	1466	csasgaauGfuGfAfAfagucaucgacL96	2562	sense	21
GUCGAUGACUUUCACAUUCUGGC	1467	gsUfscgaUfgAfCfuuucAfcAfuucugsgsc	2563	antis	23
AGAAUGUGAAAGUCAUCGACA	1468	asgsaaugUfgAfAfAfgucaucgacaL96	2564	sense	21
UGUCGAUGACUUUCACAUUCUGG	1469	usGfsucgAfuGfAfcuuuCfaCfauucusgsg	2565	antis	23
GUGCCAGAAUGUGAAAGUCAU	1470	gsusgccaGfaAfUfGfugaaagucauL96	2566	sense	21
AUGACUUUCACAUUCUGGCACCC	1471	asUfsgacUfuUfCfacauUfcUfggcacscsc	2567	antis	23
GGUGCCAGAAUGUGAAAGUCA	1472	gsgsugccAfgAfAfUfgugaaagucaL96	2568	sense	21
UGACUUUCACAUUCUGGCACCCA	1473	usGfsacuUfuCfAfcauuCfuGfgcaccscsa	2569	antis	23
AGAUGUCCUCGAGAUACUAAA	1474	asgsauguCfcUfCfGfagauacuaaaL96	2570	sense	21
UUUAGUAUCUCGAGGACAUCUUG	1475	usUfsuagUfaUfCfucgaGfgAfcaucususg	2571	antis	23
GAUGUCCUCGAGAUACUAAAG	1476	gsasugucCfuCfGfAfgauacuaaagL96	2572	sense	21
CUUUAGUAUCUCGAGGACAUCUU	1477	csUfsuuaGfuAfUfcucgAfgGfacaucsusu	2573	antis	23
UUCAAGAUGUCCUCGAGAUAC	1478	ususcaagAfuGfUfCfcucgagauacL96	2574	sense	21
GUAUCUCGAGGACAUCUUGAACA	1479	gsUfsaucUfcGfAfggacAfuCfuugaascsa	2575	antis	23
GUUCAAGAUGUCCUCGAGAUA	1480	gsusucaaGfaUfGfUfccucgagauaL96	2576	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UAUCUCGAGGACAU CUUGAACAC	1481	usAfsucuCfgAfGfgaca UfcUfugaacsasc	2577	antis	23
GUGGACUUGCUGCA UAUGUGG	1482	gsusggacUfuGfCfUfgc auauguggL96	2578	sense	21
CCACAUAUGCAGCA AGUCCACUG	1483	csCfsacaUfaUfGfcagc AfaGfuccacsusg	2579	antis	23
UGGACUUGCUGCAU AUGUGGC	1484	usgsgacuUfgCfUfGfca uauguggcL96	2580	sense	21
GCCACAUAUGCAGC AAGUCCACU	1485	gsCfscacAfuAfUfgcag CfaAfguccascsu	2581	antis	23
GACAGUGGACUUGC UGCAUAU	1486	gsascaguGfgAfCfUfug cugcauauL96	2582	sense	21
AUAUGCAGCAAGUC CACUGUCGU	1487	asUfsaugCfaGfCfaagu CfcAfcugucsgsu	2583	antis	23
CGACAGUGGACUUG CUGCAUA	1488	csgsacagUfgGfAfCfuu gcugcauaL96	2584	sense	21
UAUGCAGCAAGUCC ACUGUCGUC	1489	usAfsugcAfgCfAfaguc CfaCfugucgsusc	2585	antis	23
AACCAGUACUUUAU CAUUUUC	1490	asasccagUfaCfUfUfua ucauuuucL96	2586	sense	21
GAAAAUGAUAAAGU ACUGGUUUC	1491	gsAfsaaaUfgAfUfaaag UfaCfugguususc	2587	antis	23
ACCAGUACUUUAUC AUUUUCU	1492	ascscaguAfcUfUfUfau cauuuucuL96	2588	sense	21
AGAAAAUGAUAAAG UACUGGUUU	1493	asGfsaaaAfuGfAfuaaa GfuAfcuggususu	2589	antis	23
UUGAAACCAGUACU UUAUCAU	1494	ususgaaaCfcAfGfUfac uuuaucauL96	2590	sense	21
AUGAUAAAGUACUG GUUUCAAAA	1495	asUfsgauAfaAfGfuacu GfgUfuucaasasa	2591	antis	23
UUUGAAACCAGUAC UUUAUCA	1496	ususugaaAfcCfAfGfua cuuuaucaL96	2592	sense	21
UGAUAAAGUACUGG UUUCAAAAU	1497	usGfsauaAfaGfUfacug GfuUfucaaasasu	2593	antis	23
CGAGAAGUCACCAA GAAGCUA	1498	csgsagaaGfuCfAfCfca agaagcuaL96	2594	sense	21
UAGCUUCUUGGUGA CUUCUCGGU	1499	usAfsgcuUfcUfUfUfggug AfcUfucucgsgsu	2595	antis	23
GAGAAGUCACCAAG AAGCUAG	1500	gsasgaagUfcAfCfCfaa gaagcuagL96	2596	sense	21
CUAGCUUCUUGGUG ACUUCUCGG	1501	csUfsagcUfuCfUfuggu GfaCfuucucsgsg	2597	antis	23
GGACCGAGAAGUCA CCAAGAA	1502	gsgsaccgAfgAfAfGfuc accaagaaL96	2598	sense	21
UUCUUGGUGACUUC UCGGUCCUU	1503	usUfscuuGfgUfGfacuu CfuCfgguccsusu	2599	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AGGACCGAGAAGUCACCAAGA	1504	asgsgaccGfaGfAfAfgucaccaagaL96	2600	sense	21
UCUUGGUGACUUCUCGGUCCUUG	1505	usCfsuugGfuGfAfcuucUfcGfguccususg	2601	antis	23
UCAAAGUGUUGGUAAUGCCUG	1506	uscsaaagUfgUfUfGfguaaugccugL96	2602	sense	21
CAGGCAUUACCAACACUUUGAAC	1507	csAfsggcAfuUfAfccaaCfaCfuuugasasc	2603	antis	23
CAAAGUGUUGGUAAUGCCUGA	1508	csasaaguGfuUfGfGfuaaugccugaL96	2604	sense	21
UCAGGCAUUACCAACACUUUGAA	1509	usCfsaggCfaUfUfaccaAfcAfcuuugsasa	2605	antis	23
AGGUUCAAAGUGUUGGUAAUG	1510	asgsguucAfaAfGfUfgugguaaugL96	2606	sense	21
CAUUACCAACACUUUGAACCUGA	1511	csAfsuuaCfcAfAfcacuUfuGfaaccusgsa	2607	antis	23
CAGGUUCAAAGUGUUGGUAAU	1512	csasgguuCfaAfAfGfuguugguaauL96	2608	sense	21
AUUACCAACACUUUGAACCUGAG	1513	asUfsuacCfaAfCfacuuUfgAfaccugsasg	2609	antis	23
UAUUACUUGACAAAGAGACAC	1514	usasuuacUfuGfAfCfaaagagacacL96	2610	sense	21
GUGUCUCUUUGUCAAGUAAUACA	1515	gsUfsgucUfcUfUfugucAfaGfuaauascsa	2611	antis	23
AUUACUUGACAAAGAGACACU	1516	asusuacuUfgAfCfAfaagagacacuL96	2612	sense	21
AGUGUCUCUUUGUCAAGUAAUAC	1517	asGfsuguCfuCfUfuuguCfaAfguaausasc	2613	antis	23
CAUGUAUUACUUGACAAAGAG	1518	csasuguaUfuAfCfUfugacaaagagL96	2614	sense	21
CUCUUUGUCAAGUAAUACAUGCU	1519	csUfscuuUfgUfCfaaguAfaUfacaugscsu	2615	antis	23
GCAUGUAUUACUUGACAAAGA	1520	gscsauguAfuUfAfCfuugacaaagaL96	2616	sense	21
UCUUUGUCAAGUAAUACAUGCUG	1521	usCfsuuuGfuCfAfaguaAfuAfcaugcsusg	2617	antis	23
AAAGUCAUCGACAAGACAUUG	1522	asasagucAfuCfGfAfcaagacauugL96	2618	sense	21
CAAUGUCUUGUCGAUGACUUUCA	1523	csAfsaugUfcUfUfgucgAfuGfacuuuscsa	2619	antis	23
AAGUCAUCGACAAGACAUUGG	1524	asasgucaUfcGfAfCfaagacauuggL96	2620	sense	21
CCAAUGUCUUGUCGAUGACUUUC	1525	csCfsaauGfuCfUfugucGfaUfgacuususc	2621	antis	23
UGUGAAAGUCAUCGACAAGAC	1526	usgsugaaAfgUfCfAfucgacaagacL96	2622	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GUCUUGUCGAUGAC UUUCACAUU	1527	gsUfscuuGfuCfGfauga CfuUfucacasusu	2623	antis	23
AUGUGAAAGUCAUC GACAAGA	1528	asusgugaAfaGfUfCfau cgacaagaL96	2624	sense	21
UCUUGUCGAUGACU UUCACAUUC	1529	usCfsuugUfcGfAfugac UfuUfcacaususc	2625	antis	23
AUAUGUGGCUAAAG CAAUAGA	1530	asusauguGfgCfUfAfaa gcaauagaL96	2626	sense	21
UCUAUUGCUUUAGC CACAUAUGC	1531	usCfsuauUfgCfUfuuag CfcAfcauausgsc	2627	antis	23
UAUGUGGCUAAAGC AAUAGAC	1532	usasugugGfcUfAfAfag caauagacL96	2628	sense	21
GUCUAUUGCUUUAG CCACAUAUG	1533	gsUfscuaUfuGfCfuuua GfcCfacauasusg	2629	antis	23
CUGCAUAUGUGGCU AAAGCAA	1534	csusgcauAfuGfUfGfgc uaaagcaaL96	2630	sense	21
UUGCUUUAGCCACA UAUGCAGCA	1535	usUfsgcuUfuAfGfccac AfuAfugcagscsa	2631	antis	23
GCUGCAUAUGUGGC UAAAGCA	1536	gscsugcaUfaUfGfUfgg cuaaagcaL96	2632	sense	21
UGCUUUAGCCACAU AUGCAGCAA	1537	usGfscuuUfaGfCfcaca UfaUfgcagcsasa	2633	antis	23
AGACGACAGUGGAC UUGCUGC	1538	asgsacgaCfaGfUfGfga cuugcugcL96	2634	sense	21
GCAGCAAGUCCACU GUCGUCUCC	1539	gsCfsagcAfaGfUfccac UfgUfcgucuscsc	2635	antis	23
GACGACAGUGGACU UGCUGCA	1540	gsascgacAfgUfGfGfac uugcugcaL96	2636	sense	21
UGCAGCAAGUCCAC UGUCGUCUC	1541	usGfscagCfaAfGfucca CfuGfucgucsusc	2637	antis	23
UUGGAGACGACAGU GGACUUG	1542	ususggagAfcGfAfCfag uggacuugL96	2638	sense	21
CAAGUCCACUGUCG UCUCCAAAA	1543	csAfsaguCfcAfCfuguc GfuCfuccaasasa	2639	antis	23
UUUGGAGACGACAG UGGACUU	1544	ususuggaGfaCfGfAfca guggacuuL96	2640	sense	21
AAGUCCACUGUCGU CUCCAAAAU	1545	asAfsgucCfaCfUfgucg UfcUfccaaasasu	2641	antis	23
GGCCACCUCCUCAA UUGAAGA	1546	gsgsccacCfuCfCfUfca auugaagaL96	2642	sense	21
UCUUCAAUUGAGGA GGUGGCCCA	1547	usCfsuucAfaUfUfgagg AfgGfuggccscsa	2643	antis	23
GCCACCUCCUCAAU UGAAGAA	1548	gscscaccUfcCfUfCfaa uugaagaaL96	2644	sense	21
UUCUUCAAUUGAGG AGGUGGCCC	1549	usUfscuuCfaAfUfugag GfaGfguggcscsc	2645	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CCUGGGCCACCUCC UCAAUUG	1550	cscsugggCfcAfCfCfuc cucaauugL96	2646	sense	21
CAAUUGAGGAGGUG GCCCAGGAA	1551	csAfsauuGfaGfGfaggu GfgCfccaggsasa	2647	antis	23
UCCUGGGCCACCUC CUCAAUU	1552	uscscuggGfcCfAfCfcu ccucaauuL96	2648	sense	21
AAUUGAGGAGGUGG CCCAGGAAC	1553	asAfsuugAfgGfAfggug GfcCfcaggasasc	2649	antis	23
UGUAUGUUACUUCU UAGAGAG	1554	usgsuaugUfuAfCfUfuc uuagagagL96	2650	sense	21
CUCUCUAAGAAGUA ACAUACAUC	1555	csUfscucUfaAfGfaagu AfaCfauacasusc	2651	antis	23
GUAUGUUACUUCUU AGAGAGA	1556	gsusauguUfaCfUfUfcu uagagagaL96	2652	sense	21
UCUCUCUAAGAAGU AACAUACAU	1557	usCfsucuCfuAfAfgaag UfaAfcauacsasu	2653	antis	23
AGGAUGUAUGUUAC UUCUUAG	1558	asgsgaugUfaUfGfUfua cuucuuagL96	2654	sense	21
CUAAGAAGUAACAU ACAUCCUAA	1559	csUfsaagAfaGfUfaaca UfaCfauccusasa	2655	antis	23
UAGGAUGUAUGUUA CUUCUUA	1560	usasggauGfuAfUfGfuu acuucuuaL96	2656	sense	21
UAAGAAGUAACAUA CAUCCUAAA	1561	usAfsagaAfgUfAfacau AfcAfuccuasasa	2657	antis	23
AAAUGUUUUAGGAU GUAUGUU	1562	asasauguUfuUfAfGfga uguauguuL96	2658	sense	21
AACAUACAUCCUAA AACAUUUGG	1563	asAfscauAfcAfUfccua AfaAfcauuusgsg	2659	antis	23
AAUGUUUUAGGAUG UAUGUUA	1564	asasuguuUfuAfGfGfau guauguuaL96	2660	sense	21
UAACAUACAUCCUA AAACAUUUG	1565	usAfsacaUfaCfAfuccu AfaAfacauususg	2661	antis	23
AUCCAAAUGUUUUA GGAUGUA	1566	asusccaaAfuGfUfUfuu aggauguaL96	2662	sense	21
UACAUCCUAAAACA UUUGGAUAU	1567	usAfscauCfcUfAfaaac AfuUfuggausasu	2663	antis	23
UAUCCAAAUGUUUU AGGAUGU	1568	usasuccaAfaUfGfUfuu uaggauguL96	2664	sense	21
ACAUCCUAAAACAU UUGGAUAUA	1569	asCfsaucCfuAfAfaaca UfuUfggauasusa	2665	antis	23
AUGGGUGGCGGUAA UUGGUGA	1570	asusggguGfgCfGfGfua auuggugaL96	2666	sense	21
UCACCAAUUACCGC CACCCAUUC	1571	usCfsaccAfaUfUfaccg CfcAfcccaususc	2667	antis	23
UGGGUGGCGGUAAU UGGUGAU	1572	usgsggugGfcGfGfUfaa uuggugauL96	2668	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AUCACCAAUUACCG CCACCCAUU	1573	asUfscacCfaAfUfuacc GfcCfacccasusu	2669	antis	23
UGGAAUGGGUGGCG GUAAUUG	1574	usgsgaauGfgGfUfGfgc gguaauugL96	2670	sense	21
CAAUUACCGCCACC CAUUCCAAU	1575	csAfsauuAfcCfGfccac CfcAfuuccasasu	2671	antis	23
UUGGAAUGGGUGGC GGUAAUU	1576	ususggaaUfgGfGfUfgg cgguaauuL96	2672	sense	21
AAUUACCGCCACCC AUUCCAAUU	1577	asAfsuuaCfcGfCfcacc CfaUfuccaasusu	2673	antis	23
UUCAAAGUGUUGGU AAUGCCU	1578	ususcaaaGfuGfUfUfgg uaaugccuL96	2674	sense	21
AGGCAUUACCAACA CUUUGAACC	1579	asGfsgcaUfuAfCfcaac AfcUfuugaascsc	2675	antis	23
UCAAAGUGUUGGUA AUGCCUG	1580	uscsaaagUfgUfUfGfgu aaugccugL96	2676	sense	21
CAGGCAUUACCAAC ACUUUGAAC	1581	csAfsggcAfuUfAfccaa CfaCfuuugasasc	2677	antis	23
CAGGUUCAAAGUGU UGGUAAU	1582	csasgguuCfaAfAfGfug uugguaauL96	2678	sense	21
AUUACCAACACUUU GAACCUGAG	1583	asUfsuacCfaAfCfacuu UfgAfaccugsasg	2679	antis	23
UCAGGUUCAAAGUG UUGGUAA	1584	uscsagguUfcAfAfAfgu guugguaaL96	2680	sense	21
UUACCAACACUUUG AACCUGAGC	1585	usUfsaccAfaCfAfcuuu GfaAfccugasgsc	2681	antis	23
CCACCUCCUCAAUU GAAGAAG	1586	cscsaccuCfcUfCfAfau ugaagaagL96	2682	sense	21
CUUCUUCAAUUGAG GAGGUGGCC	1587	csUfsucuUfcAfAfuuga GfgAfgguggscsc	2683	antis	23
CACCUCCUCAAUUG AAGAAGU	1588	csasccucCfuCfAfAfuu gaagaaguL96	2684	sense	21
ACUUCUUCAAUUGA GGAGGUGGC	1589	asCfsuucUfuCfAfauug AfgGfaggugsgsc	2685	antis	23
UGGGCCACCUCCUC AAUUGAA	1590	usgsggccAfcCfUfCfcu caauugaaL96	2686	sense	21
UUCAAUUGAGGAGG UGGCCCAGG	1591	usUfscaaUfuGfAfggag GfuGfgcccasgsg	2687	antis	23
CUGGGCCACCUCCU CAAUUGA	1592	csusgggcCfaCfCfUfcc ucaauugaL96	2688	sense	21
UCAAUUGAGGAGGU GGCCCAGGA	1593	usCfsaauUfgAfGfgagg UfgGfcccagsgsa	2689	antis	23
GAGUGGGUGCCAGA AUGUGAA	1594	gsasguggGfuGfCfCfag aaugugaaL96	2690	sense	21
UUCACAUUCUGGCA CCCACUCAG	1595	usUfscacAfuUfCfuggc AfcCfcacucsasg	2691	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
AGUGGGUGCCAGAAUGUGAAA	1596	asgsugggUfgCfCfAfgaaugugaaaL96	2692	sense	21
UUUCACAUUCUGGCACCCACUCA	1597	usUfsucaCfaUfUfcuggCfaCfccacuscsa	2693	antis	23
CUCUGAGUGGGUGCCAGAAUG	1598	csuscugaGfuGfGfGfugccagaaugL96	2694	sense	21
CAUUCUGGCACCCACUCAGAGCC	1599	csAfsuucUfgGfCfacccAfcUfcagagscsc	2695	antis	23
GCUCUGAGUGGGUGCCAGAAU	1600	gscsucugAfgUfGfGfgugccagaauL96	2696	sense	21
AUUCUGGCACCCACUCAGAGCCA	1601	asUfsucuGfgCfAfcccaCfuCfagagcscsa	2697	antis	23
GCACUGAUGUUCUGAAAGCUC	1602	gscsacugAfuGfUfUfcugaaagcucL96	2698	sense	21
GAGCUUUCAGAACAUCAGUGCCU	1603	gsAfsgcuUfuCfAfgaacAfuCfagugcscsu	2699	antis	23
CACUGAUGUUCUGAAAGCUCU	1604	csascugaUfgUfUfCfugaaagcucuL96	2700	sense	21
AGAGCUUUCAGAACAUCAGUGCC	1605	asGfsagcUfuUfCfagaaCfaUfcagugscsc	2701	antis	23
AAAGGCACUGAUGUUCUGAAA	1606	asasaggcAfcUfGfAfuguucugaaaL96	2702	sense	21
UUUCAGAACAUCAGUGCCUUUCC	1607	usUfsucaGfaAfCfaucaGfuGfccuuuscsc	2703	antis	23
GAAAGGCACUGAUGUUCUGAA	1608	gsasaaggCfaCfUfGfauguucugaaL96	2704	sense	21
UUCAGAACAUCAGUGCCUUUCCG	1609	usUfscagAfaCfAfucagUfgCfcuuucscsg	2705	antis	23
GGGAAGGUGGAAGUCUUCCUG	1610	gsgsgaagGfuGfGfAfagucuuccugL96	2706	sense	21
CAGGAAGACUUCCACCUUCCCUU	1611	csAfsggaAfgAfCfuuccAfcCfuucccsusu	2707	antis	23
GGAAGGUGGAAGUCUUCCUGG	1612	gsgsaaggUfgGfAfAfgucuuccuggL96	2708	sense	21
CCAGGAAGACUUCCACCUUCCCU	1613	csCfsaggAfaGfAfcuucCfaCfcuuccscsu	2709	antis	23
GGAAGGGAAGGUGGAAGUCUU	1614	gsgsaaggGfaAfGfGfuggaagucuuL96	2710	sense	21
AAGACUUCCACCUUCCCUUCCAC	1615	asAfsgacUfuCfCfCfaccuUfcCfcuuccsasc	2711	antis	23
UGGAAGGGAAGGUGGAAGUCU	1616	usgsgaagGfgAfAfGfguggaagucuL96	2712	sense	21
AGACUUCCACCUUCCCUUCCACA	1617	asGfsacuUfcCfAfccuuCfcCfuuccascsa	2713	antis	23
UGCUAAAUCAGUACUUCCAAA	1618	usgscuaaAfuCfAfGfuacuuccaaaL96	2714	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UUUGGAAGUACUGAUUUAGCAUG	1619	usUfsuggAfaGfUfacugAfuUfuagcasusg	2715	antis	23
GCUAAAUCAGUACUUCCAAAG	1620	gscsuaaaUfcAfGfUfacuuccaaagL96	2716	sense	21
CUUUGGAAGUACUGAUUUAGCAU	1621	csUfsuugGfaAfGfuacuGfaUfuuagcsasu	2717	antis	23
AACAUGCUAAAUCAGUACUUC	1622	asascaugCfuAfAfAfucaguacuucL96	2718	sense	21
GAAGUACUGAUUUAGCAUGUUGU	1623	gsAfsaguAfcUfGfauuuAfgCfauguusgsu	2719	antis	23
CAACAUGCUAAAUCAGUACUU	1624	csasacauGfcUfAfAfaucaguacuuL96	2720	sense	21
AAGUACUGAUUUAGCAUGUUGUU	1625	asAfsguaCfuGfAfuuuaGfcAfuguugsusu	2721	antis	23
CCACAACUCAGGAUGAAAAAU	1626	cscsacaaCfuCfAfGfgaugaaaaauL96	2722	sense	21
AUUUUUCAUCCUGAGUUGUGGCG	1627	asUfsuuuUfcAfUfccugAfgUfuguggscsg	2723	antis	23
CACAACUCAGGAUGAAAAAUU	1628	csascaacUfcAfGfGfaugaaaaauuL96	2724	sense	21
AAUUUUUCAUCCUGAGUUGUGGC	1629	asAfsuuuUfuCfAfuccuGfaGfuugugsgsc	2725	antis	23
GCCGCCACAACUCAGGAUGAA	1630	gscscgccAfcAfAfCfucaggaugaaL96	2726	sense	21
UUCAUCCUGAGUUGUGGCGGCAG	1631	usUfscauCfcUfGfaguuGfuGfgcggcsasg	2727	antis	23
UGCCGCCACAACUCAGGAUGA	1632	usgsccgcCfaCfAfAfcucaggaugaL96	2728	sense	21
UCAUCCUGAGUUGUGGCGGCAGU	1633	usCfsaucCfuGfAfguugUfgGfcggcasgsu	2729	antis	23
GCAACCGUCUGGAUGAUGUGC	1634	gscsaaccGfuCfUfGfgaugaugugcL96	2730	sense	21
GCACAUCAUCCAGACGGUUGCCC	1635	gsCfsacaUfcAfUfccagAfcGfguugcscsc	2731	antis	23
CAACCGUCUGGAUGAUGUGCG	1636	csasaccgUfcUfGfGfaugaugugcgL96	2732	sense	21
CGCACAUCAUCCAGACGGUUGCC	1637	csGfscacAfuCfAfuccaGfaCfgguugscsc	2733	antis	23
CUGGGCAACCGUCUGGAUGAU	1638	csusgggcAfaCfCfGfucuggaugauL96	2734	sense	21
AUCAUCCAGACGGUUGCCCAGGU	1639	asUfscauCfcAfGfacggUfuGfcccagsgsu	2735	antis	23
CCUGGGCAACCGUCUGGAUGA	1640	cscsugggCfaAfCfCfcuguggaugaL96	2736	sense	21
UCAUCCAGACGGUUGCCCAGGUA	1641	usCfsaucCfaGfAfcgguUfgCfccaggsusa	2737	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GCAAAUGAUGAAGAAACUUUG	1642	gscsaaauGfaUfGfAfagaaacuuugL96	2738	sense	21
CAAAGUUUCUUCAUCAUUUGCCC	1643	csAfsaagUfuUfCfuucaUfcAfuuugcscsc	2739	antis	23
CAAAUGAUGAAGAAACUUUGG	1644	csasaaugAfuGfAfAfgaaacuuuggL96	2740	sense	21
CCAAAGUUUCUUCAUCAUUUGCC	1645	csCfsaaaGfuUfUfcuucAfuCfauuugscsc	2741	antis	23
UGGGGCAAAUGAUGAAGAAAC	1646	usgsgggcAfaAfUfGfaugaagaaacL96	2742	sense	21
GUUUCUUCAUCAUUUGCCCCAGA	1647	gsUfsuucUfuCfAfucauUfuGfccccasgsa	2743	antis	23
CUGGGGCAAAUGAUGAAGAAA	1648	csusggggCfaAfAfUfgaugaagaaaL96	2744	sense	21
UUUCUUCAUCAUUUGCCCCAGAC	1649	usUfsucuUfcAfUfcauuUfgCfcccagsasc	2745	antis	23
CCAAGGCUGUGUUUGUGGGGA	1650	cscsaaggCfuGfUfGfuuugugggggaL96	2746	sense	21
UCCCCACAAACACAGCCUUGGCG	1651	usCfscccAfcAfAfacacAfgCfcuuggscsg	2747	antis	23
CAAGGCUGUGUUUGUGGGGAG	1652	csasaggcUfgUfGfUfuugugggagL96	2748	sense	21
CUCCCCACAAACACAGCCUUGGC	1653	csUfscccCfaCfAfaacaCfaGfccuugsgsc	2749	antis	23
GGCGCCAAGGCUGGUUUGUG	1654	gsgscgccAfaGfGfCfuguuuugugL96	2750	sense	21
CACAAACACAGCCUUGGCGCCAA	1655	csAfscaaAfcAfCfagccUfuGfgcgccsasa	2751	antis	23
UGGCGCCAAGGCUGUGUUUGU	1656	usgsgcgcCfaAfGfGfcuguguuuguL96	2752	sense	21
ACAAACACAGCCUUGGCGCCAAG	1657	asCfsaaaCfaCfAfgccuUfgGfcgccasasg	2753	antis	23
ACUGCCGCCACAACUCAGGAU	1658	ascsugccGfcCfAfCfaacucaggauL96	2754	sense	21
AUCCUGAGUUGUGGCGGCAGUUU	1659	asUfsccuGfaGfUfugugGfcGfgcagususu	2755	antis	23
CUGCCGCCACAACUCAGGAUG	1660	csusgccgCfcAfCfAfacucaggaugL96	2756	sense	21
CAUCCUGAGUUGUGGCGGCAGUU	1661	csAfsuccUfgAfGfuuguGfgCfggcagsusu	2757	antis	23
UCAAACUGCCGCCACAACUCA	1662	uscsaaacUfgCfCfGfccacaacucaL96	2758	sense	21
UGAGUUGUGGCGGCAGUUUGAAU	1663	usGfsaguUfgUfGfgcggCfaGfuuugasasu	2759	antis	23
UUCAAACUGCCGCCACAACUC	1664	ususcaaaCfuGfCfCfgccacaacucL96	2760	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GAGUUGUGGCGGCAGUUUGAAUC	1665	gsAfsguuGfuGfGfcggcAfgUfuugaasusc	2761	antis	23
GGGAAGAUAUCAAAUGGCUGA	1666	gsgsgaagAfuAfUfCfaaauggcugaL96	2762	sense	21
UCAGCCAUUUGAUAUCUUCCCAG	1667	usCfsagcCfaUfUfugauAfuCfuucccsasg	2763	antis	23
GGAAGAUAUCAAAUGGCUGAG	1668	gsgsaagaUfaUfCfAfaauggcugagL96	2764	sense	21
CUCAGCCAUUUGAUAUCUUCCCA	1669	csUfscagCfcAfUfuugaUfaUfcuuccscsa	2765	antis	23
AGCUGGGAAGAUAUCAAAUGG	1670	asgscuggGfaAfGfAfuaucaaauggL96	2766	sense	21
CCAUUUGAUAUCUUCCCAGCUGA	1671	csCfsauuUfgAfUfaucuUfcCfcagcusgsa	2767	antis	23
CAGCUGGGAAGAUAUCAAAUG	1672	csasgcugGfgAfAfGfauaucaaaugL96	2768	sense	21
CAUUUGAUAUCUUCCCAGCUGAU	1673	csAfsuuuGfaUfAfucuuCfcCfagcugsasu	2769	antis	23
AAUCAGUACUUCCAAAGUCUA	1674	asasucagUfaCfUfUfccaaagucuaL96	2770	sense	21
UAGACUUUGGAAGUACUGAUUUA	1675	usAfsgacUfuUfGfgaagUfaCfugauususa	2771	antis	23
AUCAGUACUUCCAAAGUCUAU	1676	asuscaguAfcUfUfUfCfcaaagucuauL96	2772	sense	21
AUAGACUUUGGAAGUACUGAUUU	1677	asUfsagaCfuUfUfggaaGfuAfcugaususu	2773	antis	23
GCUAAAUCAGUACUUCCAAAG	1678	gscsuaaaUfcAfGfUfacuuccaaagL96	2774	sense	21
CUUUGGAAGUACUGAUUUAGCAU	1679	csUfsuugGfaAfGfuacuGfaUfuuagcsasu	2775	antis	23
UGCUAAAUCAGUACUUCCAAA	1680	usgscuaaAfuCfAfGfuacuuccaaaL96	2776	sense	21
UUUGGAAGUACUGAUUUAGCAUG	1681	usUfsuggAfaGfUfacugAfuUfuagcasusg	2777	antis	23
UCAGCAUGCCAAUAUGUGUGG	1682	uscsagcaUfgCfCfAfauaugugguggL96	2778	sense	21
CCACACAUAUUGGCAUGCUGACC	1683	csCfsacaCfaUfAfuuggCfaUfgcugascsc	2779	antis	23
CAGCAUGCCAAUAUGUGUGGG	1684	csasgcauGfcCfAfAfuaugugugggL96	2780	sense	21
CCCACACAUAUUGGCAUGCUGAC	1685	csCfscacAfcAfUfauugGfcAfugcugsasc	2781	antis	23
AGGGUCAGCAUGCCAAUAUGU	1686	asgsggucAfgCfAfUfgccaauauguL96	2782	sense	21
ACAUAUUGGCAUGCUGACCCUCU	1687	asCfsauaUfuGfGfcaugCfuGfacccuscsu	2783	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GAGGGUCAGCAUGCCAAUAUG	1688	gsasggguCfaGfCfAfugccaauaugL96	2784	sense	21
CAUAUUGGCAUGCUGACCCUCUG	1689	csAfsuauUfgGfCfaugcUfgAfcccucsusg	2785	antis	23
GCAUAUGUGGCUAAAGCAAUA	1690	gscsauauGfuGfGfCfuaaagcaauaL96	2786	sense	21
UAUUGCUUUAGCCACAUAUGCAG	1691	usAfsuugCfuUfUfagccAfcAfuaugcsasg	2787	antis	23
CAUAUGUGGCUAAAGCAAUAG	1692	csasuaugUfgGfCfUfaaagcaauagL96	2788	sense	21
CUAUUGCUUUAGCCACAUAUGCA	1693	csUfsauuGfcUfUfuagcCfaCfauaugscsa	2789	antis	23
UGCUGCAUAUGUGGCUAAAGC	1694	usgscugcAfuAfUfGfuggcuaaagcL96	2790	sense	21
GCUUUAGCCACAUAUGCAGCAAG	1695	gsCfsuuuAfgCfCfacauAfuGfcagcasasg	2791	antis	23
UUGCUGCAUAUGUGGCUAAAG	1696	ususgcugCfaUfAfUfguggcuaaagL96	2792	sense	21
CUUUAGCCACAUAUGCAGCAAGU	1697	csUfsuuaGfcCfAfcauaUfgCfagcaasgsu	2793	antis	23
AAAUGAUGAAGAAACUUUGGC	1698	asasaugaUfgAfAfGfaaacuuuggcL96	2794	sense	21
GCCAAAGUUUCUUCAUCAUUUGC	1699	gsCfscaaAfgUfUfucuuCfaUfcauuusgsc	2795	antis	23
AAUGAUGAAGAAACUUUGGCU	1700	asasugauGfaAfGfAfaacuuuggcuL96	2796	sense	21
AGCCAAAGUUUCUUCAUCAUUUG	1701	asGfsccaAfaGfUfuucuUfcAfucauususg	2797	antis	23
GGGCAAAUGAUGAAGAAACUU	1702	gsgsgcaaAfuGfAfUfgaagaaacuuL96	2798	sense	21
AAGUUUCUUCAUCAUUUGCCCCA	1703	asAfsguuUfcUfUfcaucAfuUfugcccscsa	2799	antis	23
GGGGCAAAUGAUGAAGAAACU	1704	gsgsggcaAfaUfGfAfugaagaaacuL96	2800	sense	21
AGUUUCUUCAUCAUUUGCCCCAG	1705	asGfsuuuCfuUfCfaucaUfuUfgccccsasg	2801	antis	23
GAGAUACUAAAGGAAGAAUUC	1706	gsasgauaCfuAfAfAfggaagaauucL96	2802	sense	21
GAAUUCUUCCUUUAGUAUCUCGA	1707	gsAfsauuCfuUfCfcuuuAfgUfaucucsgsa	2803	antis	23
AGAUACUAAAGGAAGAAUUCC	1708	asgsauacUfaAfAfGfgaagaauuccL96	2804	sense	21
GGAAUUCUUCCUUUAGUAUCUCG	1709	gsGfsaauUfcUfUfccuuUfaGfuaucuscsg	2805	antis	23
CCUCGAGAUACUAAAGGAAGA	1710	cscsucgaGfaUfAfCfuaaaggaagaL96	2806	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UCUUCCUUUAGUAUCUCGAGGAC	1711	usCfsuucCfuUfUfaguaUfcUfcgaggsasc	2807	antis	23
UCCUCGAGAUACUAAAGGAAG	1712	uscscucgAfgAfUfAfcuaaaggaagL96	2808	sense	21
CUUCCUUUAGUAUCUCGAGGACA	1713	csUfsuccUfuUfAfguauCfuCfgaggascsa	2809	antis	23
ACAACUCAGGAUGAAAAAUUU	1714	ascsaacuCfaGfGfAfugaaaaauuuL96	2810	sense	21
AAAUUUUUCAUCCUGAGUUGUGG	1715	asAfsauuUfuUfCfauccUfgAfguugusgsg	2811	antis	23
CAACUCAGGAUGAAAAAUUUU	1716	csasacucAfgGfAfUfgaaaaauuuuL96	2812	sense	21
AAAAUUUUUCAUCCUGAGUUGUG	1717	asAfsaauUfuUfUfcaucCfuGfaguugsusg	2813	antis	23
CGCCACAACUCAGGAUGAAAA	1718	csgsccacAfaCfUfCfaggaugaaaaL96	2814	sense	21
UUUUCAUCCUGAGUUGUGGCGGC	1719	usUfsuucAfuCfCfugagUfuGfuggcgsgsc	2815	antis	23
CCGCCACAACUCAGGAUGAAA	1720	cscsgccaCfaAfCfUfcaggaugaaaL96	2816	sense	21
UUUCAUCCUGAGUUGUGGCGGCA	1721	usUfsucaUfcCfUfgaguUfgUfggcggscsa	2817	antis	23
AGGGAAGGUGGAAGUCUUCCU	1722	asgsggaaGfgUfGfGfaagucuuccuL96	2818	sense	21
AGGAAGACUUCCACCUUCCCUUC	1723	asGfsgaaGfaCfUfuccaCfcUfucccususc	2819	antis	23
GGGAAGGUGGAAGUCUUCCUG	1724	gsgsgaagGfuGfGfAfagucuuccugL96	2820	sense	21
CAGGAAGACUUCCACCUUCCCUU	1725	csAfsggaAfgAfCfuuccAfcCfuucccsusu	2821	antis	23
UGGAAGGGAAGGUGGAAGUCU	1726	usgsgaagGfgAfAfGfuggaagucuL96	2822	sense	21
AGACUUCCACCUUCCCUUCCACA	1727	asGfsacuUfcCfAfccuuCfcCfuuccascsa	2823	antis	23
GUGGAAGGGAAGGUGGAAGUC	1728	gsusggaaGfgGfAfAfggugaagucL96	2824	sense	21
GACUUCCACCUUCCCUUCCACAG	1729	gsAfscuuCfcAfCfcuucCfcUfuccacsasg	2825	antis	23
GGCGAGCUUGCCACUGUGAGA	1730	gsgscgagCfuUfGfCfcacugugagaL96	2826	sense	21
UCUCACAGUGGCAAGCUCGCCGU	1731	usCfsucaCfaGfUfggcaAfgCfucgccsgsu	2827	antis	23
GCGAGCUUGCCACUGUGAGAG	1732	gscsgagcUfuGfCfCfacugugagagL96	2828	sense	21
CUCUCACAGUGGCAAGCUCGCCG	1733	csUfscucAfcAfGfuggcAfaGfcucgcscsg	2829	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GGACGGCGAGCUUG CCACUGU	1734	gsgsacggCfgAfGfCfuu gccacuguL96	2830	sense	21
ACAGUGGCAAGCUC GCCGUCCAC	1735	asCfsaguGfgCfAfagcu CfgCfcguccsasc	2831	antis	23
UGGACGGCGAGCUU GCCACUG	1736	usgsgacgGfcGfAfGfcu ugccacugL96	2832	sense	21
CAGUGGCAAGCUCG CCGUCCACA	1737	csAfsgugGfcAfAfgcuc GfcCfguccascsa	2833	antis	23
AUGUGCGUAACAGA UUCAAAC	1738	asusgugcGfuAfAfCfag auucaaacL96	2834	sense	21
GUUUGAAUCUGUUA CGCACAUCA	1739	gsUfsuugAfaUfCfuguu AfcGfcacauscsa	2835	antis	23
UGUGCGUAACAGAU UCAAACU	1740	usgsugcgUfaAfCfAfga uucaaacuL96	2836	sense	21
AGUUUGAAUCUGUU ACGCACAUC	1741	asGfsuuuGfaAfUfcugu UfaCfgcacasusc	2837	antis	23
GAUGAUGUGCGUAA CAGAUUC	1742	gsasugauGfuGfCfGfua acagauucL96	2838	sense	21
GAAUCUGUUACGCA CAUCAUCCA	1743	gsAfsaucUfgUfUfacgc AfcAfucaucscsa	2839	antis	23
GGAUGAUGUGCGUA ACAGAUU	1744	gsgsaugaUfgUfGfCfgu aacagauuL96	2840	sense	21
AAUCUGUUACGCAC AUCAUCCAG	1745	asAfsucuGfuUfAfcgca CfaUfcauccsasg	2841	antis	23
GGGUCAGCAUGCCA AUAUGUG	1746	gsgsgucaGfcAfUfGfcc aauaugugL96	2842	sense	21
CACAUAUUGGCAUG CUGACCCUC	1747	csAfscauAfuUfGfgcau GfcUfgacccsusc	2843	antis	23
GGUCAGCAUGCCAA UAUGUGU	1748	gsgsucagCfaUfGfCfca auauguguL96	2844	sense	21
ACACAUAUUGGCAU GCUGACCCU	1749	asCfsacaUfaUfUfggca UfgCfugaccscsu	2845	antis	23
CAGAGGGUCAGCAU GCCAAUA	1750	csasgaggGfuCfAfGfca ugccaauaL96	2846	sense	21
UAUUGGCAUGCUGA CCCUCUGUC	1751	usAfsuugGfcAfUfgcug AfcCfcucugsusc	2847	antis	23
ACAGAGGGUCAGCA UGCCAAU	1752	ascsagagGfgUfCfAfgc augccaauL96	2848	sense	21
AUUGGCAUGCUGAC CCUCUGUCC	1753	asUfsuggCfaUfGfcuga CfcCfucuguscsc	2849	antis	23
GCUUGAAUGGGAUC UUGGUGU	1754	gscsuugaAfuGfGfGfau cuugguguL96	2850	sense	21
ACACCAAGAUCCCA UUCAAGCCA	1755	asCfsaccAfaGfAfuccc AfuUfcaagcscsa	2851	antis	23
CUUGAAUGGGAUCU UGGUGUC	1756	csusugaaUfgGfGfAfuc uuggugucL96	2852	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GACACCAAGAUCCCAUUCAAGCC	1757	gsAfscacCfaAfGfauccCfaUfucaagscsc	2853	antis	23
CAUGGCUUGAAUGGGAUCUUG	1758	csasuggcUfuGfAfAfuggaucuugL96	2854	sense	21
CAAGAUCCCAUUCAAGCCAUGUU	1759	csAfsagaUfcCfCfauucAfaGfccaugsusu	2855	antis	23
ACAUGGCUUGAAUGGGAUCUU	1760	ascsauggCfuUfGfAfaugggaucuuL96	2856	sense	21
AAGAUCCCAUUCAAGCCAUGUUU	1761	asAfsgauCfcCfAfuucaAfgCfcaugususu	2857	antis	23
UCAAAUGGCUGAGAAGACUGA	1762	uscsaaauGfgCfUfGfagaagacugaL96	2858	sense	21
UCAGUCUUCUCAGCCAUUUGAUA	1763	usCfsaguCfuUfCfucagCfcAfuuugasusa	2859	antis	23
CAAAUGGCUGAGAAGACUGAC	1764	csasaaugGfcUfGfAfgaagacugacL96	2860	sense	21
GUCAGUCUUCUCAGCCAUUUGAU	1765	gsUfscagUfcUfUfcucaGfcCfauuugsasu	2861	antis	23
GAUAUCAAAUGGCUGAGAAGA	1766	gsasuaucAfaAfUfGfgcugagaagaL96	2862	sense	21
UCUUCUCAGCCAUUUGAUAUCUU	1767	usCfsuucUfcAfGfccauUfuGfauaucsusu	2863	antis	23
AGAUAUCAAAUGGCUGAGAAG	1768	asgsauauCfaAfAfUfggcugagaagL96	2864	sense	21
CUUCUCAGCCAUUUGAUAUCUUC	1769	csUfsucuCfaGfCfcauuUfgAfuaucususc	2865	antis	23
GAAAGUCAUCGACAAGACAUU	1770	gsasaaguCfaUfCfGfacaagacauuL96	2866	sense	21
AAUGUCUUGUCGAUGACUUUCAC	1771	asAfsuguCfuUfGfucgaUfgAfcuuucsasc	2867	antis	23
AAAGUCAUCGACAAGACAUUG	1772	asasagucAfuCfGfAfcaagacauugL96	2868	sense	21
CAAUGUCUUGUCGAUGACUUUCA	1773	csAfsaugUfcUfUfgucgAfuGfacuuuscsa	2869	antis	23
AUGUGAAAGUCAUCGACAAGA	1774	asusgugaAfaGfUfCfaucgacaagaL96	2870	sense	21
UCUUGUCGAUGACUUUCACAUUC	1775	usCfsuugUfcGfAfugacUfuUfcacaususc	2871	antis	23
AAUGUGAAAGUCAUCGACAAG	1776	asasugugAfaAfGfUfcaucgacaagL96	2872	sense	21
CUUGUCGAUGACUUUCACAUUCU	1777	csUfsuguCfgAfUfgacuUfuCfacauuscsu	2873	antis	23
GGCUAAUUUGUAUCAAUGAUU	1778	gsgscuaaUfuUfGfUfaucaaugauuL96	2874	sense	21
AAUCAUUGAUACAAAUUAGCCGG	1779	asAfsucaUfuGfAfuacaAfaUfuagccsgsg	2875	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GCUAAUUUGUAUCAAUGAUUA	1780	gscsuaauUfuGfUfAfucaaugauuaL96	2876	sense	21
UAAUCAUUGAUACAAAUUAGCCG	1781	usAfsaucAfuUfGfauacAfaAfuuagcscsg	2877	antis	23
CCCCGGCUAAUUUGUAUCAAU	1782	cscsccggCfuAfAfUfuuguaucaauL96	2878	sense	21
AUUGAUACAAAUUAGCCGGGGGA	1783	asUfsugaUfaCfAfaauuAfgCfcggggsgsa	2879	antis	23
CCCCCGGCUAAUUUGUAUCAA	1784	cscsccccgGfcUfAfAfuuuguaucaaL96	2880	sense	21
UUGAUACAAAUUAGCCGGGGGAG	1785	usUfsgauAfcAfAfauuaGfcCfgggggsasg	2881	antis	23
UGUCGACUUCUGUUUUAGGAC	1786	usgsucgaCfuUfCfUfguuuuaggacL96	2882	sense	21
GUCCUAAAACAGAAGUCGACAGA	1787	gsUfsccuAfaAfAfcagaAfgUfcgacasgsa	2883	antis	23
GUCGACUUCUGUUUUAGGACA	1788	gsuscgacUfuCfUfGfuuuuaggacaL96	2884	sense	21
UGUCCUAAAACAGAAGUCGACAG	1789	usGfsuccUfaAfAfacagAfaGfucgacsasg	2885	antis	23
GAUCUGUCGACUUCUGUUUUA	1790	gsasucugUfcGfAfCfuucuguuuuaL96	2886	sense	21
UAAAACAGAAGUCGACAGAUCUG	1791	usAfsaaaCfaGfAfagucGfaCfagaucsusg	2887	antis	23
AGAUCUGUCGACUUCUGUUUU	1792	asgsaucuGfuCfGfAfcuucuguuuuL96	2888	sense	21
AAAACAGAAGUCGACAGAUCUGU	1793	asAfsaacAfgAfAfgucgAfcAfgaucusgsu	2889	antis	23
CCGAGAAGUCACCAAGAAGCU	1794	cscsgagaAfgUfCfAfccaagaagcuL96	2890	sense	21
AGCUUCUUGGUGACUUCUCGGUC	1795	asGfscuuCfuUfGfgugaCfuUfcucggsusc	2891	antis	23
CGAGAAGUCACCAAGAAGCUA	1796	csgsagaaGfuCfAfCfcaagaagcuaL96	2892	sense	21
UAGCUUCUUGGUGACUUCUCGGU	1797	usAfsgcuUfcUfUfggugAfcUfucucgsgsu	2893	antis	23
AGGACCGAGAAGUCACCAAGA	1798	asgsgaccGfaGfAfAfgucaccaagaL96	2894	sense	21
UCUUGGUGACUUCUCGGUCCUUG	1799	usCfsuugGfuGfAfcuucUfcGfguccususg	2895	antis	23
AAGGACCGAGAAGUCACCAAG	1800	asasggacCfgAfGfAfagucaccaagL96	2896	sense	21
CUUGGUGACUUCUCGGUCCUUGU	1801	csUfsuggUfgAfCfuucuCfgGfuccuusgsu	2897	antis	23
AAACAUGGCUUGAAUGGGAUC	1802	asasacauGfgCfUfUfgaaugggaucL96	2898	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
GAUCCCAUUCAAGC CAUGUUUAA	1803	gsAfsuccCfaUfUfcaag CfcAfuguuusasa	2899	antis	23
AACAUGGCUUGAAU GGGAUCU	1804	asascaugGfcUfUfGfaa ugggaucuL96	2900	sense	21
AGAUCCCAUUCAAG CCAUGUUUA	1805	asGfsaucCfcAfUfucaa GfcCfauguususa	2901	antis	23
UGUUAAACAUGGCU UGAAUGG	1806	usgsuuaaAfcAfUfGfgc uugaauggL96	2902	sense	21
CCAUUCAAGCCAUG UUUAACAGC	1807	csCfsauuCfaAfGfccau GfuUfuaacasgsc	2903	antis	23
CUGUUAAACAUGGC UUGAAUG	1808	csusguuaAfaCfAfUfgg cuugaaugL96	2904	sense	21
CAUUCAAGCCAUGU UUAACAGCC	1809	csAfsuucAfaGfCfcaug UfuUfaacagscsc	2905	antis	23
GACUUGCUGCAUAU GUGGCUA	1810	gsascuugCfuGfCfAfua uguggcuaL96	2906	sense	21
UAGCCACAUAUGCA GCAAGUCCA	1811	usAfsgccAfcAfUfaugc AfgCfaagucscsa	2907	antis	23
ACUUGCUGCAUAUG UGGCUAA	1812	ascsuugcUfgCfAfUfau guggcuaaL96	2908	sense	21
UUAGCCACAUAUGC AGCAAGUCC	1813	usUfsagcCfaCfAfuaug CfaGfcaaguscsc	2909	antis	23
AGUGGACUUGCUGC AUAUGUG	1814	asgsuggaCfuUfGfCfug cauaugugL96	2910	sense	21
CACAUAUGCAGCAA GUCCACUGU	1815	csAfscauAfuGfCfagca AfgUfccacusgsu	2911	antis	23
CAGUGGACUUGCUG CAUAUGU	1816	csasguggAfcUfUfGfcu gcauauguL96	2912	sense	21
ACAUAUGCAGCAAG UCCACUGUC	1817	asCfsauaUfgCfAfgcaa GfuCfcacugsusc	2913	antis	23
UAAAUCAGUACUUC CAAAGUC	1818	usasaaucAfgUfAfCfuu ccaaagucL96	2914	sense	21
GACUUUGGAAGUAC UGAUUUAGC	1819	gsAfscuuUfgGfAfagua CfuGfauuuasgsc	2915	antis	23
AAAUCAGUACUUCC AAAGUCU	1820	asasaucaGfuAfCfUfuc caaagucuL96	2916	sense	21
AGACUUUGGAAGUA CUGAUUUAG	1821	asGfsacuUfuGfGfaagu AfcUfgauuusasg	2917	antis	23
AUGCUAAAUCAGUA CUUCCAA	1822	asusgcuaAfaUfCfAfgu acuuccaaL96	2918	sense	21
UUGGAAGUACUGAU UUAGCAUGU	1823	usUfsggaAfgUfAfcuga UfuUfagcausgsu	2919	antis	23
CAUGCUAAAUCAGU ACUUCCA	1824	csasugcuAfaAfUfCfag uacuuccaL96	2920	sense	21
UGGAAGUACUGAUU UAGCAUGUU	1825	usGfsgaaGfuAfCfugau UfuAfgcaugsusu	2921	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UCCUCAAUUGAAGA AGUGGCG	1826	uscscucaAfuUfGfAfag aaguggcgL96	2922	sense	21
CGCCACUUCUUCAA UUGAGGAGG	1827	csGfsccaCfuUfCfuuca AfuUfgaggasgsg	2923	antis	23
CCUCAAUUGAAGAA GUGGCGG	1828	cscsucaaUfuGfAfAfga aguggcggL96	2924	sense	21
CCGCCACUUCUUCA AUUGAGGAG	1829	csCfsgccAfcUfUfcuuc AfaUfugaggsasg	2925	antis	23
CACCUCCUCAAUUG AAGAAGU	1830	csasccucCfuCfAfAfuu gaagaaguL96	2926	sense	21
ACUUCUUCAAUUGA GGAGGUGGC	1831	asCfsuucUfuCfAfauug AfgGfaggugsgsc	2927	antis	23
CCACCUCCUCAAUU GAAGAAG	1832	cscsaccuCfcUfCfAfau ugaagaagL96	2928	sense	21
CUUCUUCAAUUGAG GAGGUGGCC	1833	csUfsucuUfcAfAfuuga GfgAfgguggscsc	2929	antis	23
CAAGAUGUCCUCGA GAUACUA	1834	csasagauGfuCfCfUfcg agauacuaL96	2930	sense	21
UAGUAUCUCGAGGA CAUCUUGAA	1835	usAfsguaUfcUfCfgagg AfcAfucuugsasa	2931	antis	23
AAGAUGUCCUCGAG AUACUAA	1836	asasgaugUfcCfUfCfga gauacuaaL96	2932	sense	21
UUAGUAUCUCGAGG ACAUCUUGA	1837	usUfsaguAfuCfUfcgag GfaCfaucuusgsa	2933	antis	23
UGUUCAAGAUGUCC UCGAGAU	1838	usgsuucaAfgAfUfGfuc cucgagauL96	2934	sense	21
AUCUCGAGGACAUC UUGAACACC	1839	asUfscucGfaGfGfacau CfuUfgaacascsc	2935	antis	23
GUGUUCAAGAUGUC CUCGAGA	1840	gsusguucAfaGfAfUfgu ccucgagaL96	2936	sense	21
UCUCGAGGACAUCU UGAACACCU	1841	usCfsucgAfgGfAfcauc UfuGfaacacscsu	2937	antis	23
ACAUGCUAAAUCAG UACUUCC	1842	ascsaugcUfaAfAfUfca guacuuccL96	2938	sense	21
GGAAGUACUGAUUU AGCAUGUUG	1843	gsGfsaagUfaCfUfgauu UfaGfcaugususg	2939	antis	23
CAUGCUAAAUCAGU ACUUCCA	1844	csasugcuAfaAfUfCfag uacuuccaL96	2940	sense	21
UGGAAGUACUGAUU UAGCAUGUU	1845	usGfsgaaGfuAfCfugau UfuAfgcaugsusu	2941	antis	23
AACAACAUGCUAAA UCAGUAC	1846	asascaacAfuGfCfUfaa aucaguacL96	2942	sense	21
GUACUGAUUUAGCA UGUUGUUCA	1847	gsUfsacuGfaUfUfuagc AfuGfuuguuscsa	2943	antis	23
GAACAACAUGCUAA AUCAGUA	1848	gsasacaaCfaUfGfCfua aaucaguaL96	2944	sense	21

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
UACUGAUUUAGCAUGUUGUUCAU	1849	usAfscugAfuUfUfagcaUfgUfuguucsasu	2945	antis	23
GAAAGGCACUGAUGUUCUGAA	1850	gsasaaggCfaCfUfGfauguucugaaL96	2946	sense	21
UUCAGAACAUCAGUGCCUUUCCG	1851	usUfscagAfaCfAfucagUfgCfcuuucscsg	2947	antis	23
AAAGGCACUGAUGUUCUGAAA	1852	asasaggcAfcUfGfAfuguucugaaaL96	2948	sense	21
UUUCAGAACAUCAGUGCCUUUCC	1853	usUfsucaGfaAfCfaucaGfuGfccuuuscsc	2949	antis	23
UGCGGAAAGGCACUGAUGUUC	1854	usgscggaAfaGfGfCfacugauguucL96	2950	sense	21
GAACAUCAGUGCCUUUCCGCACA	1855	gsAfsacaUfcAfGfugccUfuUfccgcascsa	2951	antis	23
GUGCGGAAAGGCACUGAUGUU	1856	gsusgcggAfaAfGfGfcacugauguuL96	2952	sense	21
AACAUCAGUGCCUUUCCGCACAC	1857	asAfscauCfaGfUfgccuUfuCfcgcacsasc	2953	antis	23
GUCAGCAUGCCAAUAUGUGUG	1858	gsuscagcAfuGfCfCfaauaugugugL96	2954	sense	21
CACACAUAUUGGCAUGCUGACCC	1859	csAfscacAfuAfUfuggcAfuGfcugacscsc	2955	antis	23
UCAGCAUGCCAAUAUGUGUGG	1860	uscsagcaUfgCfCfAfauaugugguggL96	2956	sense	21
CCACACAUAUUGGCAUGCUGACC	1861	csCfsacaCfaUfAfuuggCfaUfgcugascsc	2957	antis	23
GAGGGUCAGCAUGCCAAUAUG	1862	gsasggguCfaGfCfAfugccaauaugL96	2958	sense	21
CAUAUUGGCAUGCUGACCCUCUG	1863	csAfsuauUfgGfCfaugcUfgAfcccucsusg	2959	antis	23
AGAGGGUCAGCAUGCCAAUAU	1864	asgsagggUfcAfGfCfaugccaauauL96	2960	sense	21
AUAUUGGCAUGCUGACCCUCUGU	1865	asUfsauuGfgCfAfugcuGfaCfccucusgsu	2961	antis	23
GAUGCUCCGGAAUGUUGCUGA	1866	gsasugcuCfcGfGfAfauguugcugaL96	2962	sense	21
UCAGCAACAUUCCGGAGCAUCCU	1867	usCfsagcAfaCfAfuuccGfgAfgcaucscsu	2963	antis	23
AUGCUCCGGAAUGUUGCUGAA	1868	asusgcucCfgGfAfAfuguugcugaaL96	2964	sense	21
UUCAGCAACAUUCCGGAGCAUCC	1869	usUfscagCfaAfCfauucCfgGfagcauscsc	2965	antis	23
CAAGGAUGCUCCGGAAUGUUG	1870	csasaggaUfgCfUfCfcggaauguugL96	2966	sense	21
CAACAUUCCGGAGCAUCCUUGGA	1871	csAfsacaUfuCfCfggagCfaUfccuugsgsa	2967	antis	23

Unmodified sequence	SEQ ID NO:	Modified sequence	SEQ ID NO:	strand	Length
CCAAGGAUGCUCCG GAAUGUU	1872	cscsaaggAfuGfCfUfcc ggaauguuL96	2968	sense	21
AACAUUCCGGAGCA UCCUUGGAU	1873	asAfscauUfcCfGfgagc AfuCfcuuggsasu	2969	antis	23
GCGUAACAGAUUCA AACUGCC	1874	gscsguaaCfaGfAfUfuc aaacugccL96	2970	sense	21
GGCAGUUUGAAUCU GUUACGCAC	1875	gsGfscagUfuUfGfaauc UfgUfuacgcsasc	2971	antis	23
CGUAACAGAUUCAA ACUGCCG	1876	csgsuaacAfgAfUfUfca aacugccgL96	2972	sense	21
CGGCAGUUUGAAUC UGUUACGCA	1877	csGfsgcaGfuUfUfgaau CfuGfuuacgscsa	2973	antis	23
AUGUGCGUAACAGA UUCAAAC	1878	asusgugcGfuAfAfCfag auucaaacL96	2974	sense	21
GUUUGAAUCUGUUA CGCACAUCA	1879	gsUfsuugAfaUfCfuguu AfcGfcacauscsa	2975	antis	23
GAUGUGCGUAACAG AUUCAAA	1880	gsasugugCfgUfAfAfca gauucaaaL96	2976	sense	21
UUUGAAUCUGUUAC GCACAUCAU	1881	usUfsugaAfuCfUfguua CfgCfacaucsasu	2977	antis	23
AGAGAAGAUGGGCU ACAAGGC	1882	asgsagaaGfaUfGfGfgc uacaaggcL96	2978	sense	21
GCCUUGUAGCCCAU CUUCUCUGC	1883	gsCfscuuGfuAfGfccca UfcUfucucusgsc	2979	antis	23
GAGAAGAUGGGCUA CAAGGCC	1884	gsasgaagAfuGfGfGfcu acaaggccL96	2980	sense	21
GGCCUUGUAGCCCA UCUUCUCUG	1885	gsGfsccuUfgUfAfgccc AfuCfuucucsusg	2981	antis	23
AGGCAGAGAAGAUG GGCUACA	1886	asgsgcagAfgAfAfGfau gggcuacaL96	2982	sense	21
UGUAGCCCAUCUUC UCUGCCUGC	1887	usGfsuagCfcCfAfucuu CfuCfugccusgsc	2983	antis	23
CAGGCAGAGAAGAU GGGCUAC	1888	csasggcaGfaGfAfAfga ugggcuacL96	2984	sense	21
GUAGCCCAUCUUCU CUGCCUGCC	1889	gsUfsagcCfcAfUfcuuc UfcUfgccugscsc	2985	antis	23

We claim:

1. A double stranded RNAi agent capable of inhibiting expression of HAO1 in a cell, wherein said double stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:1 SEQ ID NO:2, SEQ ID NO:5, or SEQ ID NO:6 and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:3 SEQ ID NO:4, SEQ ID NO:7, or SEQ ID NO:8;

wherein substantially all of the nucleotides of said sense strand and substantially all of the nucleotides of said antisense strand are modified nucleotides,

wherein at least one of said modified nucleotides is selected from the group consisting of 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 abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a nucleotide comprising a 5'-phosphorothioate group, a nucleotide comprising a 5' phosphate or 5' phosphate mimic, and a terminal nucleotide linked to a cholesteryl derivative or a dodecanoic acid bisdecylamide group, and

wherein said sense strand is conjugated to a ligand attached at the 3'-terminus.

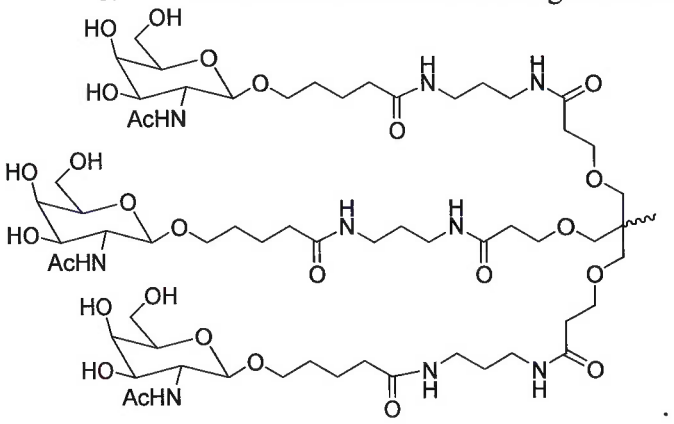
2. The double stranded RNAi agent of claim 1, wherein all of the nucleotides of said sense strand and all of the nucleotides of said antisense strand are modified nucleotides.

3. The double stranded RNAi agent of claim 1, wherein said sense strand and said antisense strand comprise a region of complementarity which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the antisense sequences listed in Table 2.

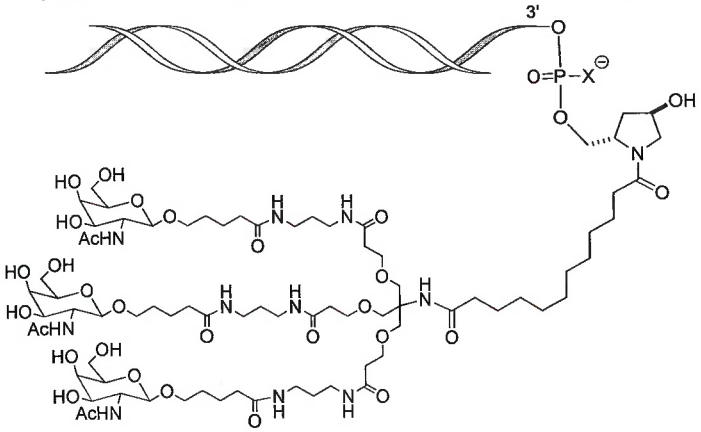
4. The double stranded RNAi agent of any claim 1, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.

5. The double stranded RNAi agent of claim 1, wherein at least one strand comprises a 3' overhang of at least 2 nucleotides.

6. The double stranded RNAi agent of claim 1, wherein the ligand is



7. The double stranded RNAi agent of claim 1, wherein the RNAi agent is conjugated to the ligand as shown in the following schematic



wherein X is O or S.

8. The double stranded RNAi agent of claim 1, wherein said agent further comprises at least one phosphorothioate or methylphosphonate internucleotide linkage.

9. The double stranded RNAi agent of claim 8, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the 3'-terminus of one strand.

10. The double stranded RNAi agent of claim 8, wherein said RNAi agent comprises 6-8 phosphorothioate internucleotide linkages.

11. The double stranded RNAi of claim 10, wherein the antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and the sense strand comprises at least two phosphorothioate internucleotide linkages at either the 5'-terminus or the 3'-terminus.

12. The double stranded RNAi agent of claim 1, wherein the base pair at the 1 position of the 5'-end of the antisense strand of the duplex is an AU base pair.

13. The double stranded RNAi agent of claim 1, wherein the RNAi agent is selected from the group consisting of AD-62994, AD-62933, and AD-65585.

14. A double stranded RNAi agent capable of inhibiting expression of HAO1 in a cell,

wherein said double stranded RNAi agent comprises a sense strand and an antisense strand forming a double stranded region,

wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of from any one of the nucleotide sequences of SEQ ID NO:1 SEQ ID NO:2, SEQ ID NO:5, or SEQ ID NO:6 and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:3 SEQ ID NO:4, SEQ ID NO:7, or SEQ ID NO:8,

wherein substantially all of the nucleotides of said sense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification,

wherein said sense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus,

wherein substantially all of the nucleotides of said antisense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification,

wherein said antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and

wherein said sense strand is conjugated to one or more GalNAc derivatives attached through a branched bivalent or trivalent linker at the 3'-terminus.

15. The double stranded RNAi agent of claim 14, wherein all of the nucleotides of said sense strand and all of the nucleotides of said antisense strand comprise a modification.

16. An RNAi agent selected from the group of RNAi agents listed in Table 1 or 2.

17. The RNAi agent of claim 14, wherein the RNAi agent is selected from the group consisting of AD-62994, AD-62933, and AD-65585.

18. Use of a double stranded RNAi agent in the manufacture of a medicament for treating a subject having Primary Hyperoxaluria 1 (PH1),

wherein said double stranded RNAi agent comprises a sense strand and an antisense strand forming a double stranded region,

wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of from any one of the nucleotide sequences of SEQ ID NO:1 SEQ ID NO:2, SEQ ID NO:5, or SEQ ID NO:6 and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the nucleotide sequences of SEQ ID NO:3 SEQ ID NO:4, SEQ ID NO:7, or SEQ ID NO:8,

wherein substantially all of the nucleotides of said antisense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoromodification,

wherein said antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus,

wherein substantially all of the nucleotides of said sense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoromodification,

wherein said sense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and,

wherein said sense strand is conjugated to one or more GalNAc derivatives attached through a branched bivalent or trivalent linker at the 3'-terminus.

19. The use of claim of claim 18, wherein all of the nucleotides of said sense strand and all of the nucleotides of said antisense strand comprise a modification.

20. The use of claim 18, wherein the subject is a human.

21. The use of claim 18, wherein the double stranded RNAi agent is to be administered at a dose of 0.01 mg/kg to 10 mg/kg or 1 mg/kg to 10 mg/kg.

22. The use of claim 21, wherein the double stranded RNAi agent is to be administered at a dose of 0.1 mg/kg, 1.0 mg/kg, or 3.0 mg/kg.

23. The use of claim 21, wherein the double stranded RNAi agent is to be administered at a dose of 1 mg/kg to 10 mg/kg.

24. The use of claim 21, wherein the double stranded RNAi agent is to be administered subcutaneously.

25. The use of claim 21, wherein the double stranded RNAi agent is to be administered intravenously.

26. The use of claim 21, wherein said RNAi agent is to be administered in two or more doses.

27. The use of claim 26, wherein said RNAi agent is to be administered at intervals selected from the group consisting of once every about 12 hours, once every about 24 hours, once every about 48 hours, once every about 72 hours, and once every about 96 hours.

28. The use of claim 26, wherein said RNAi agent is to be administered once a week for up to 2 weeks, up to 3 weeks, up to 4 weeks, up to 5 weeks, or longer.