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(54) RNA INTERFERENCE MEDIATED
INHIBITION OF PROPROTEIN
CONVERTASE SUBTILISIN KEXIN 9 (PCSK9)
GENE EXPRESSION USING SHORT
INTERFERING NUCLEIC ACID (SINA)

(76) Inventors: LEONID BEIGELMAN, SAN
MATEO, CA (US); JAMES
MCSWIGGEN, BOTHELL, WA
(US)

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A61P 9/00 (2006.01)

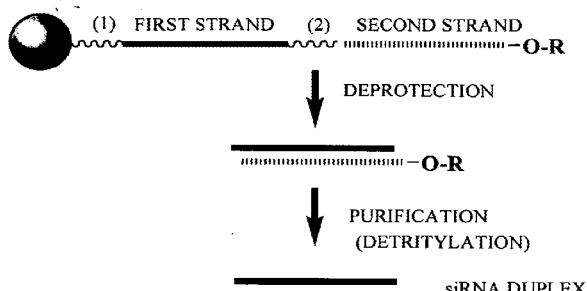
(52) U.S. Cl. 514/44 A; 536/24.5

(57) ABSTRACT

The present invention relates to compounds, compositions, and methods for the study, diagnosis, and treatment of traits, diseases and conditions that respond to the modulation of Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene expression and/or activity. Specifically, the invention relates to double stranded nucleic acid molecules including small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene expression, including cocktails of such small nucleic acid molecules and lipid nanoparticle (LNP) formulations of such small nucleic acid molecules.

Related U.S. Application Data

(63) Continuation of application No. 11/487,788, filed on Jul. 17, 2006, which is a continuation-in-part of application No. 11/369,108, filed on Mar. 6, 2006, now abandoned, which is a continuation-in-part of application No. 10/923,536, filed on Aug. 20, 2004, now abandoned.



 = SOLID SUPPORT

R = TERMINAL PROTECTING GROUP
FOR EXAMPLE:
DIMETHOXYSYTRITYL (DMT)

⁽¹⁾
~~~~~ = CLEAVABLE LINKER  
(FOR EXAMPLE: NUCLEOTIDE SUCCINATE OR  
INVERTED DEOXYABASIC SUCCINATE)

<sup>(2)</sup>  
~~~~~ = CLEAVABLE LINKER  
(FOR EXAMPLE: NUCLEOTIDE SUCCINATE OR
INVERTED DEOXYABASIC SUCCINATE)

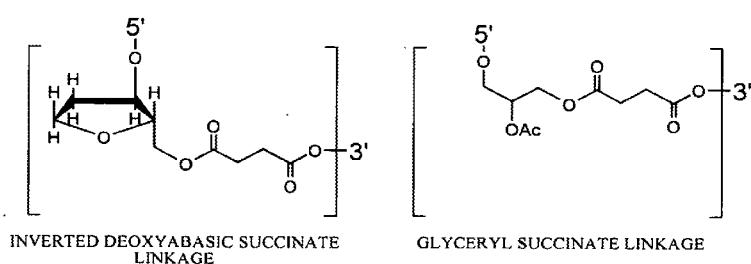


Figure 1

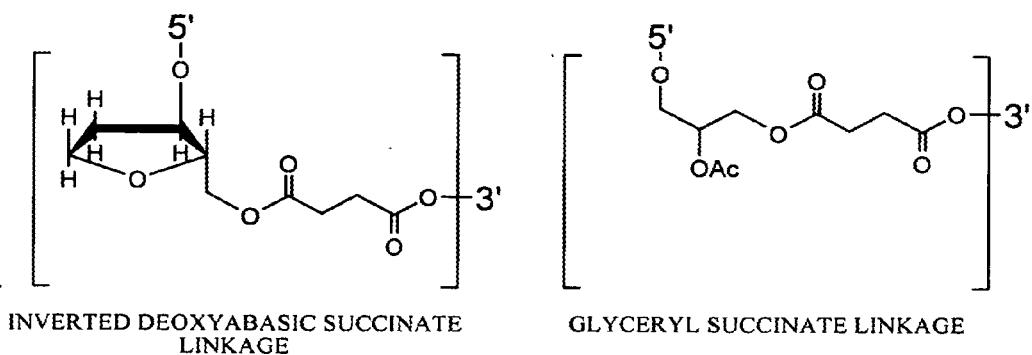
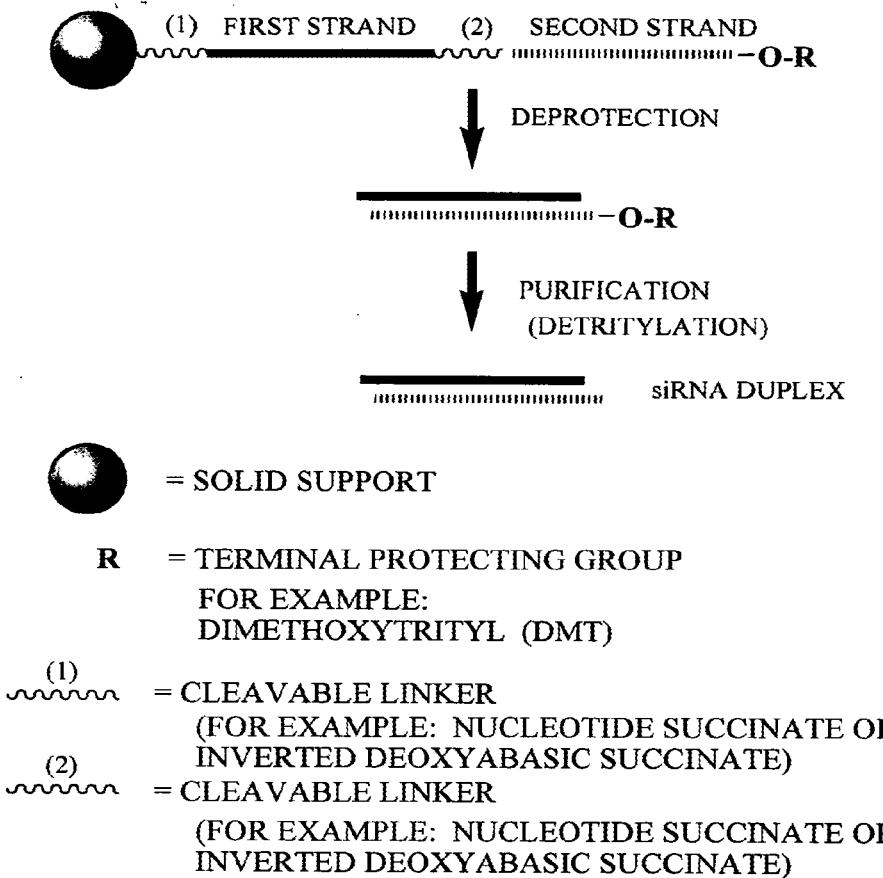


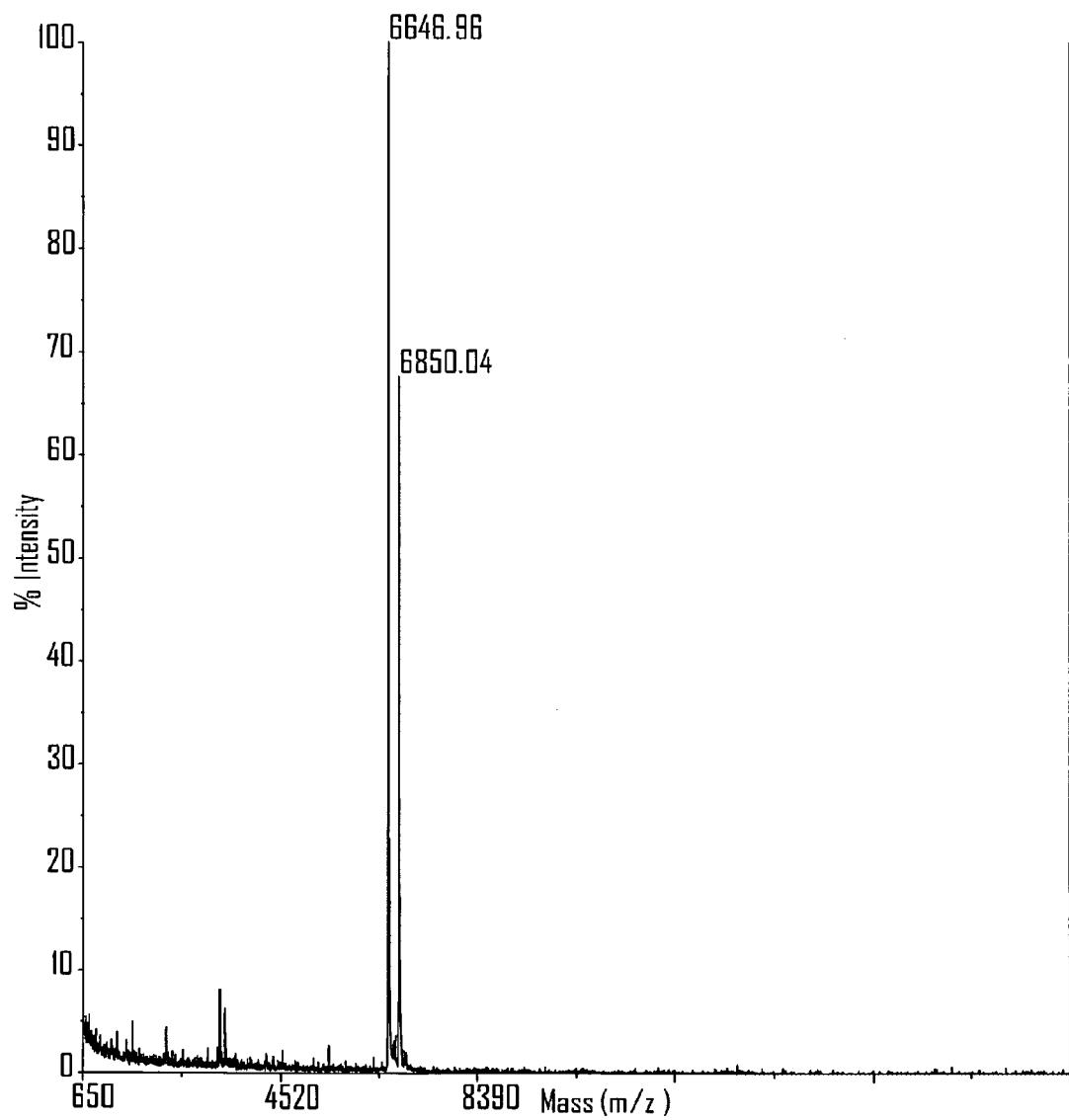
Figure 2

Figure 3

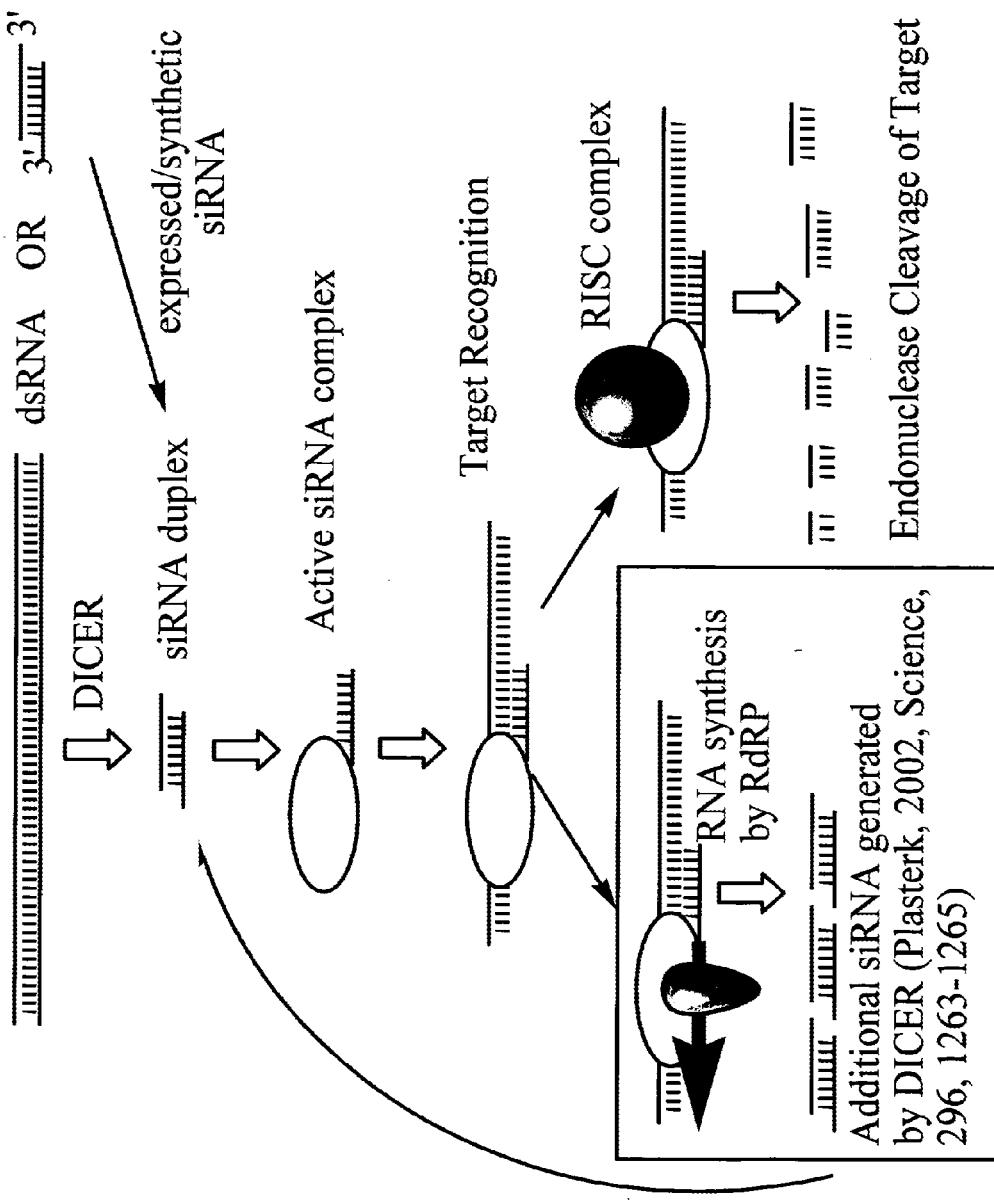


Figure 4

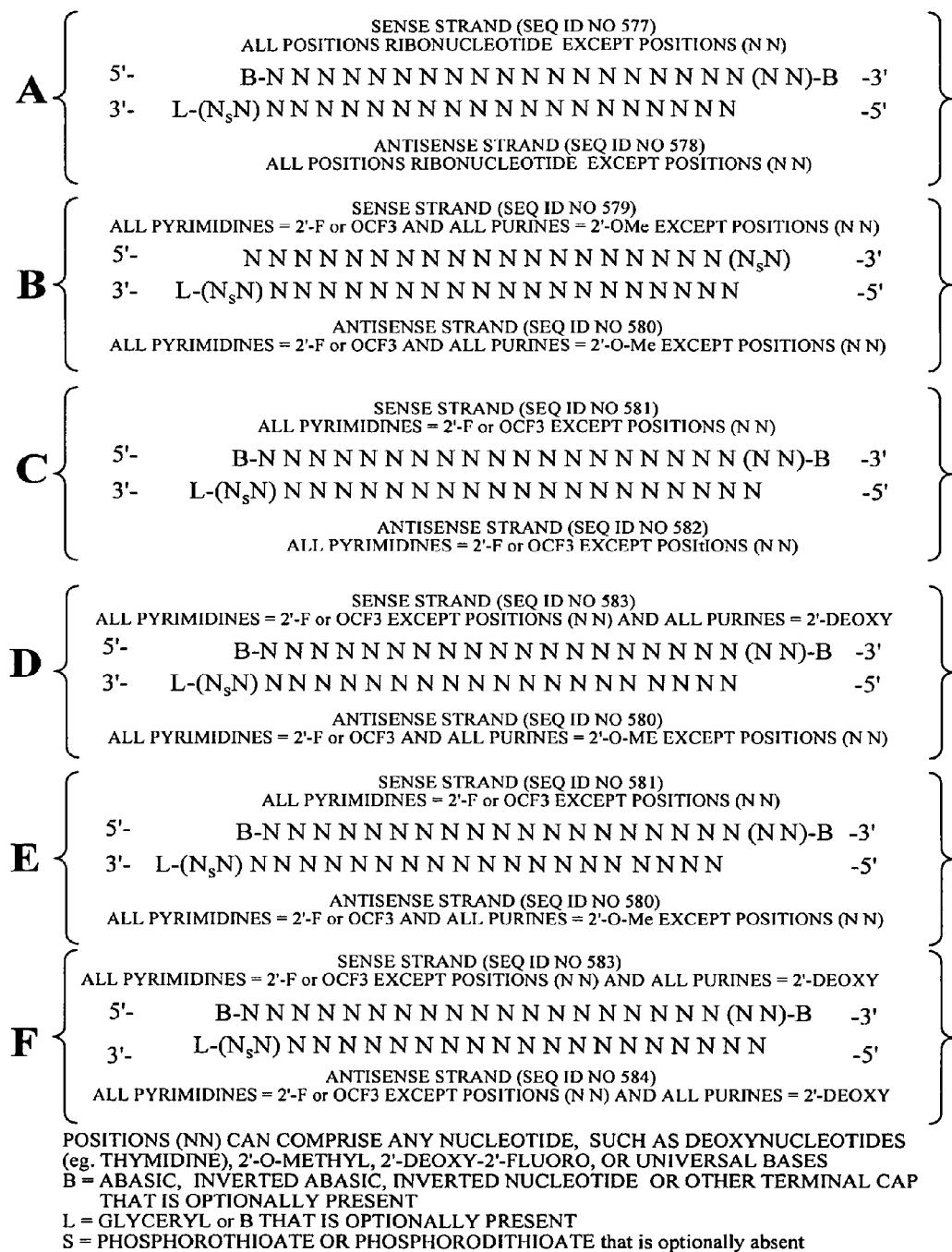
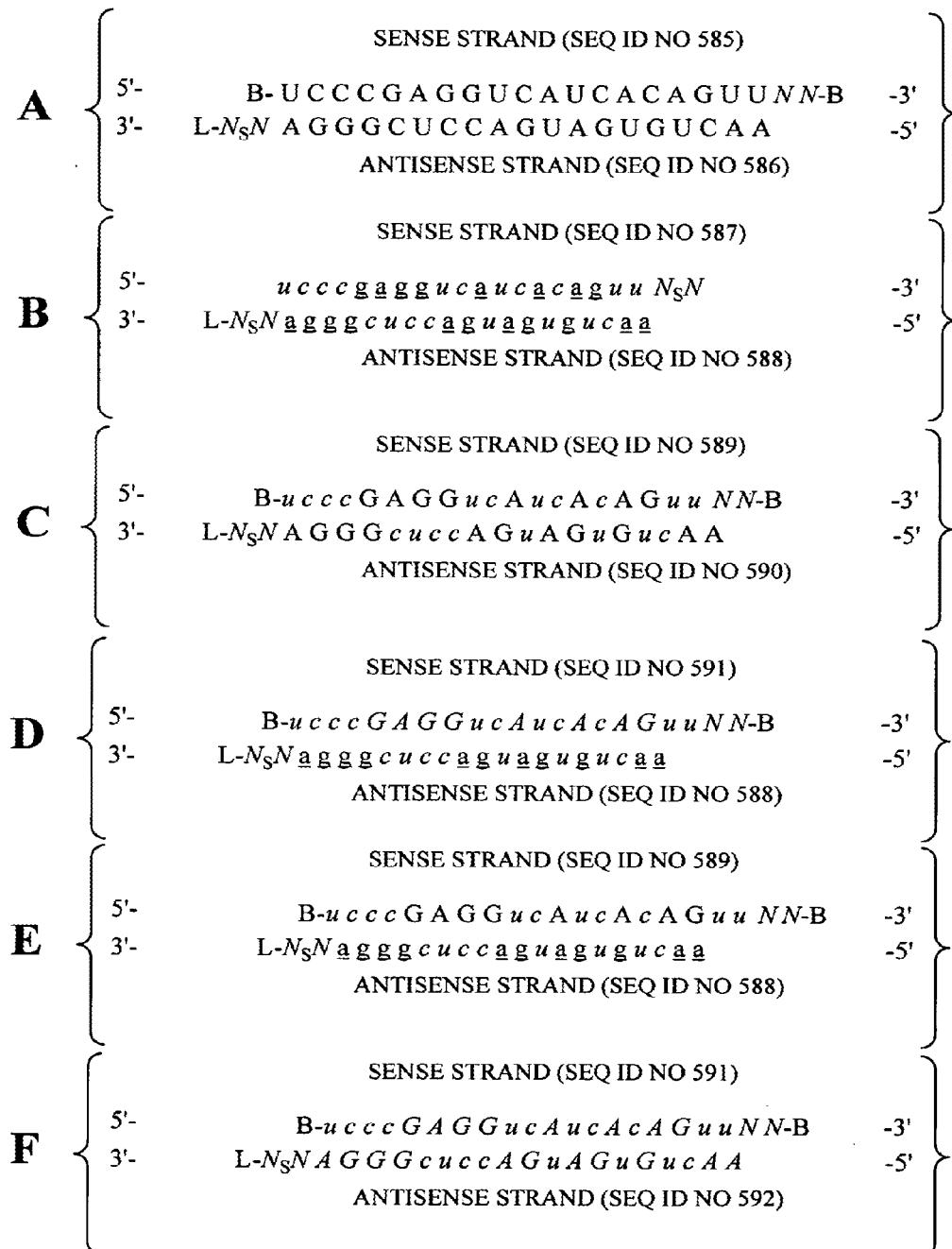


Figure 5



italic lower case = 2'-deoxy-2'-fluoro or 2'-OCF₃
underline = 2'-O-methyl

ITALIC UPPER CASE = DEOXY

N = Deoxy, 2'-OMe, 2'-deoxy-2'-fluoro, LNA etc.

B = ABASIC, INVERTED ABASIC, INVERTED NUCLEOTIDE OR OTHER TERMINAL CAP THAT IS OPTIONALY PRESENT
 L = GLYCERYL MOIETY or B OPTIONALY PRESENT
 S = PHOSPHOROTHIOATE OR PHOSPHORODITHIOATE OPTIONALY PRESENT

Figure 6A

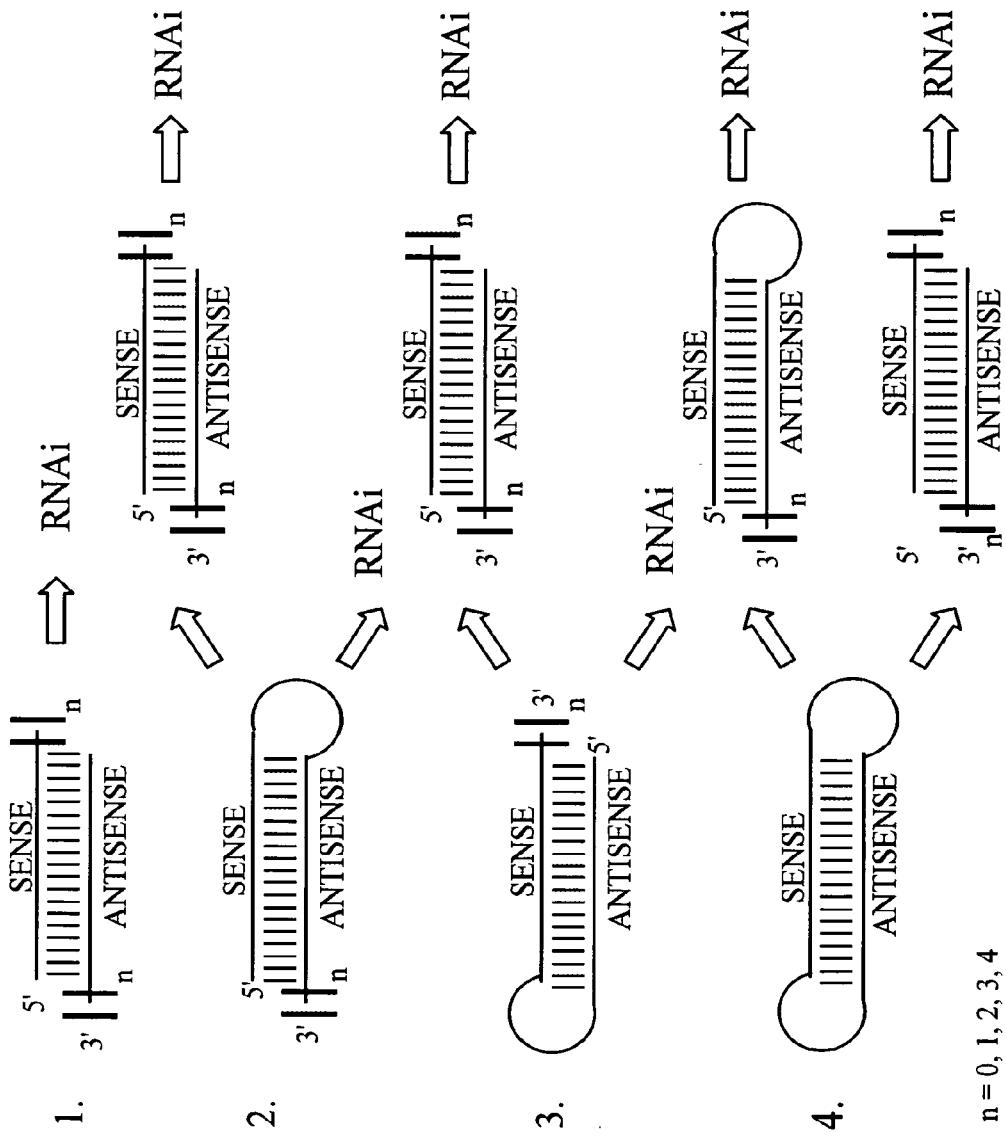


Figure 6B

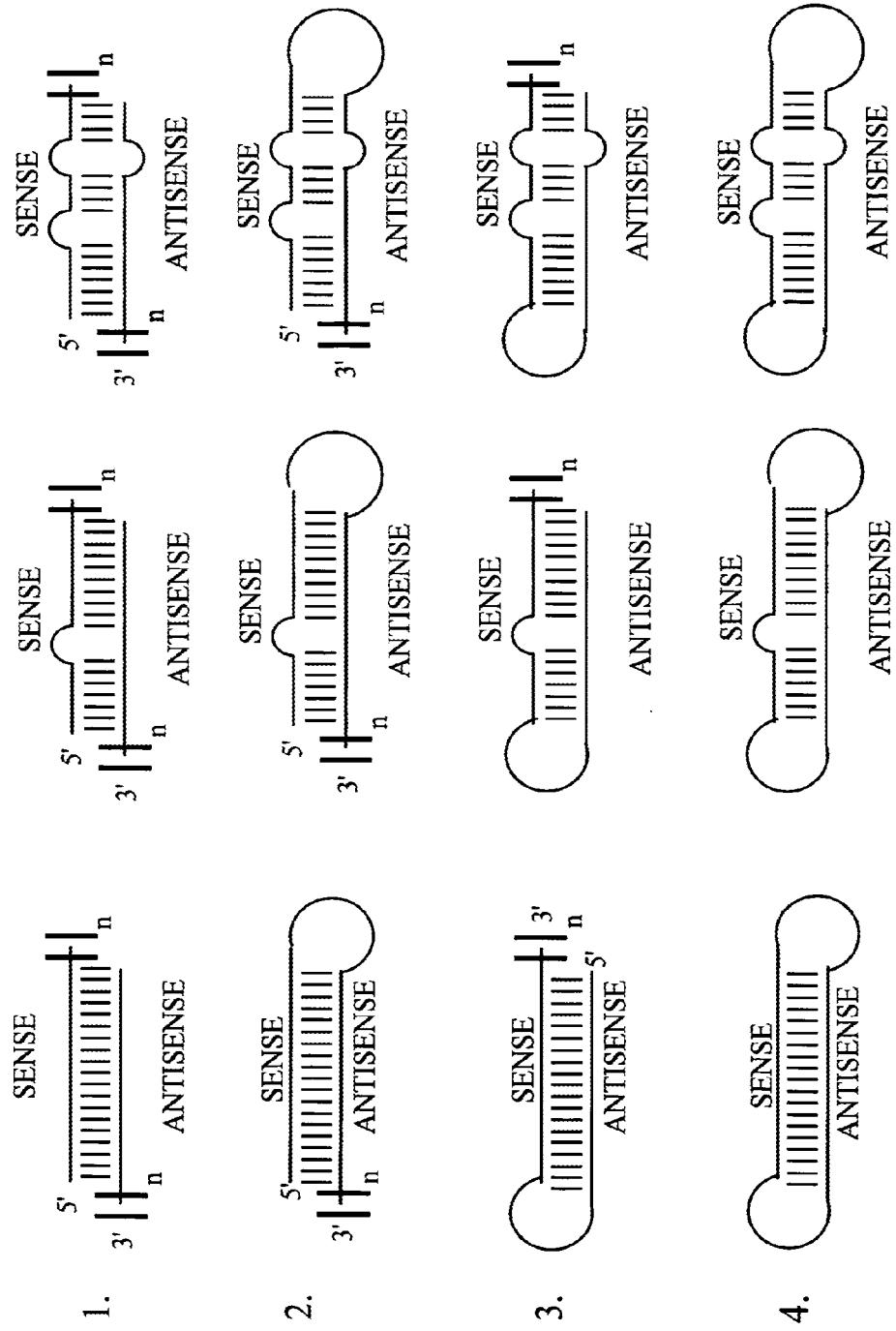
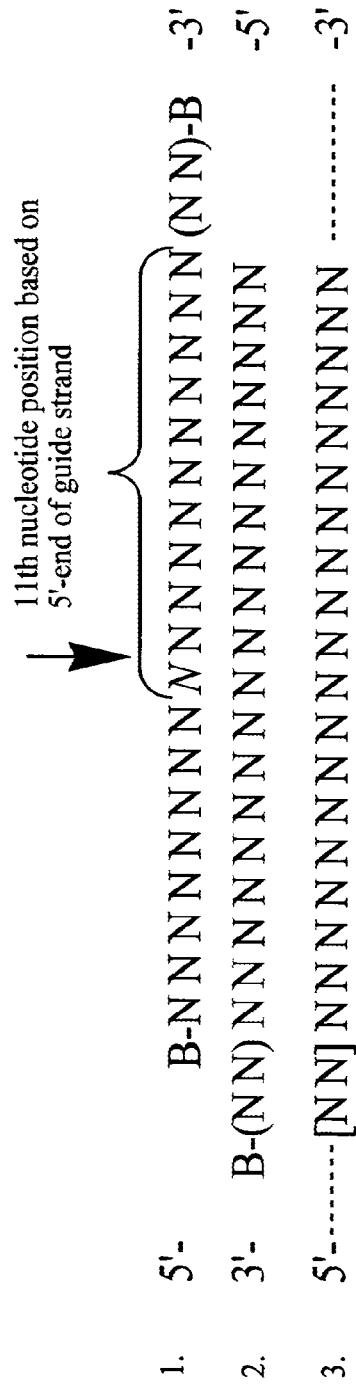


Figure 6C



1. = sense strand (passenger strand)
 2. = antisense strand (guide strand)
 3. = target polynucleotide sequence

The guide strand is complementary to the target sequence and the passenger strand is complementary to the guide strand. Overhang nucleotides (NN) in the guide strand can be complementary to nucleotides [NN] in target sequence.

Overhang nucleotides (NN) in the passenger strand can comprise nucleotides [NN] in target sequence

Position N of the passenger strand can comprise a ribonucleotide. For the representative 19 base pair 21 mer duplex shown, position N is 9 nucleotides in from the 3' end of the passenger strand. However, in duplexes of differing length, the position N is determined based on the 5'-end of the guide strand by counting 11 nucleotide positions in from the 5'-terminus of the guide strand and picking the corresponding base paired nucleotide in the passenger strand. Cleavage by Ago2 takes place

Representative 2 nucleotide overhangs are shown, but can vary for example from 0 to about 4 nucleotides between positions 10 and 11 as indicated by the arrow.

$B =$ terminal cap which can be present or absent
This generalized motif can be applied to all Stab 00-34 chemistries herein.

Figure 7

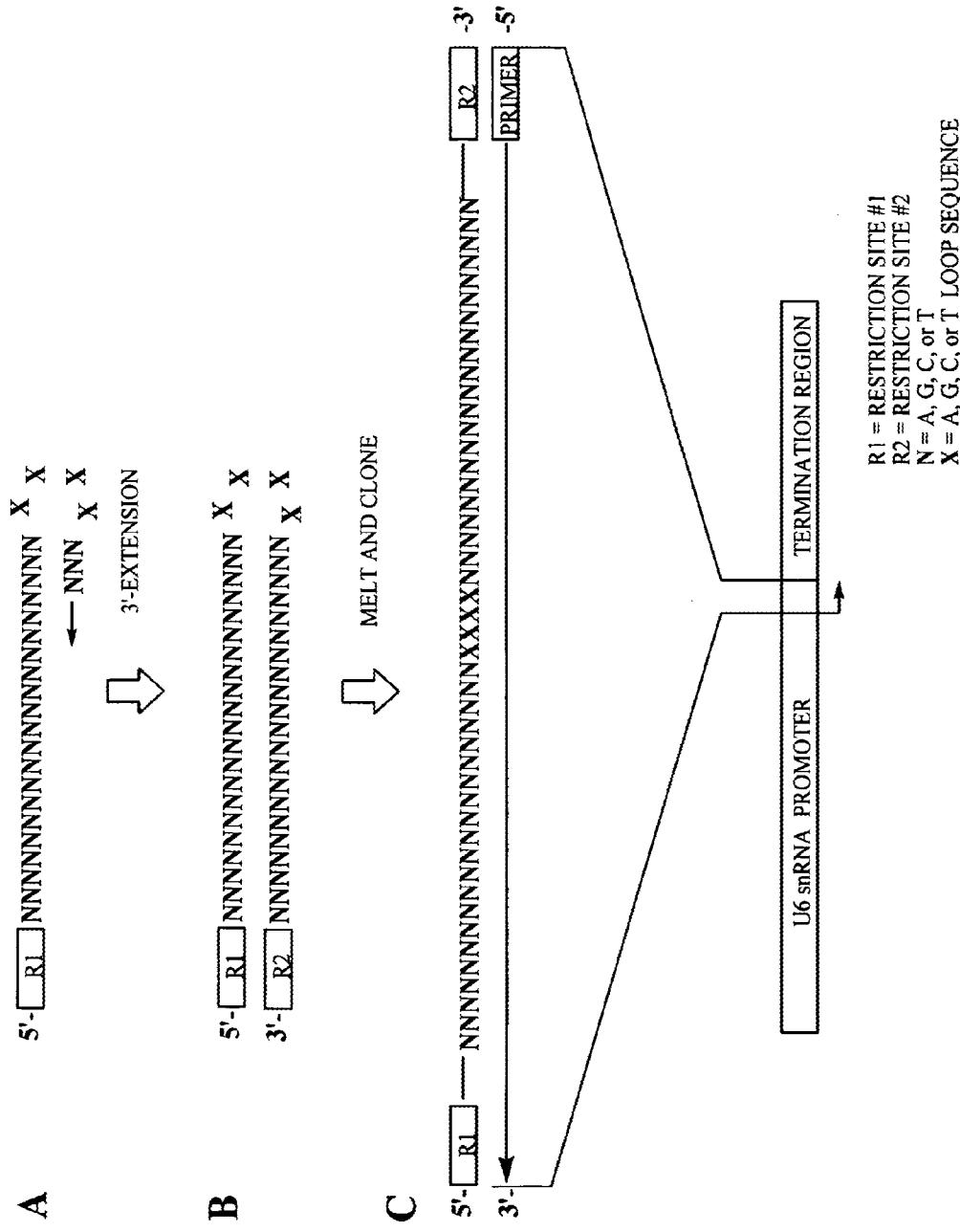


Figure 8

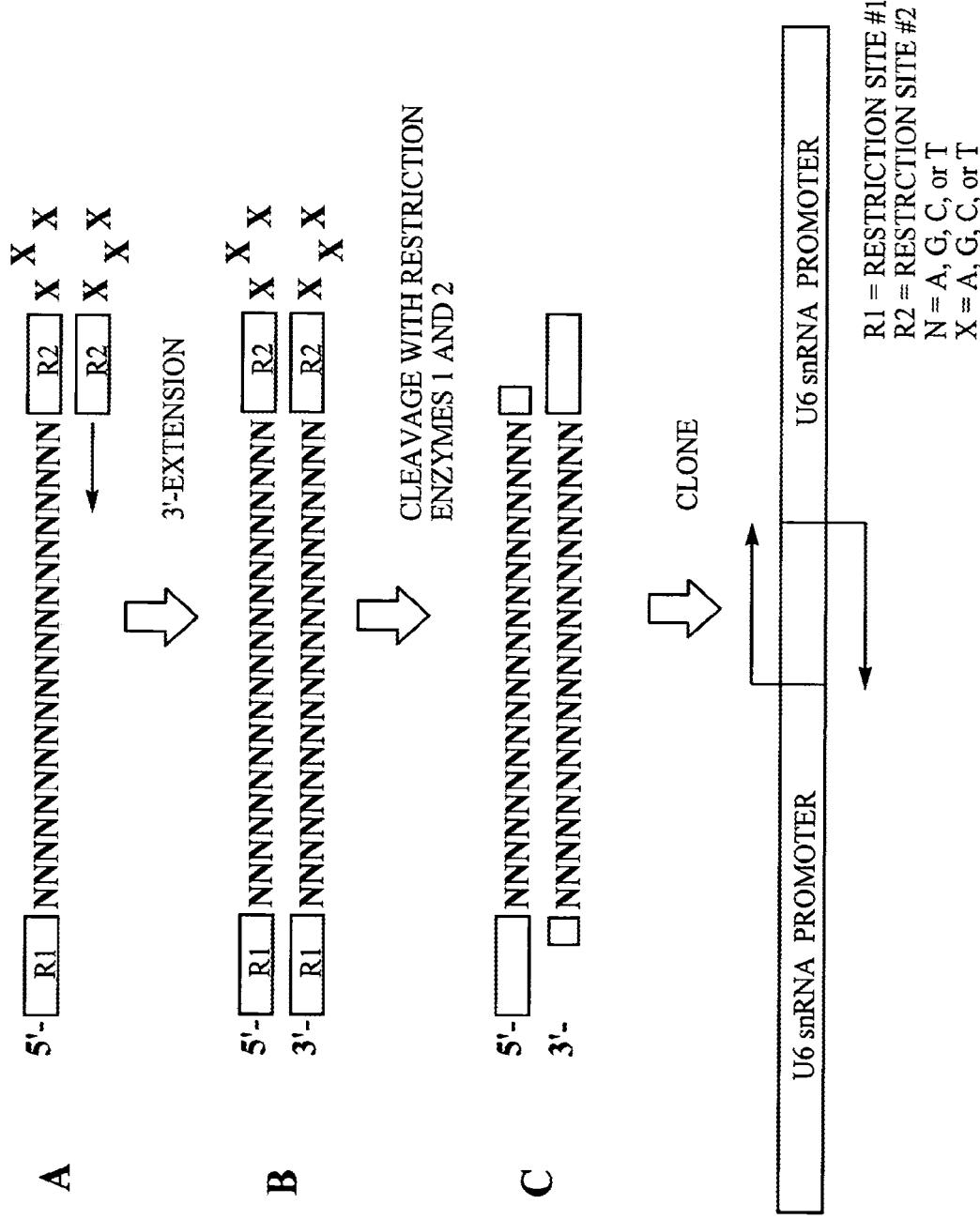


Figure 9: Target site Selection using siRNA

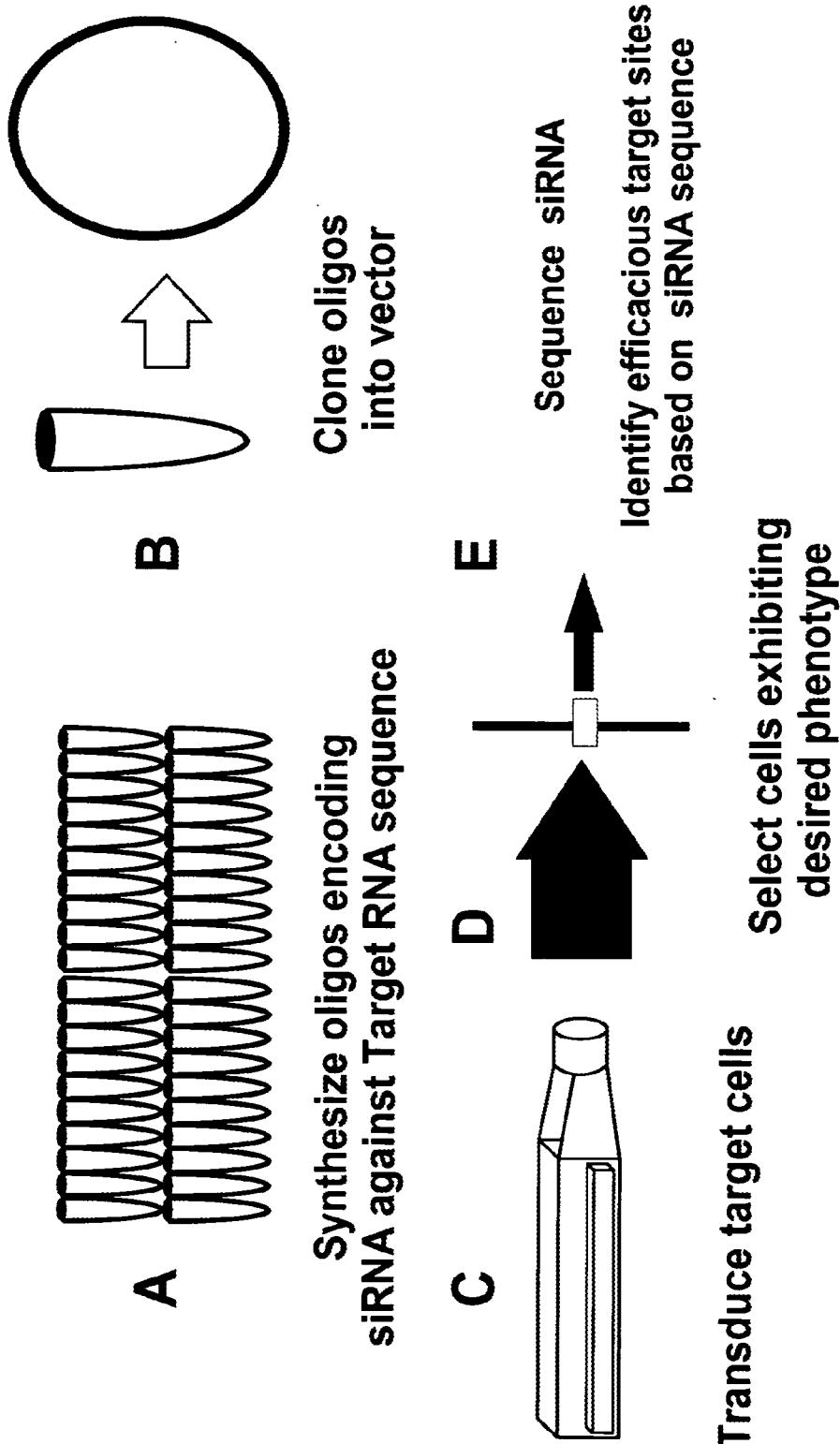
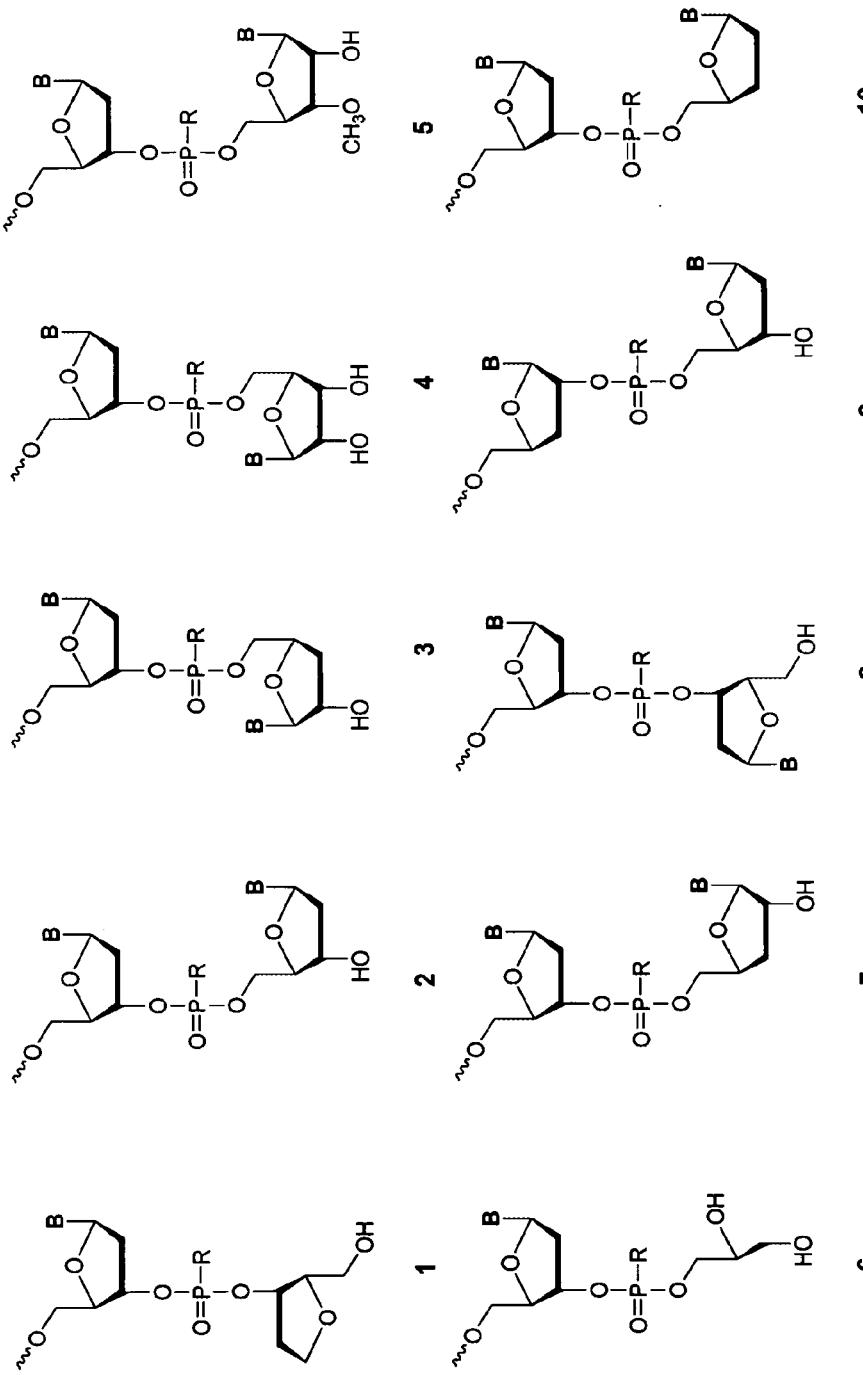


Figure 10



$\text{R} = \text{O}, \text{S}, \text{N}$, alkyl, substituted alkyl, O-alkyl , S-alkyl , alkaryl, or aralkyl
 $\text{B} = \text{Independently any nucleotide base, either naturally occurring or chemically modified, or optionally H (abasic).}$

Figure 11: Modification Strategy

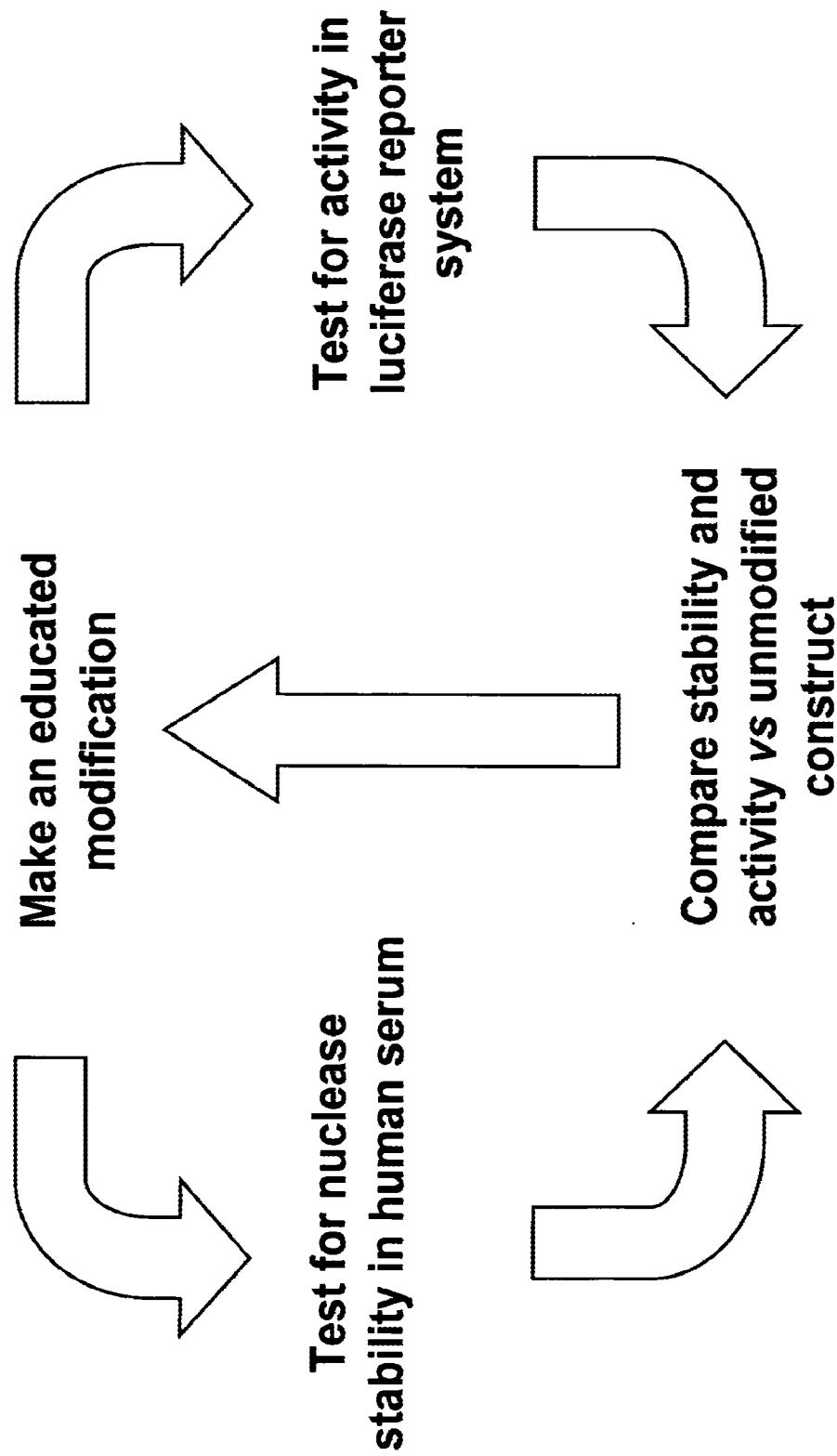


Figure 12: Phosphorylated siNA constructs

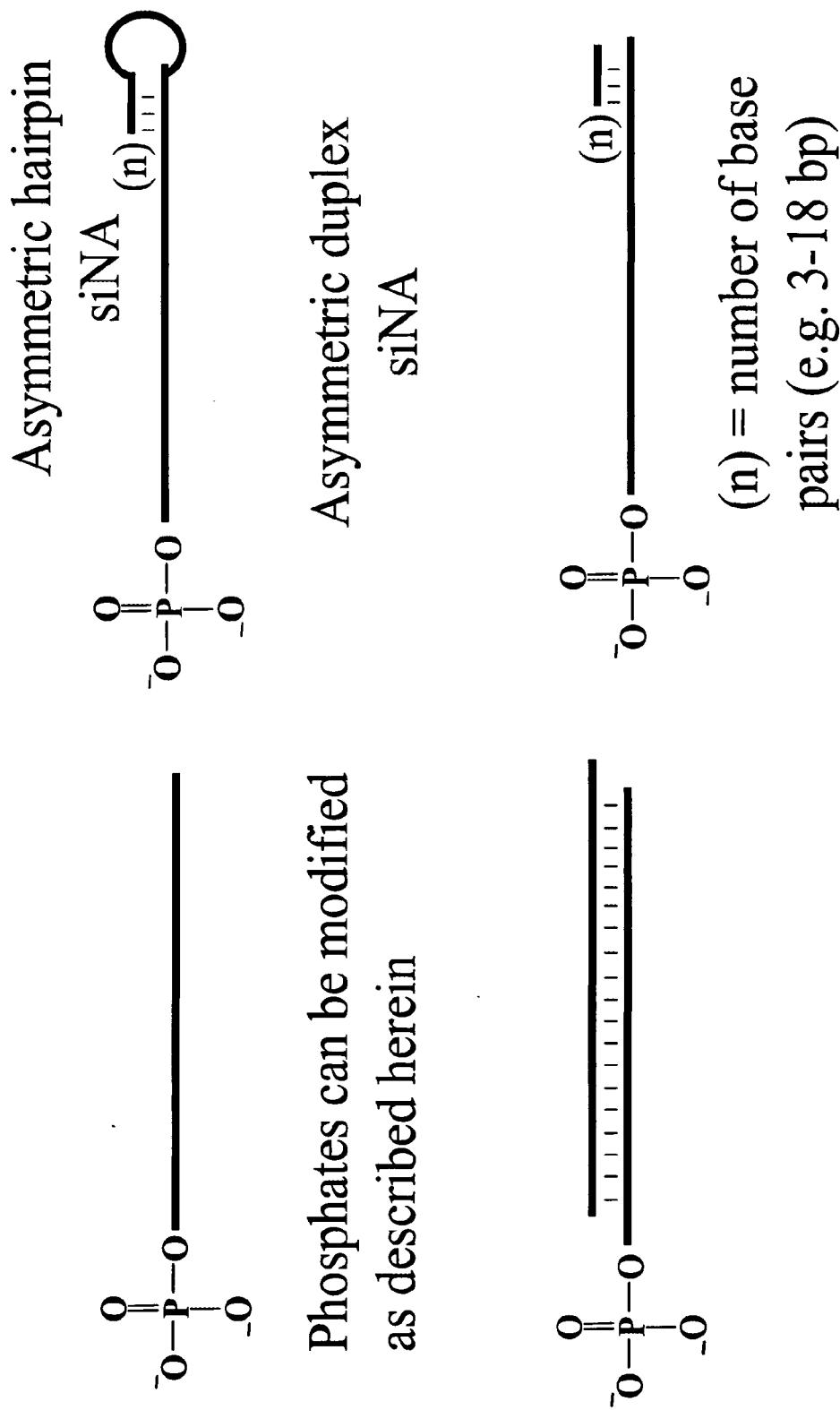


Figure 13: 5'-phosphate modifications

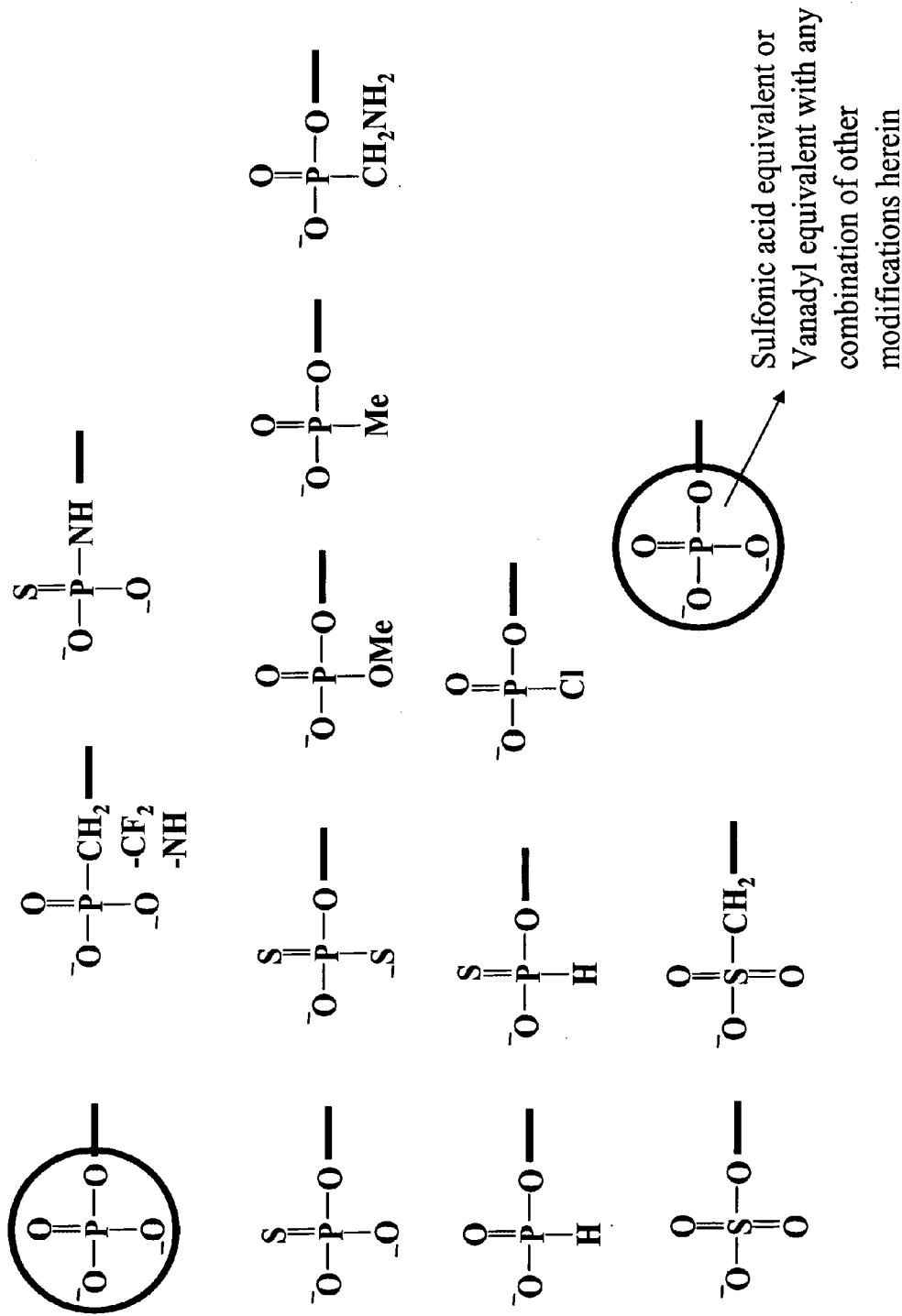


Figure 14A: Duplex forming oligonucleotide constructs that utilize Palindrome or repeat sequences

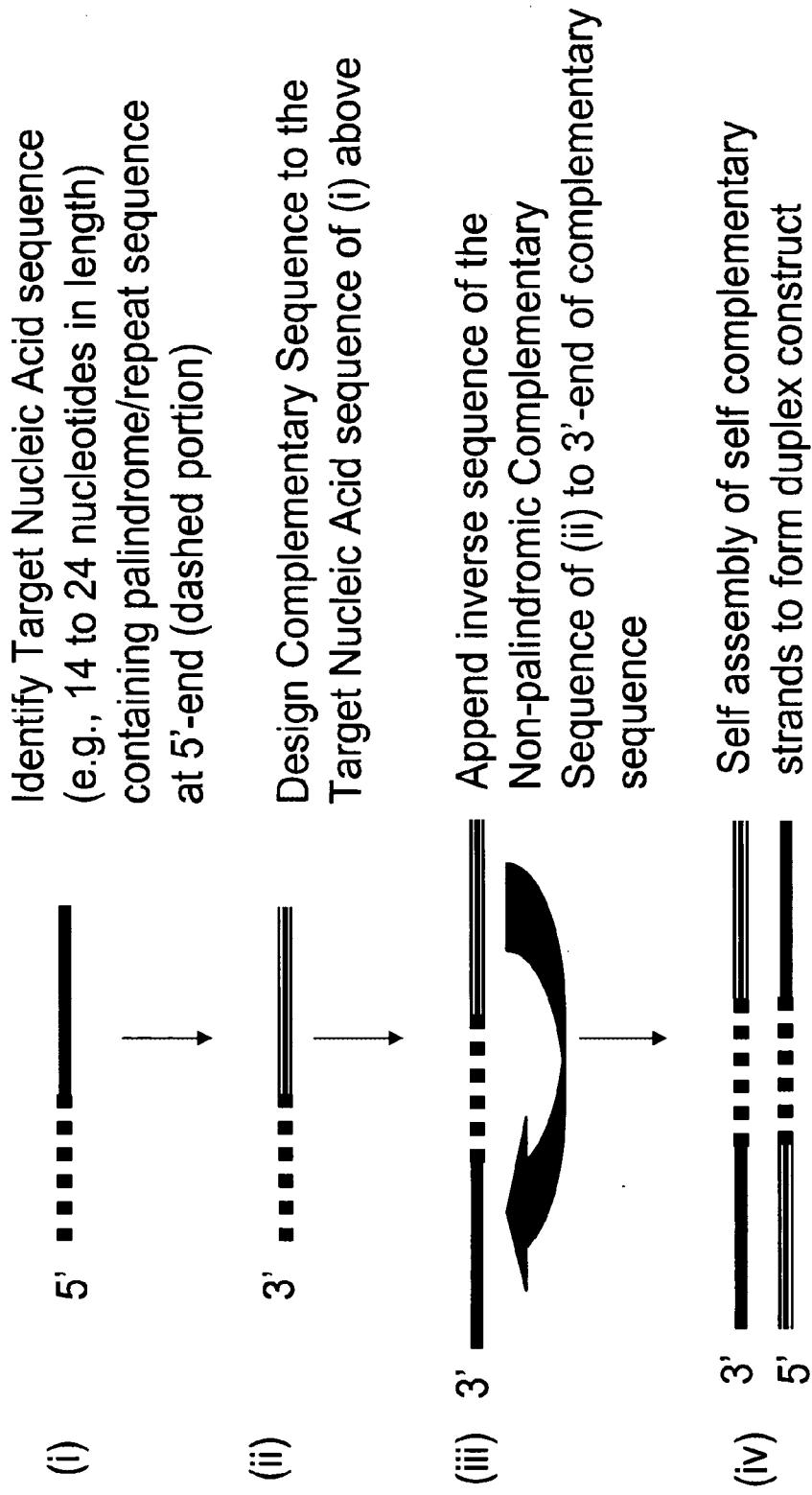


Figure 14B: Example of a duplex forming oligonucleotide sequence that utilizes a palindrome or repeat sequence

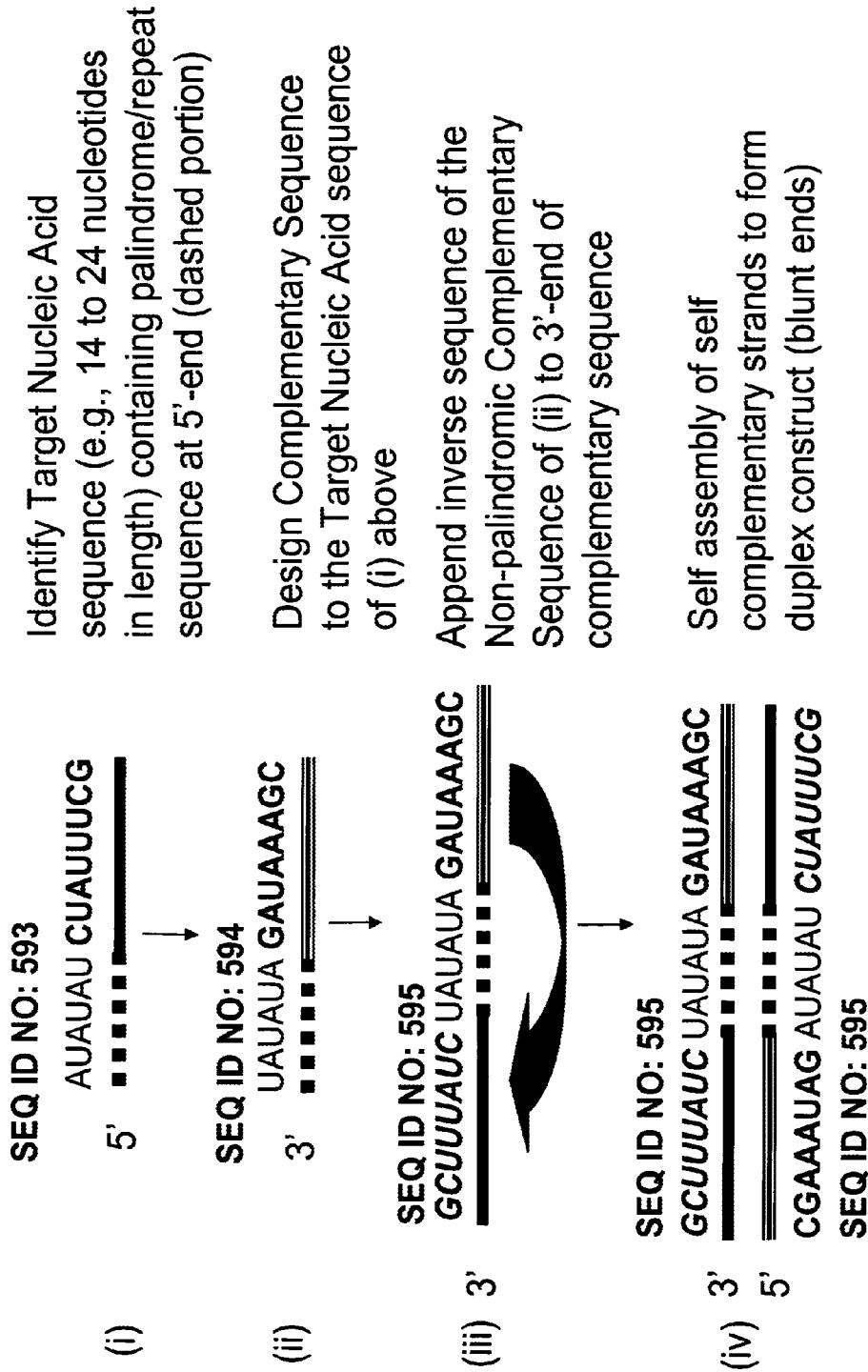


Figure 14C: Example of a duplex forming oligonucleotide sequence that utilizes a palindrome or repeat sequence, self assembly

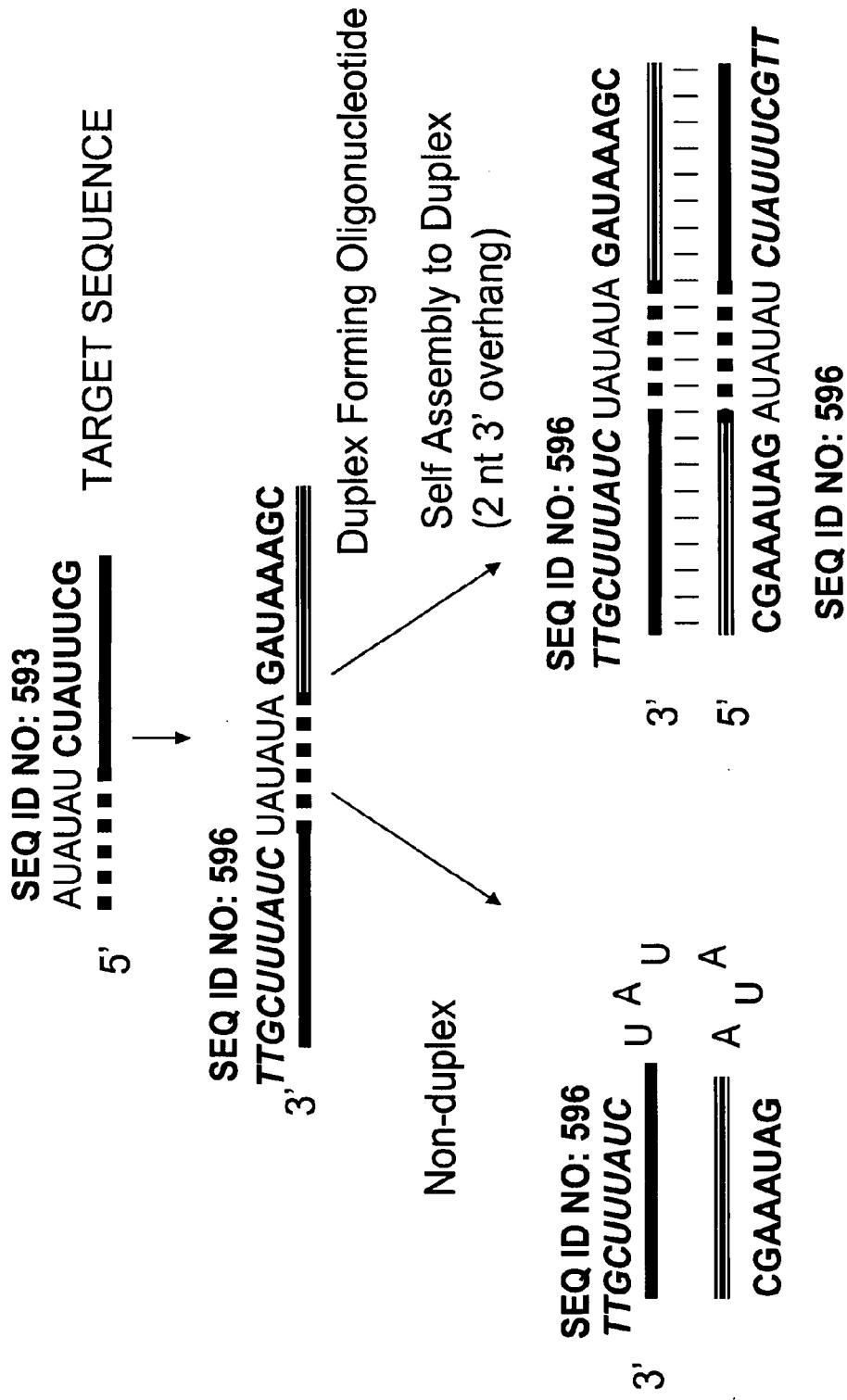


Figure 14D: Example of a duplex forming oligonucleotide sequence that utilizes a palindrome or repeat sequence, self assembly and inhibition of Target Sequence Expression

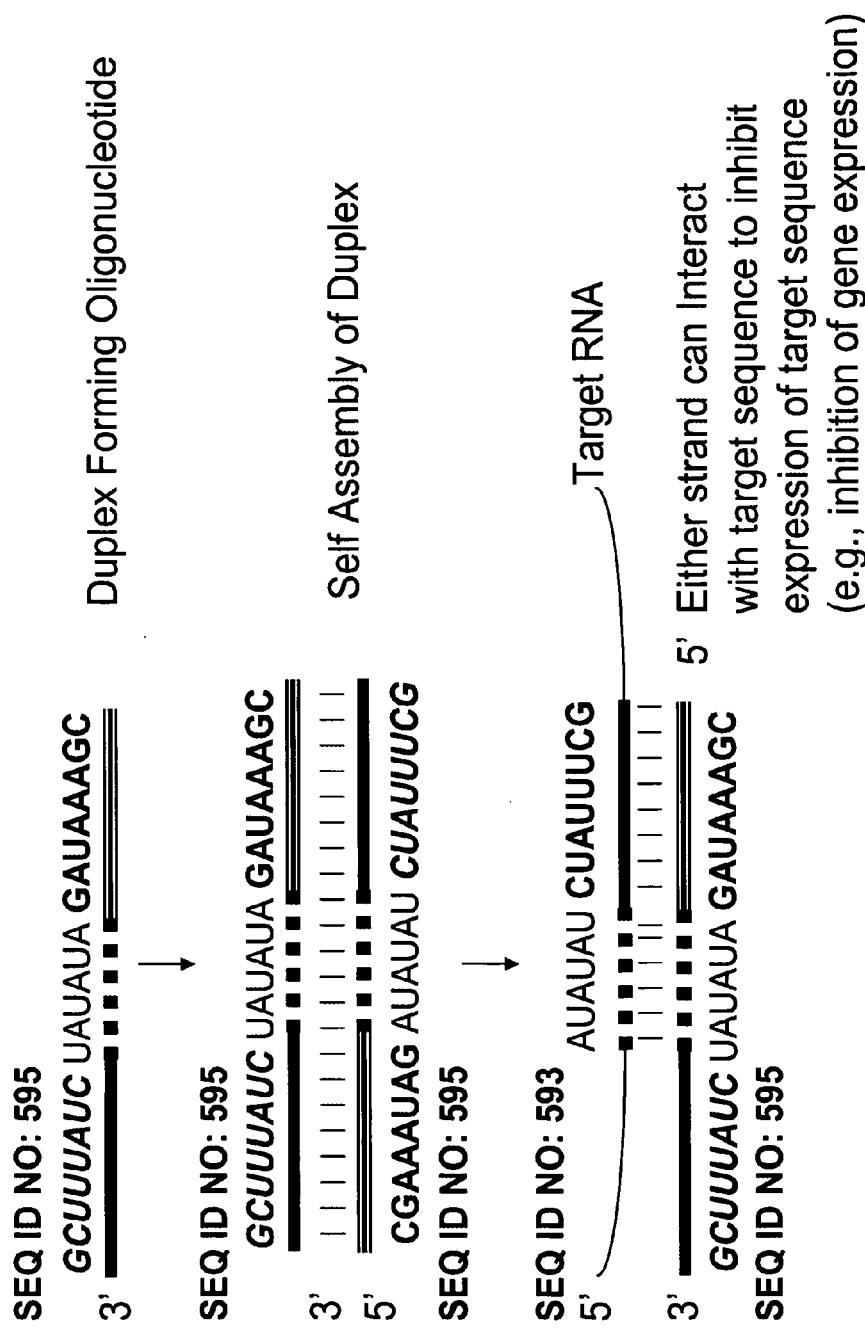


Figure 15: Duplex forming oligonucleotide constructs that utilize artificial palindrome or repeat sequences

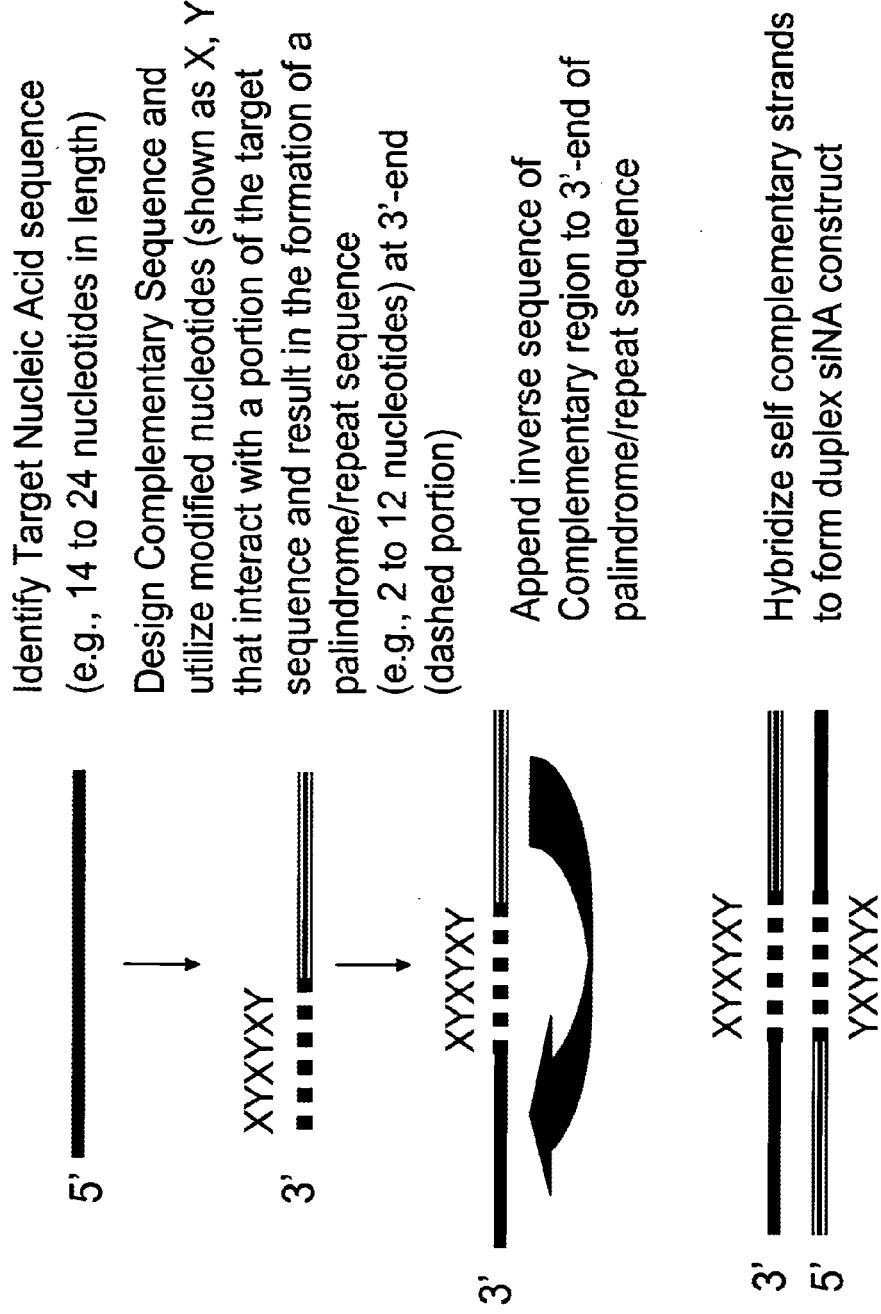


Figure 16: Examples of double stranded multifunctional siNA constructs with distinct complementary regions

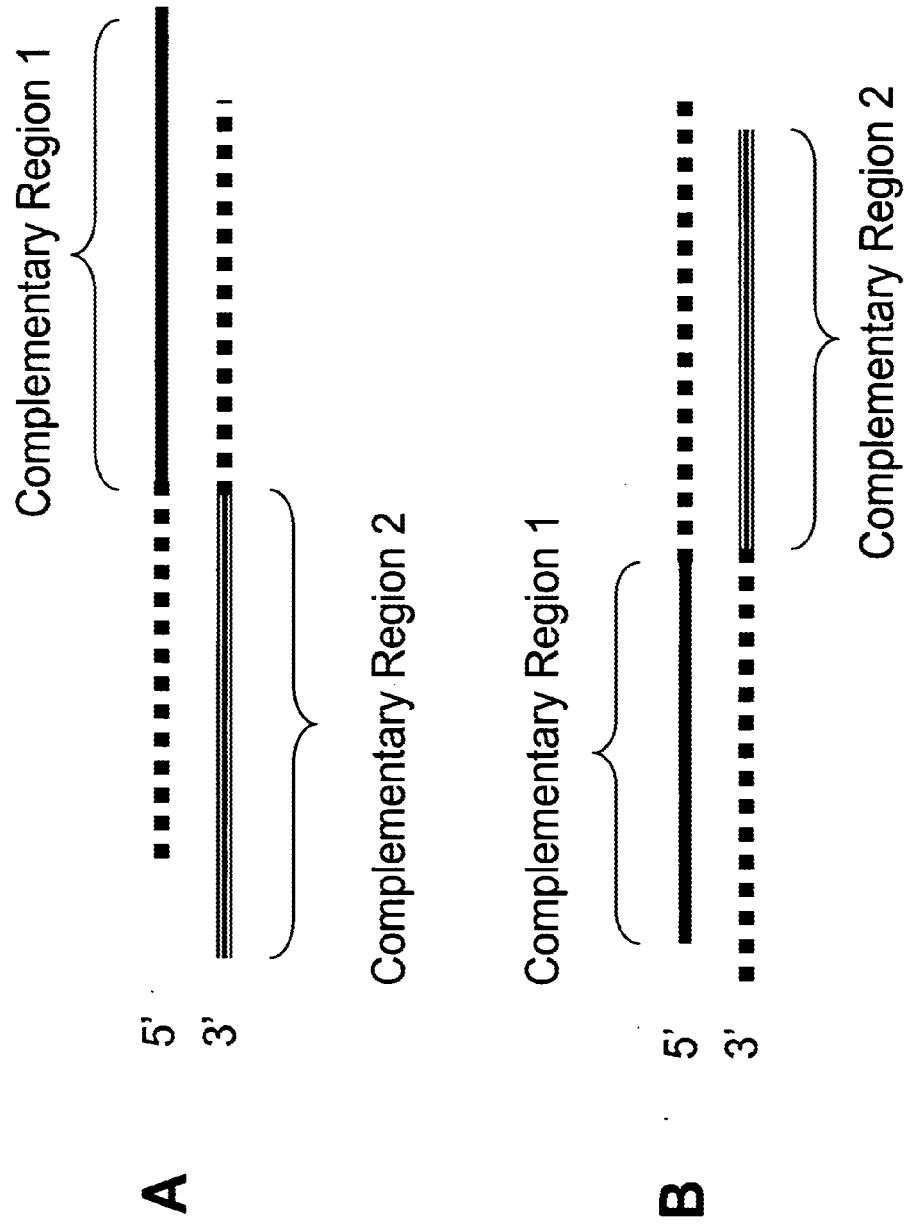


Figure 17: Examples of hairpin multifunctional siNA constructs with distinct complementary regions

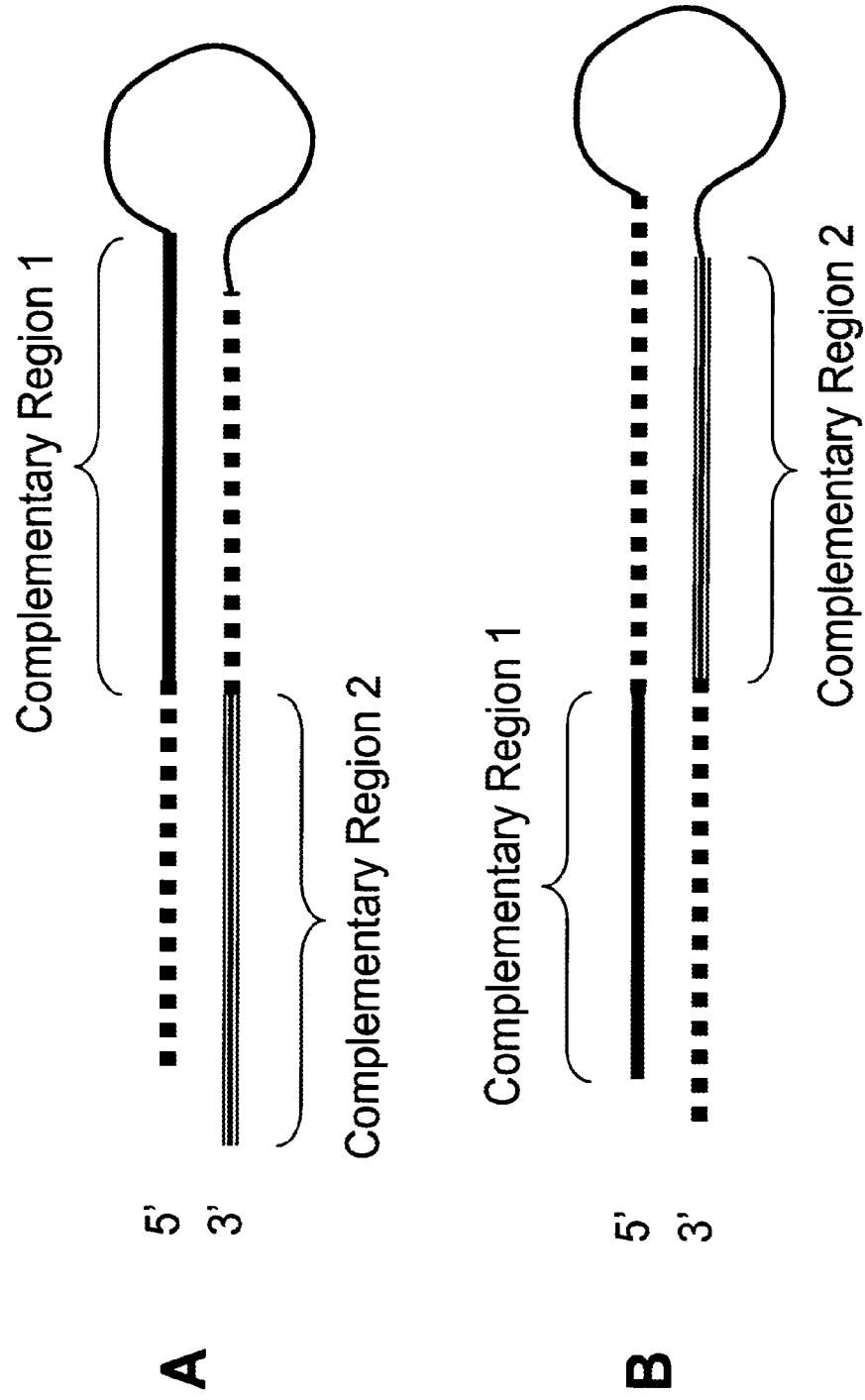


Figure 18: Examples of double stranded multifunctional siNA constructs with distinct complementary regions and a self complementary/palindrome region

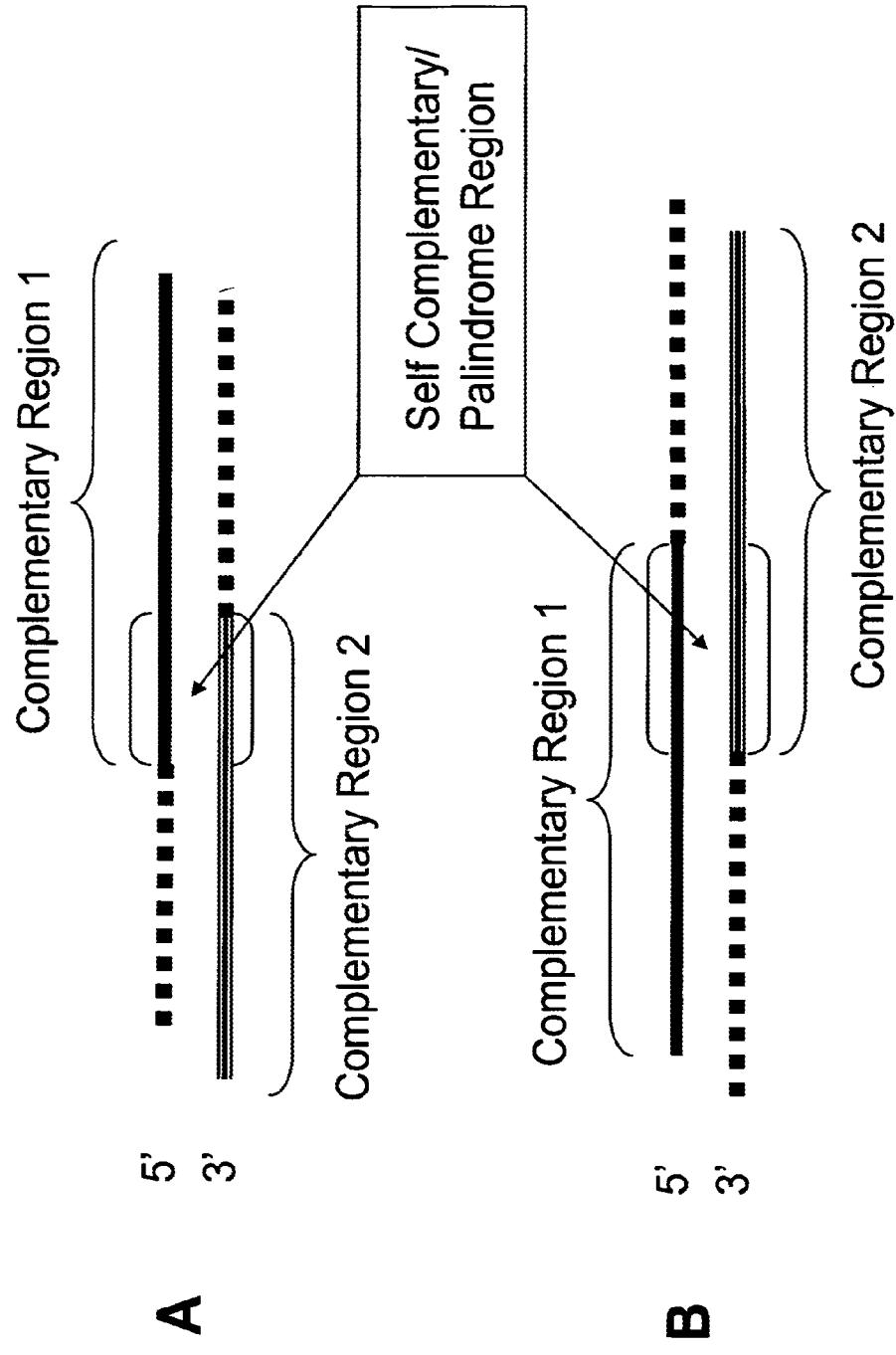


Figure 19: Examples of hairpin multifunctional siNA constructs with distinct complementary regions and a self complementary/palindrome region

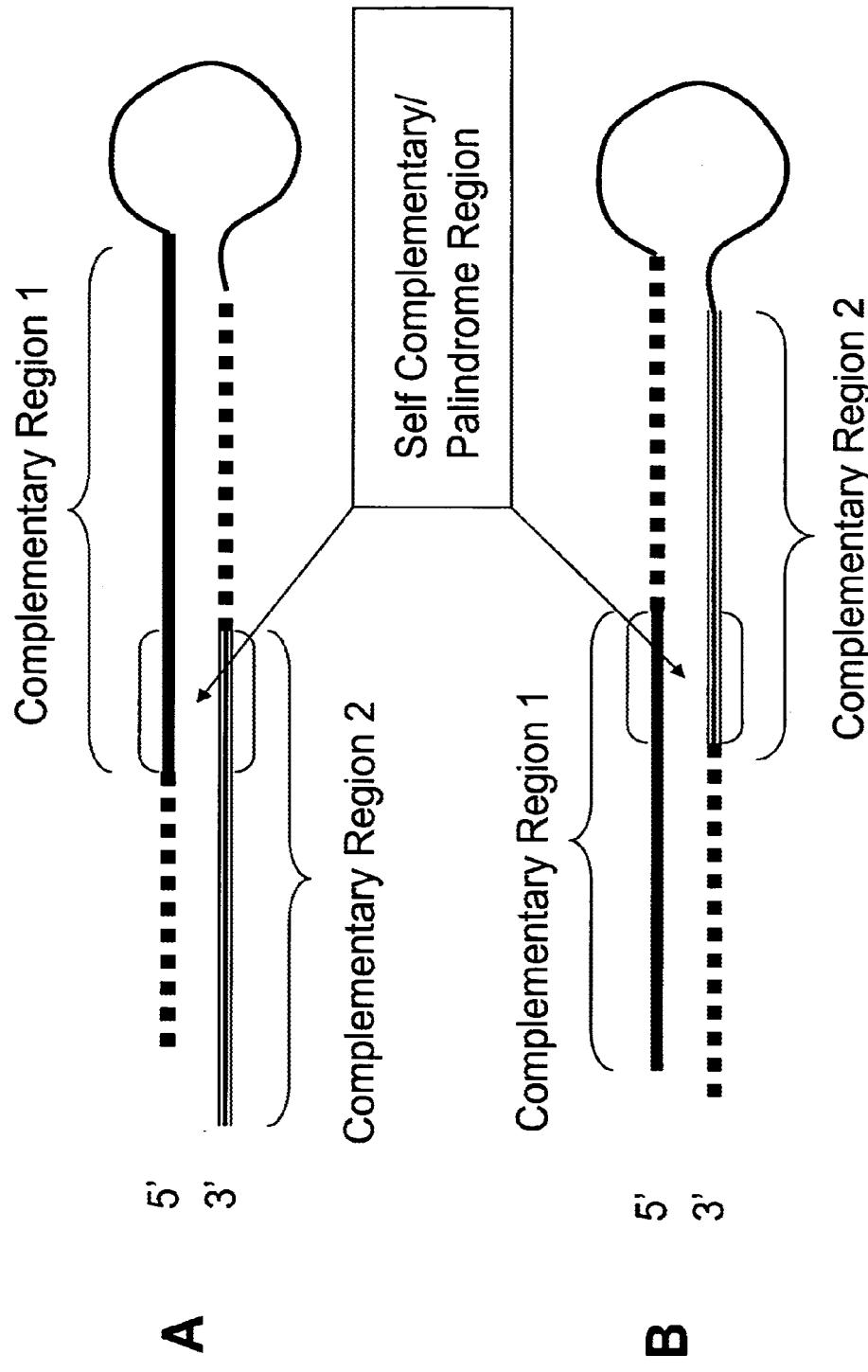


Figure 20: Example of multifunctional siNA targeting two Separate Target nucleic acid sequences

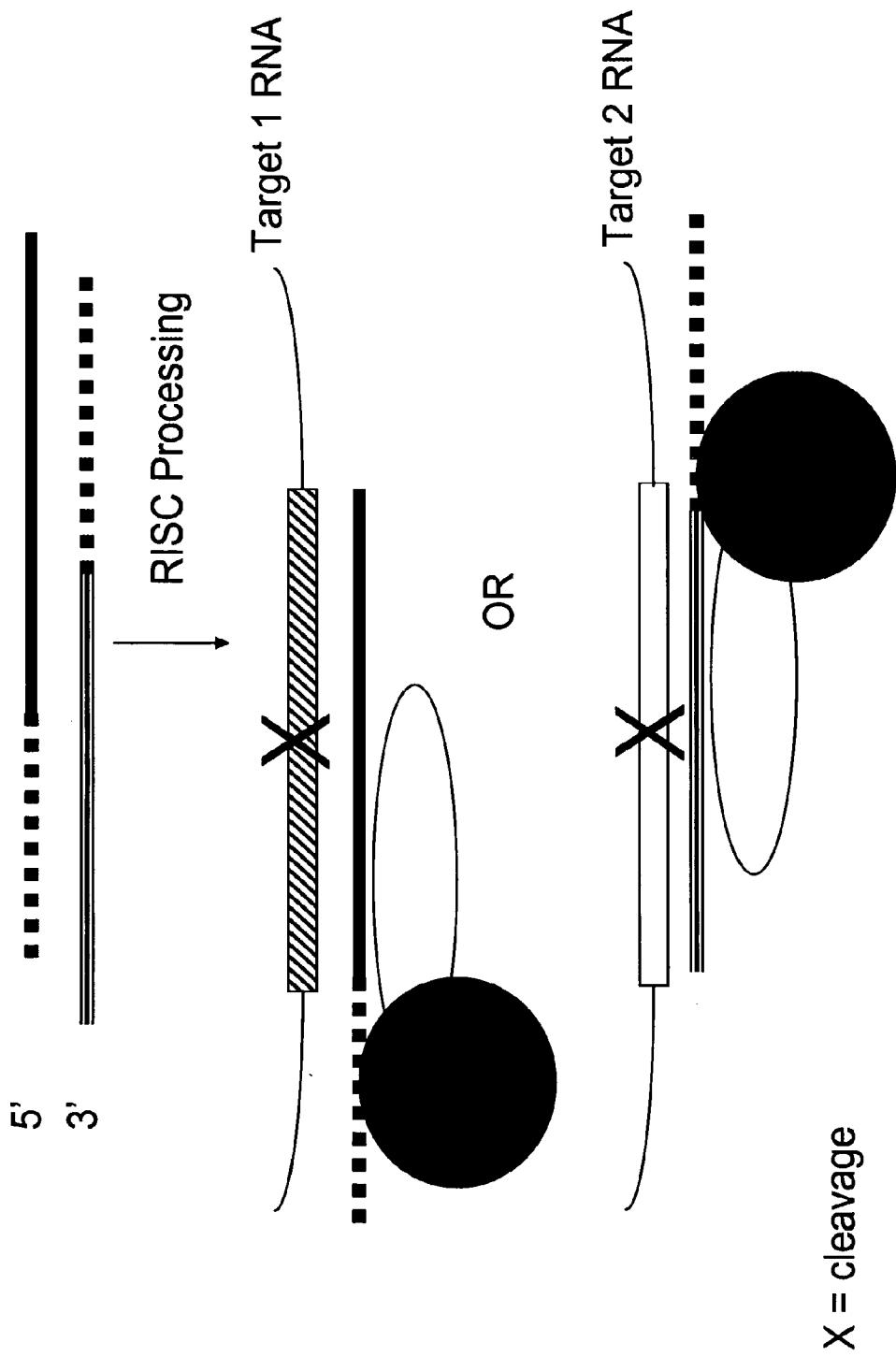


Figure 21: Example of multifunctional siNA targeting two regions within the same target nucleic acid sequence

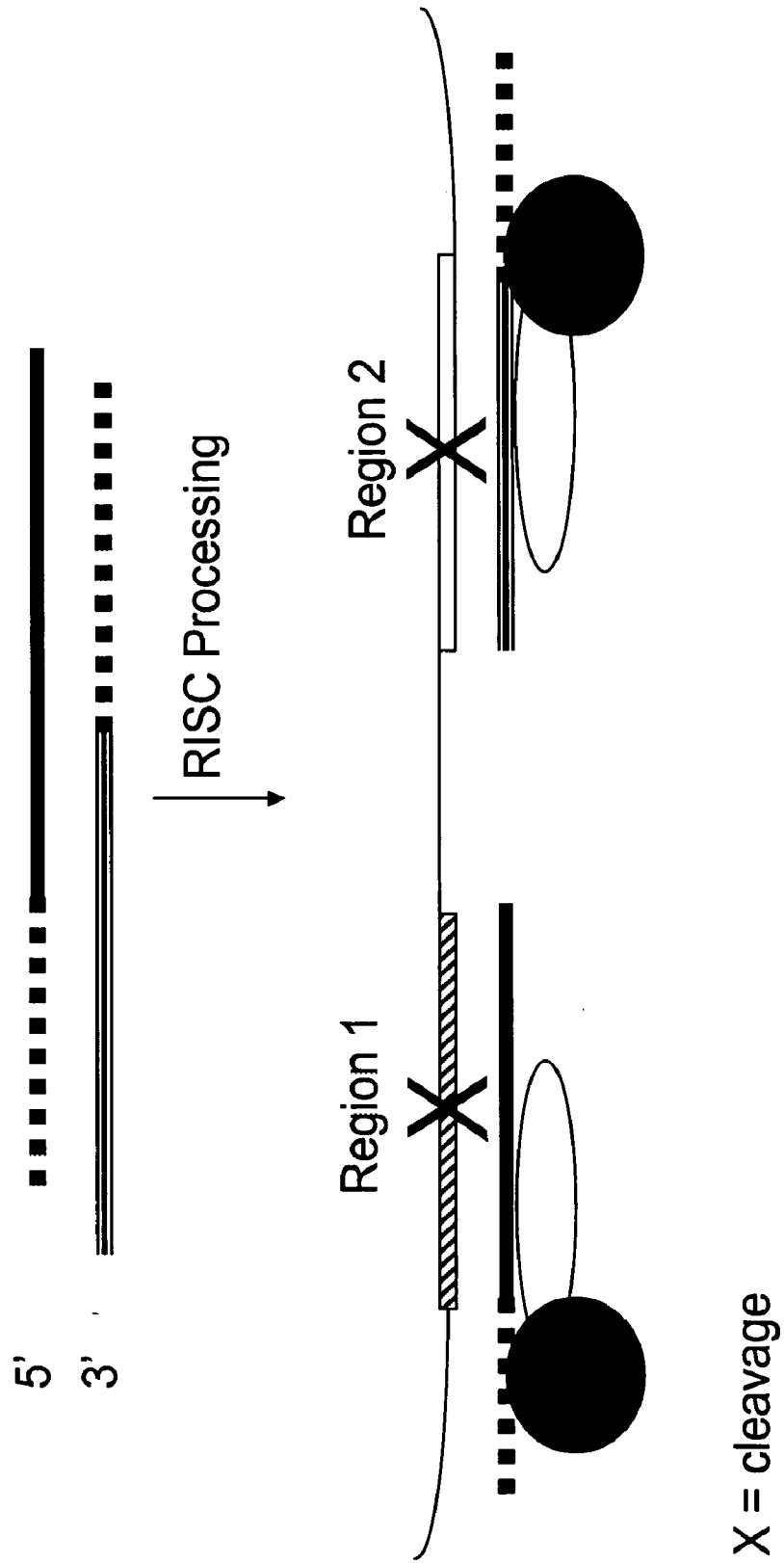
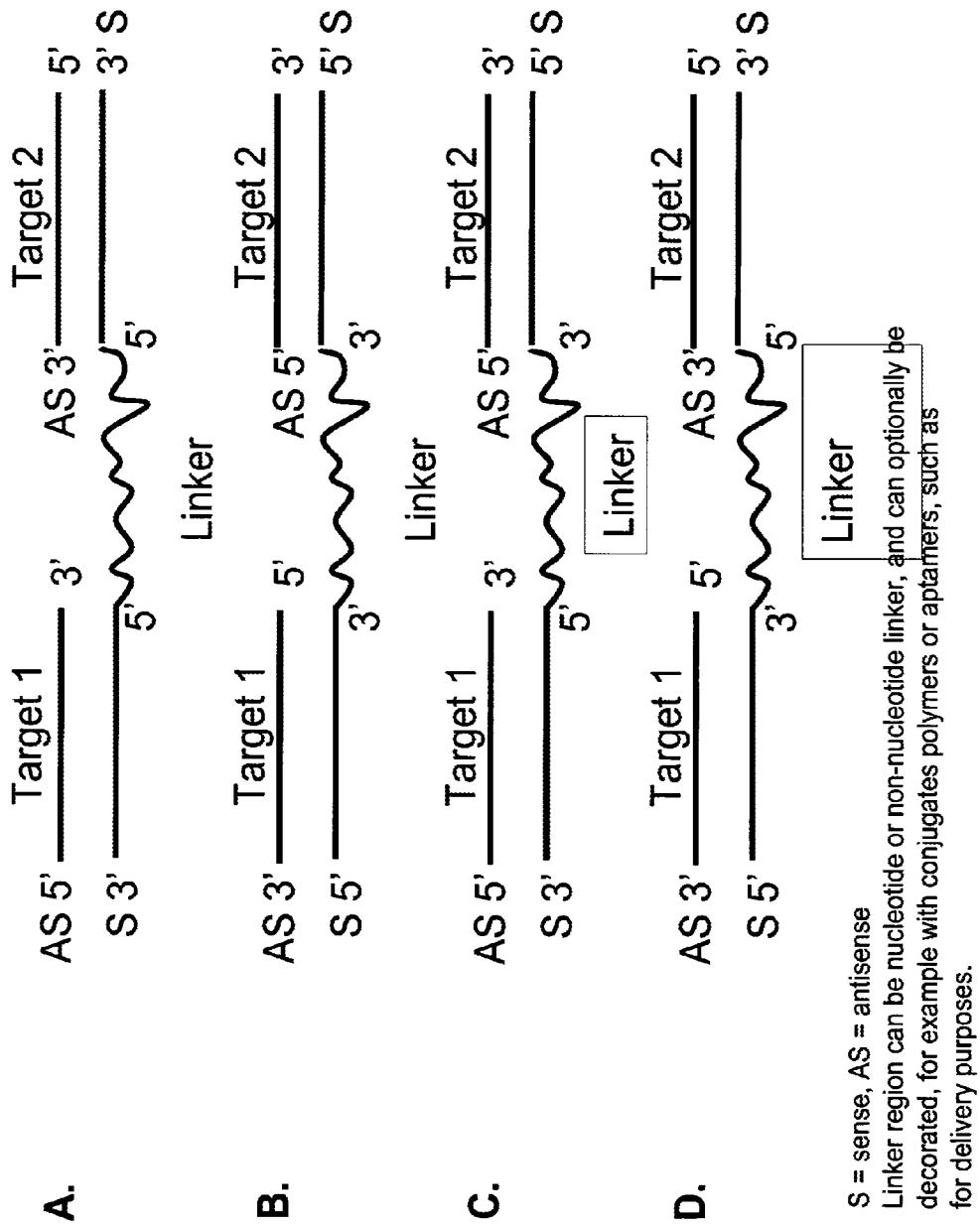


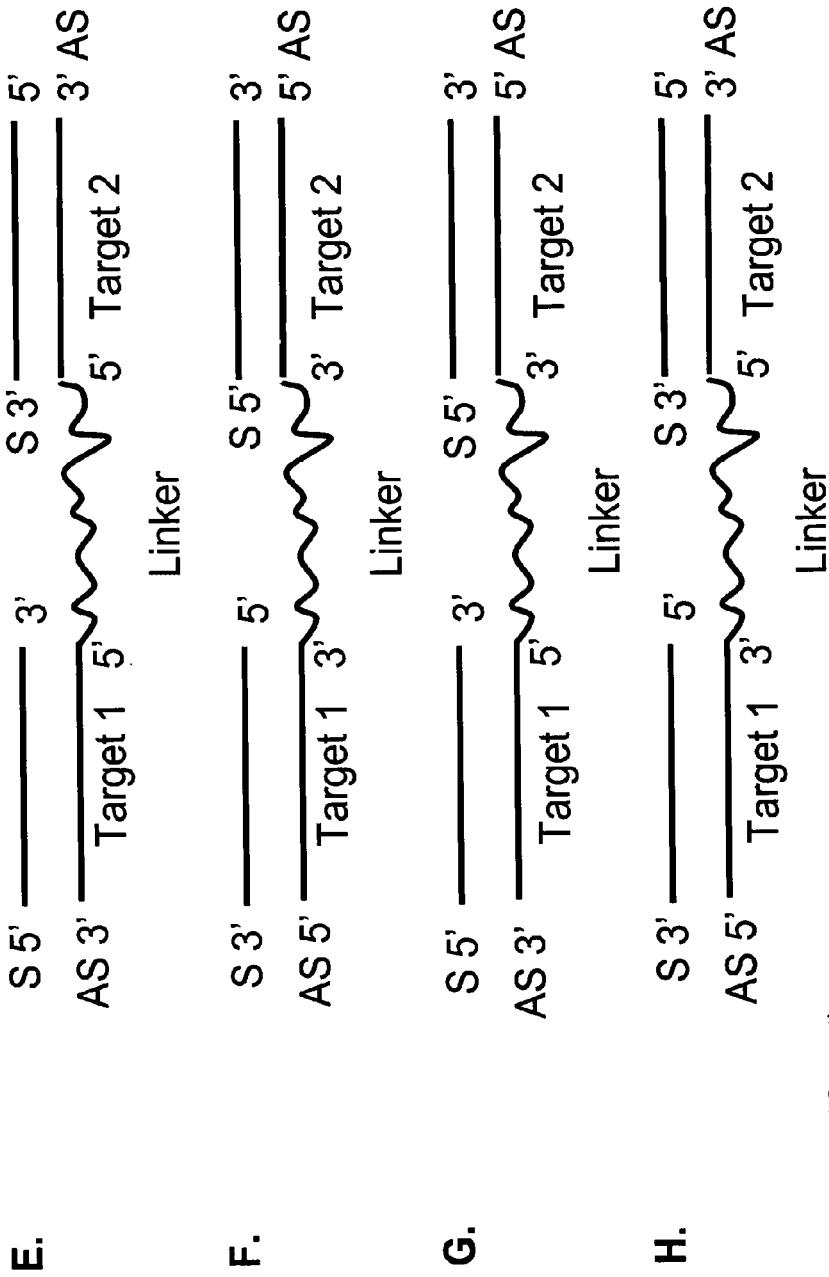
Figure 22: Tethered Multifunctional siNA design



S = sense, AS = antisense

Linker region can be nucleotide or non-nucleotide linker, and can optionally be decorated, for example with conjugates polymers or aptamers, such as for delivery purposes.

Figure 22: Tethered Multifunctional siNA design



S = sense, AS = antisense

Linker region can be nucleotide or non-nucleotide linker, and can optionally be decorated, for example with conjugates polymers or aptamers, such as for delivery purposes.

Figure 23: Dendrimer Multifunctional siNA designs

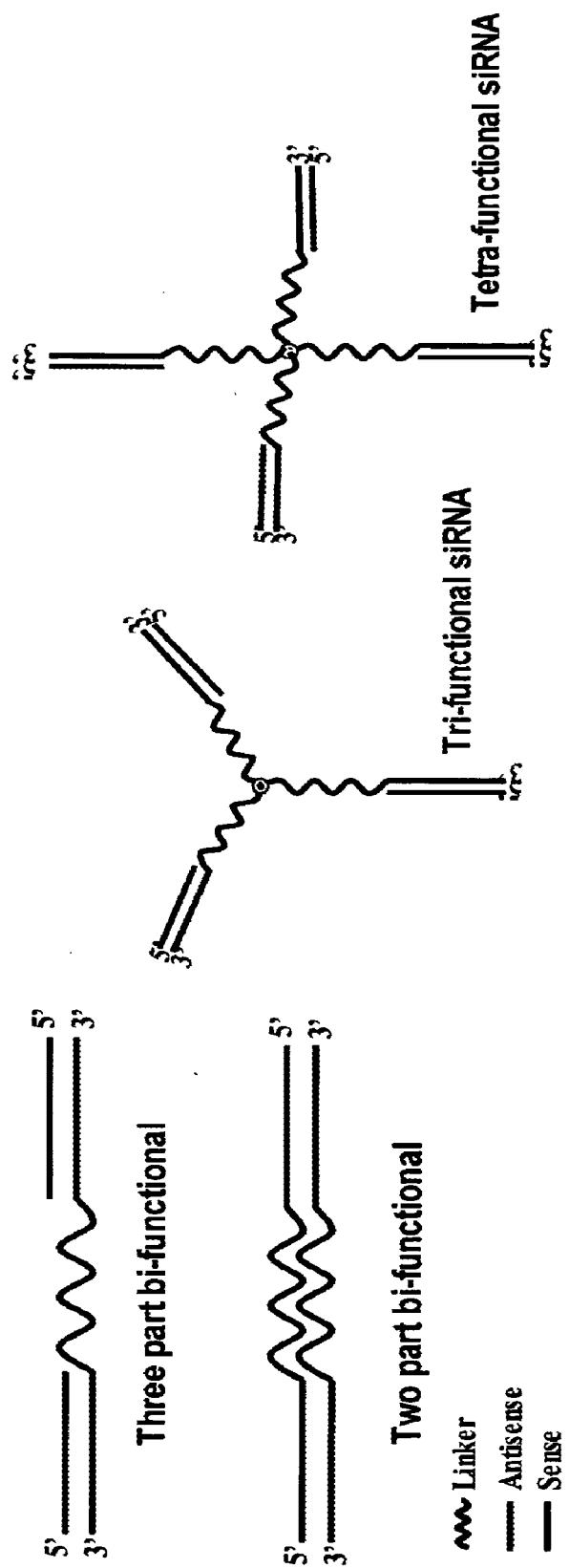


Figure 24: Supramolecular Multifunctional siNA designs

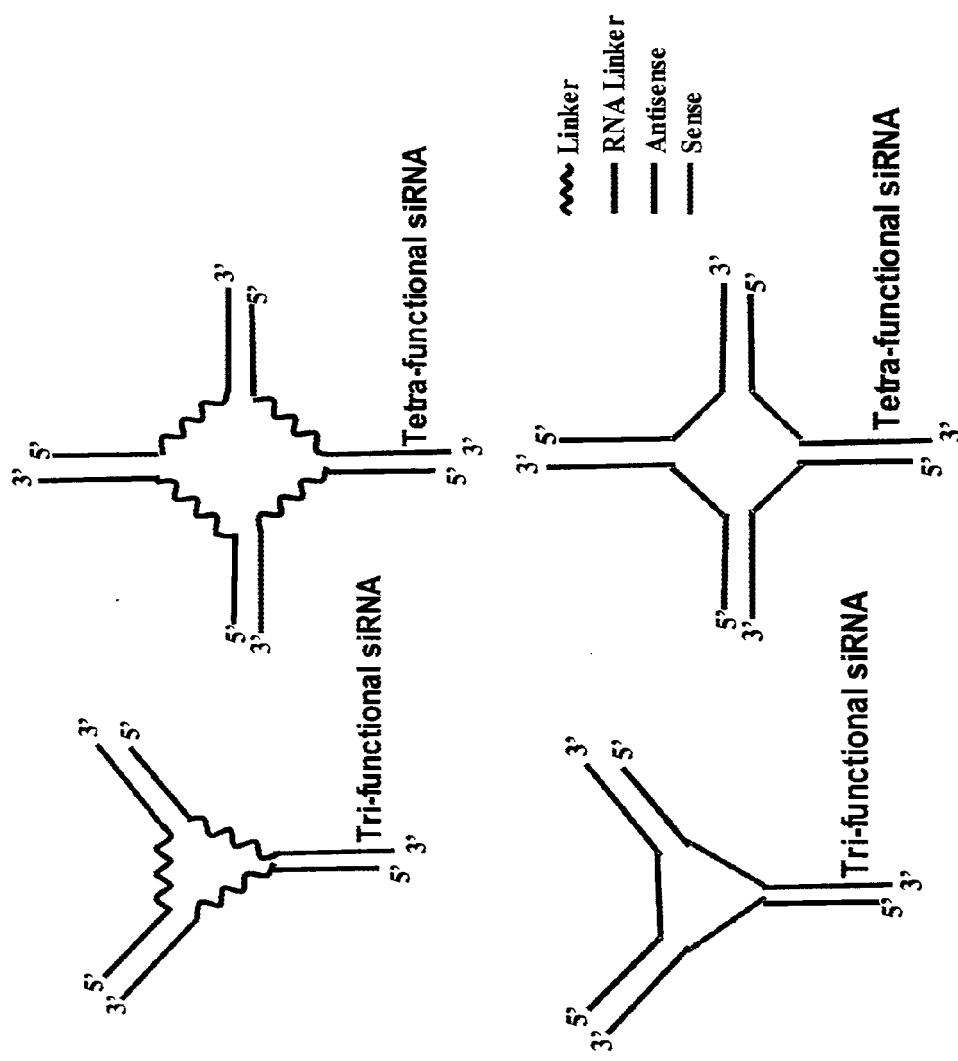


Figure 25: Dicer enabled multifunctional siNA design

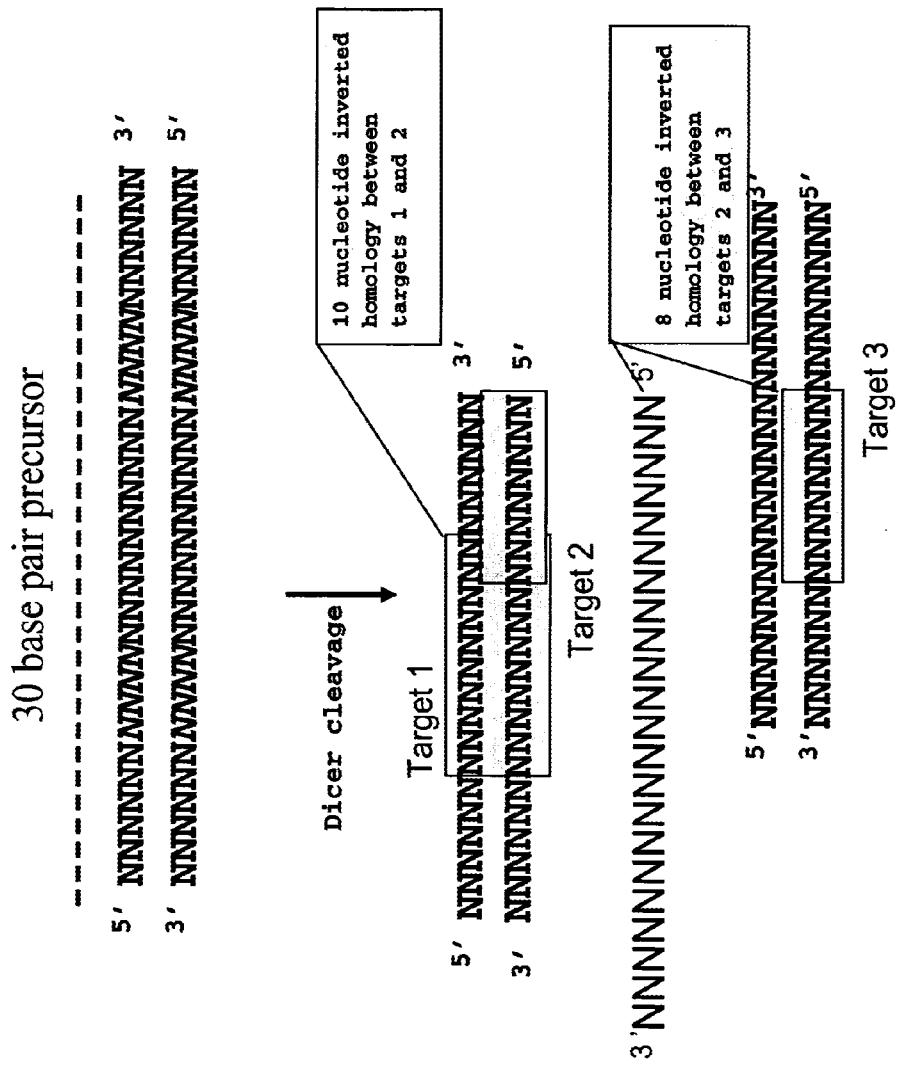


Figure 26: Dicer enabled multifunctional siNA design

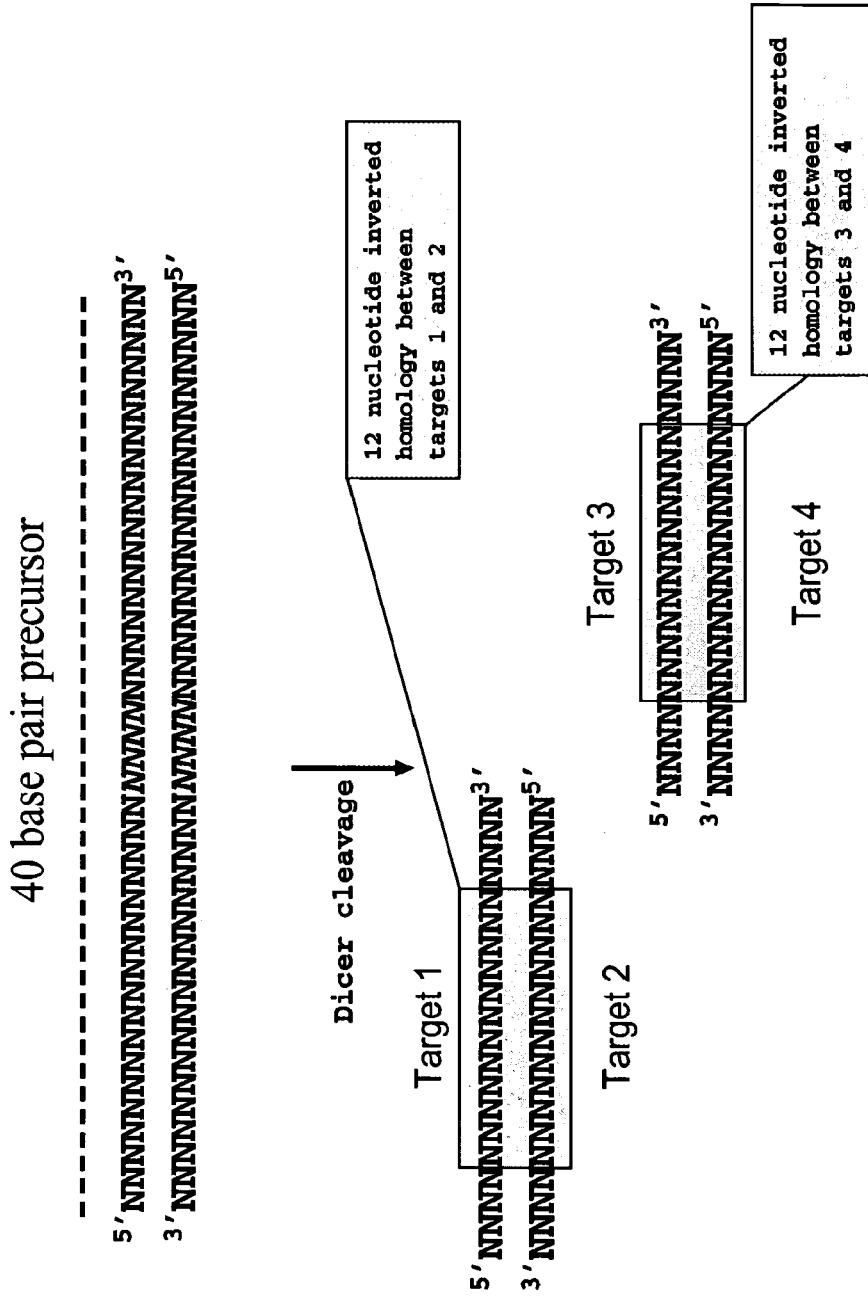


Figure 27: Additional Multifunctional siNA designs

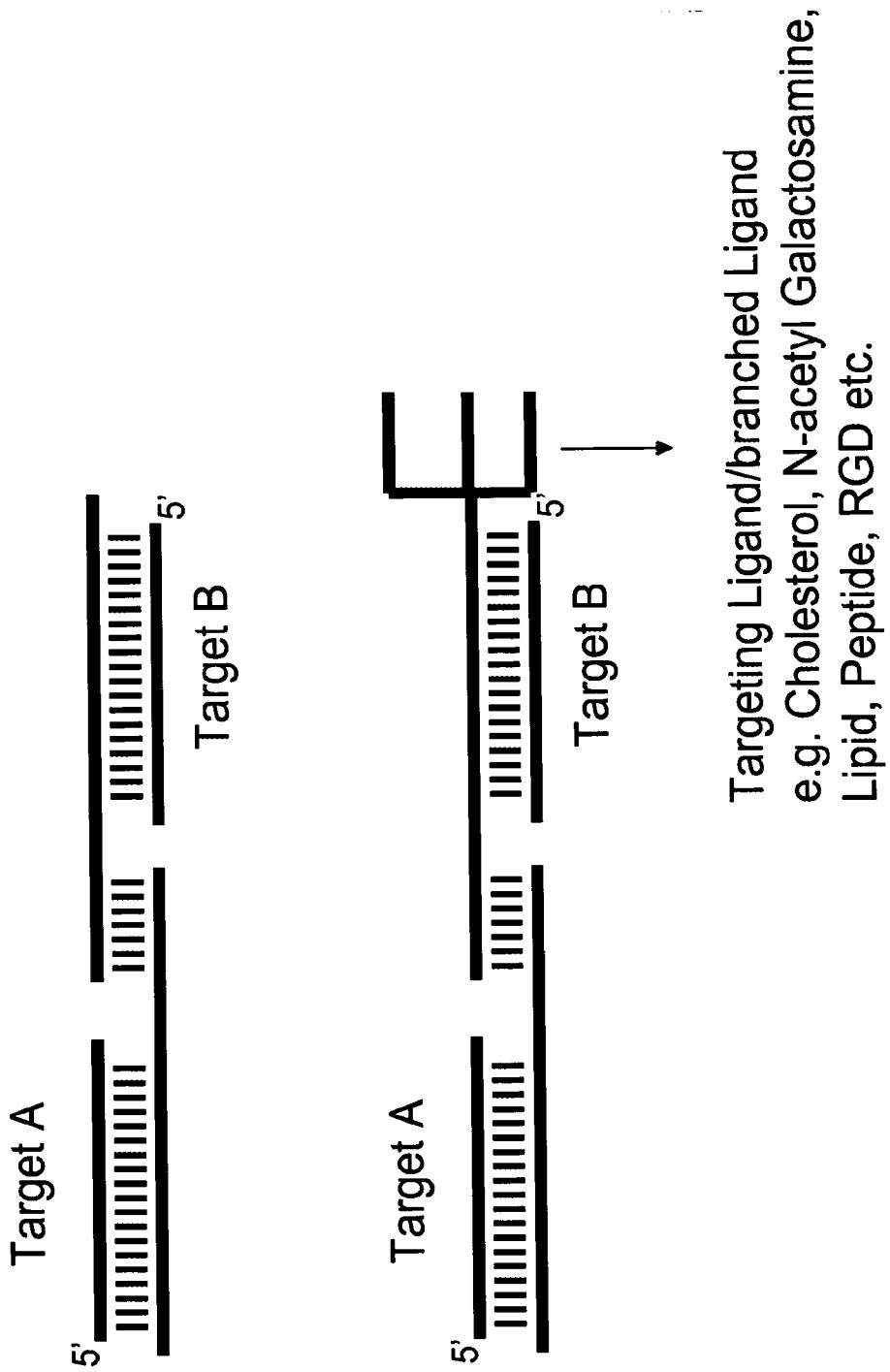


Figure 28: Additional Multifunctional siNA designs

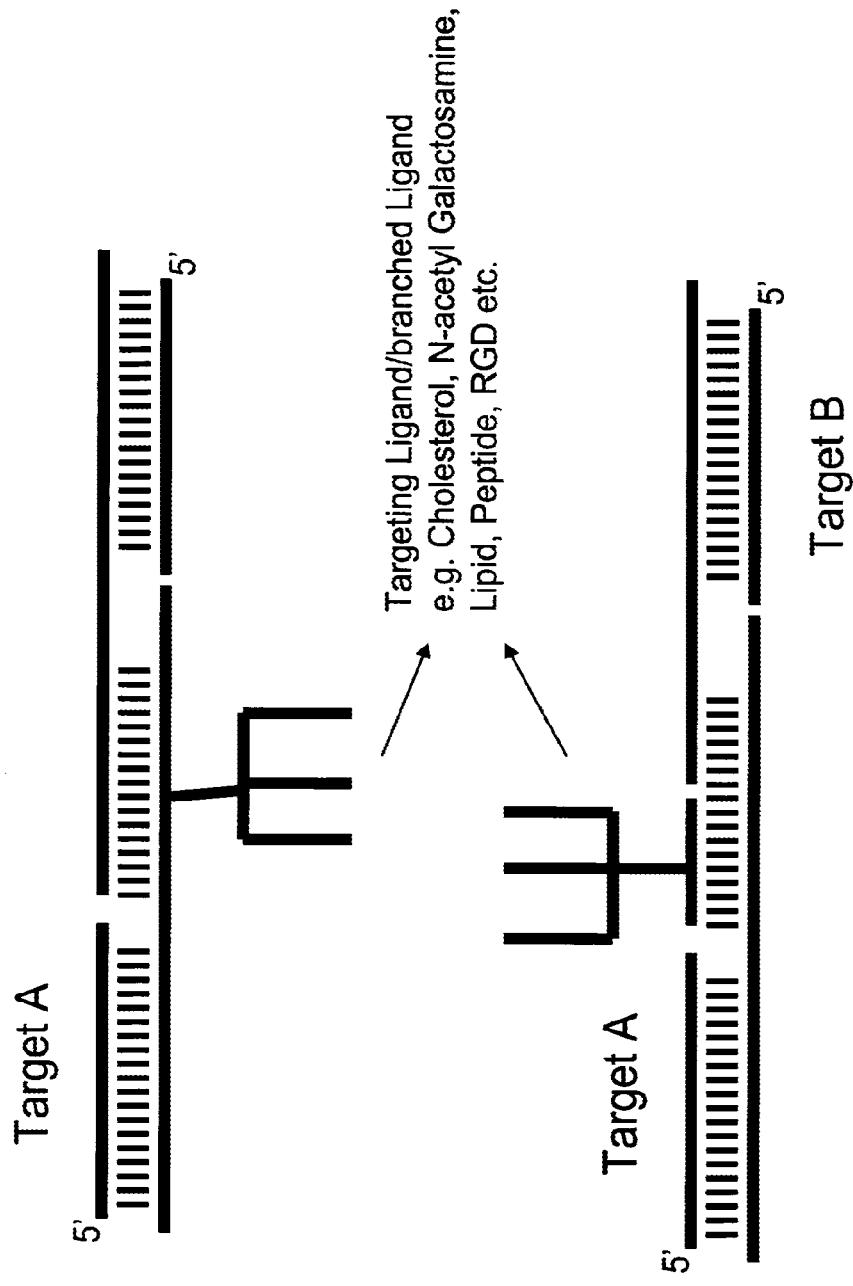
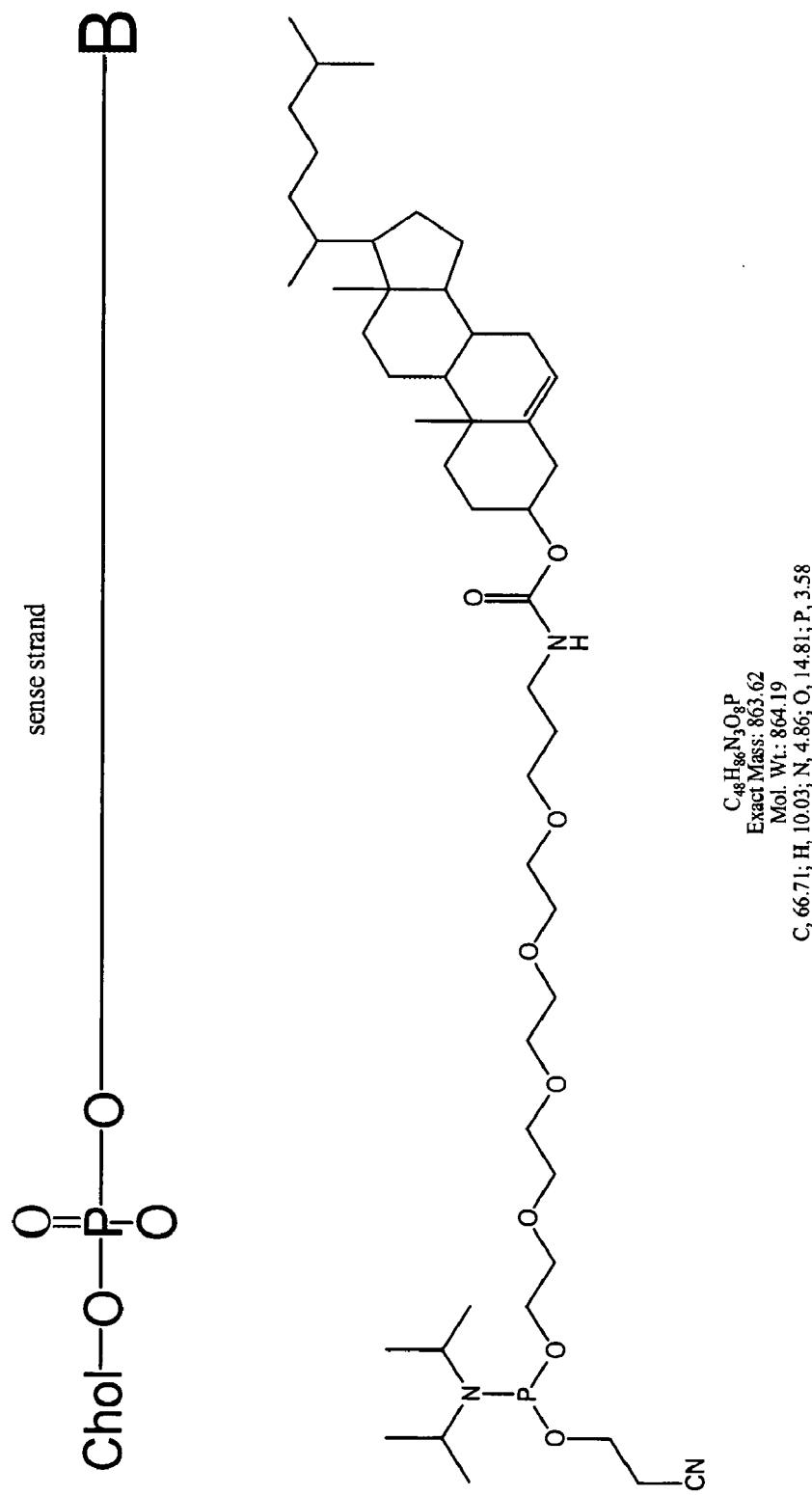


Figure 29: Cholesterol Conjugate Approach



**RNA INTERFERENCE MEDIATED
INHIBITION OF PROPROTEIN
CONVERTASE SUBTILISIN KEXIN 9 (PCSK9)
GENE EXPRESSION USING SHORT
INTERFERING NUCLEIC ACID (SINA)**

[0001] This application is a continuation of U.S. patent application Ser. No. 11/487,788 filed Jul. 17, 2006, which is a continuation-in part of U.S. patent application Ser. No. 11/369,108 filed Mar. 6, 2006 (now abandoned), which is a continuation-in-part of U.S. patent application Ser. No. 10/923,536 filed Aug. 20, 2004 (now abandoned). The instant application claims the benefit of all the listed applications, which are hereby incorporated by reference herein in their entireties, including the drawings.

FIELD OF THE INVENTION

[0002] The present invention relates to compounds, compositions, and methods for the study, diagnosis, and treatment of traits, diseases and conditions that respond to the modulation of Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene expression and/or activity. The present invention is also directed to compounds, compositions, and methods relating to traits, diseases and conditions that respond to the modulation of expression and/or activity of genes involved in Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene expression pathways or other cellular processes that mediate the maintenance or development of such traits, diseases and conditions. Specifically, the invention relates to double stranded nucleic acid molecules including small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene expression, including cocktails of such small nucleic acid molecules and lipid nanoparticle (LNP) formulations of such small nucleic acid molecules. The present invention also relates to small nucleic acid molecules, such as siNA, siRNA, and others that can inhibit the function of endogenous RNA molecules, such as endogenous micro-RNA (miRNA) (e.g., miRNA inhibitors) or endogenous short interfering RNA (siRNA), (e.g., siRNA inhibitors) or that can inhibit the function of RISC (e.g., RISC inhibitors), to modulate PCSK9 gene expression by interfering with the regulatory function of such endogenous RNAs or proteins associated with such endogenous RNAs (e.g., RISC), including cocktails of such small nucleic acid molecules and lipid nanoparticle (LNP) formulations of such small nucleic acid molecules. Such small nucleic acid molecules are useful, for example, in providing compositions to prevent, inhibit, or reduce metabolic diseases traits and conditions, including but not limited to hyperlipidemia, hypercholesterolemia, cardiovascular disease, atherosclerosis, hypertension, diabetes (e.g., type I and/or type II diabetes), insulin resistance, obesity and/or other disease states, conditions, or traits associated with PCSK9 gene expression or activity in a subject or organism.

BACKGROUND OF THE INVENTION

[0003] The following is a discussion of relevant art pertaining to RNAi. The discussion is provided only for understand-

ing of the invention that follows. The summary is not an admission that any of the work described below is prior art to the claimed invention.

[0004] RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Zamore et al., 2000, *Cell*, 101, 25-33; Fire et al., 1998, *Nature*, 391, 806; Hamilton et al., 1999, *Science*, 286, 950-951; Lin et al., 1999, *Nature*, 402, 128-129; Sharp, 1999, *Genes & Dev.*, 13:139-141; and Strauss, 1999, *Science*, 286, 886). The corresponding process in plants (Heifetz et al., International PCT Publication No. WO 99/61631) is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire et al., 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or from the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from other known mechanisms involving double stranded RNA-specific ribonucleases, such as the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L (see for example U.S. Pat. Nos. 6,107,094; 5,898,031; Clemens et al., 1997, *J. Interferon & Cytokine Res.*, 17, 503-524; Adah et al., 2001, *Curr. Med. Chem.*, 8, 1189).

[0005] The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer (Bass, 2000, *Cell*, 101, 235; Zamore et al., 2000, *Cell*, 101, 25-33; Hammond et al., 2000, *Nature*, 404, 293). Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Zamore et al., 2000, *Cell*, 101, 25-33; Bass, 2000, *Cell*, 101, 235; Bernstein et al., 2001, *Nature*, 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Zamore et al., 2000, *Cell*, 101, 25-33; Elbashir et al., 2001, *Genes Dev.*, 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner et al., 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir et al., 2001, *Genes Dev.*, 15, 188).

[0006] RNAi has been studied in a variety of systems. Fire et al., 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Bahramian and Zarbl, 1999, *Molecular and Cellular Biology*, 19, 274-283 and Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mammalian systems. Hammond et al., 2000, *Nature*, 404,

293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir et al., 2001, *Nature*, 411, 494 and Tuschl et al., International PCT Publication No. WO 01/75164, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir et al., 2001, *EMBO J.*, 20, 6877 and Tuschl et al., International PCT Publication No. WO 01/75164) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy(2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir et al., 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen et al., 2001, *Cell*, 107, 309).

[0007] Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two-nucleotide 3'-overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir et al., 2001, *EMBO J.*, 20, 6877 and Tuschl et al., International PCT Publication No. WO 01/75164). In addition, Elbashir et al., supra, also report that substitution of siRNA with 2'-O-methyl nucleotides completely abolishes RNAi activity. Li et al., International PCT Publication No. WO 00/44914, and Beach et al., International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer et al., Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge. However, Kreutzer et al. similarly fails to provide examples or guidance as to what extent these modifications would be tolerated in dsRNA molecules.

[0008] Parrish et al., 2000, *Molecular Cell*, 6, 1077-1087, tested certain chemical modifications targeting the unc-22 gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3 RNA polymerase and observed that RNAs with two phosphorothioate modified

bases also had substantial decreases in effectiveness as RNAi. Further, Parrish et al. reported that phosphorothioate modification of more than two residues greatly destabilized the RNAs in vitro such that interference activities could not be assayed. Id. at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. Id. In addition, the authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the anti-sense strand resulted in a substantial decrease in RNAi activity as well.

[0009] The use of longer dsRNA has been described. For example, Beach et al., International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl et al., International PCT Publication No. WO 01/75164, describe a *Drosophila* in vitro RNAi system and the use of specific siRNA molecules for certain functional genomic and certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li et al., International PCT Publication No. WO 00/44914, describe the use of specific long (141 bp-488 bp) enzymatically synthesized or vector expressed dsRNAs for attenuating the expression of certain target genes. Zernicka-Goetz et al., International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian cells using certain long (550 bp-714 bp), enzymatically synthesized or vector expressed dsRNA molecules. Fire et al., International PCT Publication No. WO 99/32619, describe particular methods for introducing certain long dsRNA molecules into cells for use in inhibiting gene expression in nematodes. Plaetinck et al., International PCT Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific long dsRNA molecules. Mello et al., International PCT Publication No. WO 01/29058, describe the identification of specific genes involved in dsRNA-mediated RNAi. Pachuck et al., International PCT Publication No. WO 00/63364, describe certain long (at least 200 nucleotide) dsRNA constructs. Deschamps Depaillette et al., International PCT Publication No. WO 99/07409, describe specific compositions consisting of particular dsRNA molecules combined with certain anti-viral agents. Waterhouse et al., International PCT Publication No. 99/53050 and 1998, *PNAS*, 95, 13959-13964, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using certain dsRNAs. Driscoll et al., International PCT Publication No. WO 01/49844, describe specific DNA expression constructs for use in facilitating gene silencing in targeted organisms.

[0010] Others have reported on various RNAi and gene-silencing systems. For example, Parrish et al., 2000, *Molecu-*

lar Cell, 6, 1077-1087, describe specific chemically-modified dsRNA constructs targeting the unc-22 gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb gene expression in plants using certain dsRNAs. Churikov et al., International PCT Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni et al., International PCT Publication No. WO 01/53475, describe certain methods for isolating a *Neurospora* silencing gene and uses thereof. Reed et al., International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer et al., International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain dsRNAs. Deak et al., International PCT Publication No. WO 01/72774, describe certain *Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt et al., International PCT Publication No. WO 01/92513 describe certain methods for mediating gene suppression by using factors that enhance RNAi. Tuschl et al., International PCT Publication No. WO 02/44321, describe certain synthetic siRNA constructs. Pachuk et al., International PCT Publication No. WO 00/63364, and Satishchandran et al., International PCT Publication No. WO 01/04313, describe certain methods and compositions for inhibiting the function of certain polynucleotide sequences using certain long (over 250 bp), vector expressed dsRNAs. Echeverri et al., International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer et al., International PCT Publications Nos. WO 02/055692, WO 02/055693, and EP 1144623 B1 describes certain methods for inhibiting gene expression using dsRNA. Graham et al., International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire et al., U.S. Pat. No. 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain long dsRNA (299 bp-1033 bp) constructs that mediate RNAi. Martinez et al., 2002, *Cell*, 110, 563-574, describe certain single stranded siRNA constructs, including certain 5'-phosphorylated single stranded siRNAs that mediate RNA interference in Hela cells. Harborth et al., 2003, *Antisense & Nucleic Acid Drug Development*, 13, 83-105, describe certain chemically and structurally modified siRNA molecules. Chiu and Rana, 2003, *RNA*, 9, 1034-1048, describe certain chemically and structurally modified siRNA molecules. Woolf et al., International PCT Publication Nos. WO 03/064626 and WO 03/064625 describe certain chemically modified dsRNA constructs. Hornung et al., 2005, *Nature Medicine*, 11, 263-270, describe the sequence-specific potent induction of IFN-alpha by short interfering RNA in plasmacytoid dendritic cells through TLR7. Judge et al., 2005, *Nature Biotechnology*, Published online: 20 Mar. 2005, describe the sequence-dependent stimulation of the mammalian innate immune response by synthetic siRNA. Yuki et al., International PCT Publication Nos. WO 05/049821 and WO 04/048566, describe certain methods for designing short interfering RNA sequences and certain short interfering RNA sequences with optimized activity. Saigo et al., US Patent Application Publication No. US20040539332, describe certain methods of designing oligo- or polynucleotide sequences, including short interfering RNA sequences, for achieving RNA interference. Tei et al., International PCT Publication No. WO 03/044188,

describe certain methods for inhibiting expression of a target gene, which comprises transfecting a cell, tissue, or individual organism with a double-stranded polynucleotide comprising DNA and RNA having a substantially identical nucleotide sequence with at least a partial nucleotide sequence of the target gene.

[0011] Mattick, 2005, *Science*, 309, 1527-1528; Clayterie, 2005, *Science*, 309, 1529-1530; Sethupathy et al., 2006, *RNA*, 12, 192-197; and Czech, 2006 *NEJM*, 354, 11: 1194-1195; Hutvagner et al., US 20050227256, and Tuschl et al., US 20050182005, all describe antisense molecules that can inhibit miRNA function via steric blocking and are all incorporated by reference herein in their entirety.

[0012] Lalanne et al., 2005, *Journal of Lipid Research*, 46, 1312-1319, describe certain siRNA molecules targeting PCSK9.

SUMMARY OF THE INVENTION

[0013] This invention relates to compounds, compositions, and methods useful for modulating the expression of Proprotein Convertase Subtilisin Kexin 9 (PCSK9) genes, such as those PCSK9 genes associated with the development or maintenance of metabolic diseases traits and conditions, including but not limited to hyperlipidemia, hypercholesterolemia, cardiovascular disease, atherosclerosis, hypertension, diabetes (e.g., type I and/or type II diabetes), insulin resistance, obesity and/or any other diseases, traits, and conditions that are related to PCSK9 gene expression or activity, by RNA interference (RNAi) using short interfering nucleic acid (siNA) molecules. This invention also relates to compounds, compositions, and methods useful for modulating the expression and activity of other genes involved in pathways of PCSK9 gene expression and/or activity by RNA interference (RNAi) using small nucleic acid molecules. In particular, the instant invention features small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules and methods used to modulate the expression of PCSK9 genes and/or other genes involved in pathways of PCSK9 gene expression and/or activity.

[0014] The instant invention also relates to small nucleic acid molecules, such as siNA, siRNA, and others that can inhibit the function of endogenous RNA molecules, such as endogenous micro-RNA (miRNA) (e.g., miRNA inhibitors) or endogenous short interfering RNA (siRNA), (e.g., siRNA inhibitors) or that can inhibit the function of RISC (e.g., RISC inhibitors), to modulate PCSK9 gene expression by interfering with the regulatory function of such endogenous RNAs or proteins associated with such endogenous RNAs (e.g., RISC). Such molecules are collectively referred to herein as RNAi inhibitors.

[0015] A siNA or RNAi inhibitor of the invention can be unmodified or chemically-modified. A siNA or RNAi inhibitor of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The instant invention also features various chemically-modified synthetic short interfering nucleic acid (siNA) molecules capable of modulating target gene expression or activity in cells by RNA interference (RNAi). The instant invention also features various chemically-modified synthetic short nucleic acid (siNA) molecules capable of modulating RNAi activity in cells by interacting with miRNA, siRNA, or RISC, and hence down regulating or inhibiting RNA interference

(RNAi), translational inhibition, or transcriptional silencing in a cell or organism. The use of chemically-modified siNA and/or RNAi inhibitors improves various properties of native siNA molecules and/or RNAi inhibitors through increased resistance to nuclease degradation in vivo and/or through improved cellular uptake. Further, contrary to earlier published studies, siNA molecules of the invention having multiple chemical modifications, including fully modified siNA, retains its RNAi activity. Therefore, Applicant teaches herein chemically modified siRNA that retains or improves upon the activity of native siRNA. The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, prophylactic, veterinary, diagnostic, target validation, genomic discovery, genetic engineering, and pharmacogenomic applications.

[0016] In one embodiment, the invention features one or more siNA molecules and/or RNAi inhibitors and methods that independently or in combination modulate the expression of gene(s) encoding Proprotein Convertase Subtilisin Kexin 9 (PCSK9) and/or PCSK9 pathway genes, such as genes encoding sequences comprising those sequences referred to by GenBank Accession Nos. shown in Table I, referred to herein generally as "PCSK9". The description below of the various aspects and embodiments of the invention is provided with reference to exemplary Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene referred to herein generally as PCSK9, but also known as neural apoptosis-regulated convertase 1 or NARC1. The present invention is also directed to compounds, compositions, and methods relating to traits, diseases and conditions that respond to the modulation of expression and/or activity of genes involved in Proprotein Convertase Subtilisin Kexin 9 (PCSK9) gene expression pathways or other cellular processes that mediate the maintenance or development of such traits, diseases and conditions. However, such reference is meant to be exemplary only and the various aspects and embodiments of the invention are also directed to other genes that express alternate PCSK9 genes, such as mutant PCSK9 genes, splice variants of PCSK9 genes, PCSK9 variants from species to species or subject to subject, and other PCSK9 pathway genes including certain genes described in PCT/US03/05028 and U.S. Ser. No. 10/923,536, both incorporated by reference herein. Such additional genes can be analyzed for target sites using the methods described herein for exemplary PCSK9 genes and sequences herein. Thus, the modulation and the effects of such modulation of the other genes can be performed as described herein. In other words, the term "PCSK9" as it is defined herein below and recited in the described embodiments, is meant to encompass genes associated with the development and/or maintenance of diseases, traits and conditions herein, such as genes which encode PCSK9 polypeptides, PCSK9 regulatory polynucleotides (e.g., PCSK9 miRNAs and siRNAs), mutant PCSK9 genes, and splice variants of PCSK9 genes, as well as other genes involved in PCSK9 pathways of gene expression and/or activity. Thus, each of the embodiments described herein with reference to the term "PCSK9" are applicable to all of the protein, peptide, polypeptide, and/or polynucleotide molecules covered by the term "PCSK9", as that term is defined herein. Comprehensively, such gene targets are also referred to herein generally as "target" sequences.

[0017] In one embodiment, the invention features a composition comprising two or more different siNA molecules and/or RNAi inhibitors of the invention (e.g., siNA, duplex

forming siNA, or multifunctional siNA or any combination thereof) targeting different polynucleotide targets, such as different regions of PCSK9 RNA or DNA (e.g., two different target sites such as provided herein or any combination of PCSK9 targets or PCSK9 pathway targets) or both coding and non-coding targets. Such pools of siNA molecules can provide increased therapeutic effect.

[0018] In one embodiment, the invention features a pool of two or more different siNA molecules of the invention (e.g., siNA, duplex forming siNA, or multifunctional siNA or any combination thereof) that have specificity for different polynucleotide targets, such as different regions of PCSK9 RNA or DNA (e.g., two different target sites herein or any combination of PCSK9 targets or PCSK9 pathway targets) or both coding and non-coding targets, wherein the pool comprises siNA molecules targeting about 2, 3, 4, 5, 6, 7, 8, 9, 10 or more different PCSK9 targets.

[0019] Due to the potential for sequence variability of the PCSK9 genome across different organisms or different subjects, selection of siNA molecules for broad therapeutic applications likely involve the conserved regions of the PCSK9 gene. In one embodiment, the present invention relates to siNA molecules and/or RNAi inhibitors that target conserved regions of the PCSK9 genome or regions that are conserved across different PCSK9 targets. siNA molecules and/or RNAi inhibitors designed to target conserved regions of various PCSK9 targets enable efficient inhibition of PCSK9 target gene expression in diverse patient populations.

[0020] In one embodiment, the invention features a double stranded nucleic acid molecule, such as an siNA molecule, where one of the strands comprises nucleotide sequence having complementarity to a predetermined nucleotide sequence in a PCSK9 target nucleic acid molecule, or a portion thereof. The predetermined nucleotide sequence can be a nucleotide PCSK9 target sequence, such as a sequence described herein or known in the art.

[0021] In another embodiment, the predetermined nucleotide sequence is a PCSK9 target sequence or PCSK9 pathway target sequence as is known in the art.

[0022] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, wherein said siNA molecule comprises about 15 to about 28 base pairs.

[0023] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a PCSK9 target RNA, wherein said siNA molecule comprises about 15 to about 28 base pairs.

[0024] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a PCSK9 target RNA via RNA interference (RNAi), wherein the double stranded siNA molecule comprises a first strand and a second strand, each strand of the siNA molecule is about 18 to about 28 (e.g., about 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28) nucleotides in length, the first strand of the siNA molecule comprises nucleotide sequence having sufficient complementarity to the PCSK9 target RNA for the siNA molecule to direct cleavage of the PCSK9 target RNA via RNA interference, and the second strand of said siNA molecule comprises nucleotide sequence that is complementary to the first strand. In one specific embodiment, for example, each strand of the siNA molecule is about 18 to about 27 nucleotides in length.

[0025] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a PCSK9 target RNA via RNA interference (RNAi), wherein the double stranded siNA molecule comprises a first strand and a second strand, each strand of the siNA molecule is about 18 to about 23 (e.g., about 18, 19, 20, 21, 22, or 23) nucleotides in length, the first strand of the siNA molecule comprises nucleotide sequence having sufficient complementarity to the PCSK9 target RNA for the siNA molecule to direct cleavage of the PCSK9 target RNA via RNA interference, and the second strand of said siNA molecule comprises nucleotide sequence that is complementary to the first strand.

[0026] In one embodiment, the invention features a chemically synthesized double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a PCSK9 target RNA via RNA interference (RNAi), wherein each strand of the siNA molecule is about 18 to about 28 nucleotides in length; and one strand of the siNA molecule comprises nucleotide sequence having sufficient complementarity to the PCSK9 target RNA for the siNA molecule to direct cleavage of the PCSK9 target RNA via RNA interference.

[0027] In one embodiment, the invention features a chemically synthesized double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a PCSK9 target RNA via RNA interference (RNAi), wherein each strand of the siNA molecule is about 18 to about 23 nucleotides in length; and one strand of the siNA molecule comprises nucleotide sequence having sufficient complementarity to the PCSK9 target RNA for the siNA molecule to direct cleavage of the PCSK9 target RNA via RNA interference.

[0028] In one embodiment, the invention features a siNA molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, for example, wherein the PCSK9 target gene or RNA comprises protein encoding sequence. In one embodiment, the invention features a siNA molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, for example, wherein the PCSK9 target gene or RNA comprises non-coding sequence or regulatory elements involved in PCSK9 target gene expression (e.g., non-coding RNA, miRNA, siRNA etc.).

[0029] In one embodiment, a siNA of the invention is used to inhibit the expression of PCSK9 target genes or a PCSK9 target gene family, wherein the genes or gene family sequences share sequence homology. Such homologous sequences can be identified as is known in the art, for example using sequence alignments. siNA molecules can be designed to target such homologous sequences, for example using perfectly complementary sequences or by incorporating non-canonical base pairs, for example mismatches and/or wobble base pairs, that can provide additional PCSK9 target sequences. In instances where mismatches are identified, non-canonical base pairs (for example, mismatches and/or wobble bases) can be used to generate siNA molecules that target more than one gene sequence. In a non-limiting example, non-canonical base pairs such as UU and CC base pairs are used to generate siNA molecules that are capable of PCSK9 targeting sequences for differing polynucleotide PCSK9 targets that share sequence homology. As such, one advantage of using siNAs of the invention is that a single siNA can be designed to include nucleic acid sequence that is complementary to the nucleotide sequence that is conserved between the homologous genes. In this approach, a single

siNA can be used to inhibit expression of more than one gene instead of using more than one siNA molecule to target the different genes.

[0030] In one embodiment, the invention features a siNA molecule having RNAi activity against PCSK9 target RNA (e.g., coding or non-coding RNA), wherein the siNA molecule comprises a sequence complementary to any RNA sequence, such as those sequences having GenBank Accession Nos. shown in Table I herein, or in PCT/US03/05028 and U.S. Ser. No. 10/923,536, both incorporated by reference herein. In another embodiment, the invention features a siNA molecule having RNAi activity against PCSK9 target RNA, wherein the siNA molecule comprises a sequence complementary to an RNA having variant encoding sequence, for example other mutant genes known in the art to be associated with the maintenance and/or development of diseases, traits, disorders, and/or conditions described herein or otherwise known in the art. Chemical modifications as shown in Table IV or otherwise described herein can be applied to any siNA construct of the invention. In another embodiment, a siNA molecule of the invention includes a nucleotide sequence that can interact with nucleotide sequence of a PCSK9 target gene and thereby mediate silencing of PCSK9 target gene expression, for example, wherein the siNA mediates regulation of PCSK9 target gene expression by cellular processes that modulate the chromatin structure or methylation patterns of the PCSK9 target gene and prevent transcription of the PCSK9 target gene.

[0031] In one embodiment, siNA molecules of the invention are used to down regulate or inhibit the expression of proteins arising from haplotype polymorphisms that are associated with a trait, disease or condition in a subject or organism. Analysis of genes, or protein or RNA levels can be used to identify subjects with such polymorphisms or those subjects who are at risk of developing traits, conditions, or diseases described herein. These subjects are amenable to treatment, for example, treatment with siNA molecules of the invention and any other composition useful in treating diseases related to target gene expression. As such, analysis of protein or RNA levels can be used to determine treatment type and the course of therapy in treating a subject. Monitoring of protein or RNA levels can be used to predict treatment outcome and to determine the efficacy of compounds and compositions that modulate the level and/or activity of certain proteins associated with a trait, disorder, condition, or disease.

[0032] In one embodiment of the invention a siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a PCSK9 target protein. The siNA further comprises a sense strand, wherein said sense strand comprises a nucleotide sequence of a PCSK9 target gene or a portion thereof.

[0033] In another embodiment, a siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence encoding a PCSK9 target protein or a portion thereof. The siNA molecule further comprises a sense region, wherein said sense region comprises a nucleotide sequence of a PCSK9 target gene or a portion thereof.

[0034] In another embodiment, the invention features a siNA molecule comprising nucleotide sequence, for example, nucleotide sequence in the antisense region of the siNA molecule that is complementary to a nucleotide

sequence or portion of sequence of a PCSK9 target gene. In another embodiment, the invention features a siNA molecule comprising a region, for example, the antisense region of the siNA construct, complementary to a sequence comprising a PCSK9 target gene sequence or a portion thereof.

[0035] In one embodiment, the sense region or sense strand of a siNA molecule of the invention is complementary to that portion of the antisense region or antisense strand of the siNA molecule that is complementary to a PCSK9 target polynucleotide sequence.

[0036] In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example, the antisense sequence of the siNA construct, complementary to a sequence or portion of sequence comprising sequence represented by GenBank Accession Nos. shown in Table I and in PCT/US03/05028 and U.S. Ser. No. 10/923,536, both incorporated by reference herein. Chemical modifications in Tables III and IV and described herein can be applied to any siNA construct of the invention. LNP formulations described in Table VI can be applied to any siNA molecule or combination of siNA molecules herein.

[0037] In one embodiment of the invention a siNA molecule comprises an antisense strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein the antisense strand is complementary to a PCSK9 target RNA sequence or a portion thereof, and wherein said siNA further comprises a sense strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences where at least about 15 nucleotides in each strand are complementary to the other strand.

[0038] In one embodiment, a siNA molecule of the invention (e.g., a double stranded nucleic acid molecule) comprises an antisense (guide) strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides that are complementary to a RNA sequence of PCSK9 or a portion thereof. In one embodiment, at least 15 nucleotides (e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides) of a PCSK9 RNA sequence are complementary to the antisense (guide) strand of a siNA molecule of the invention.

[0039] In one embodiment, a siNA molecule of the invention (e.g., a double stranded nucleic acid molecule) comprises a sense (passenger) strand having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides that comprise sequence of a PCSK9 RNA or a portion thereof. In one embodiment, at least 15 nucleotides (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides of a PCSK9 RNA sequence comprise the sense (passenger) strand of a siNA molecule of the invention.

[0040] In another embodiment of the invention a siNA molecule of the invention comprises an antisense region having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein the antisense region is complementary to a PCSK9 target DNA sequence, and wherein said siNA further comprises a sense region having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein said sense region and said antisense region are comprised in a linear molecule where the sense region comprises at least about 15 nucleotides that are complementary to the antisense region.

[0041] In one embodiment, a siNA molecule of the invention has RNAi activity that modulates expression of RNA encoded by a PCSK9 gene. Because PCSK9 genes can share some degree of sequence homology with each other, siNA molecules can be designed to target a class of PCSK9 genes by selecting sequences that are either shared amongst different PCSK9 targets or alternatively that are unique for a specific PCSK9 target. Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of PCSK9 polynucleotide sequences having homology among several PCSK9 gene variants so as to target a class of PCSK9 genes with one siNA molecule. Accordingly, in one embodiment, the siNA molecule of the invention modulates the expression of one or more PCSK9 isoforms or variants in a subject or organism. In another embodiment, the siNA molecule can be designed to target a sequence that is unique to a specific PCSK9 polynucleotide sequence (e.g., a single PCSK9 isoform or PCSK9 single nucleotide polymorphism (SNP)) due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity.

[0042] In one embodiment, nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are double-stranded nucleic acid molecules. In another embodiment, the siNA molecules of the invention consist of duplex nucleic acid molecules containing about 15 to about 30 base pairs between oligonucleotides comprising about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplex nucleic acid molecules with overhanging ends of about 1 to about 3 (e.g., about 1, 2, or 3) nucleotides, for example, about 21-nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide, dinucleotide, or trinucleotide overhangs. In yet another embodiment, siNA molecules of the invention comprise duplex nucleic acid molecules with blunt ends, where both ends are blunt, or alternatively, where one of the ends is blunt.

[0043] In one embodiment, a double stranded nucleic acid (e.g., siNA) molecule comprises nucleotide or non-nucleotide overhangs. By "overhang" is meant a terminal portion of the nucleotide sequence that is not base paired between the two strands of a double stranded nucleic acid molecule (see for example FIG. 6). In one embodiment, a double stranded nucleic acid molecule of the invention can comprise nucleotide or non-nucleotide overhangs at the 3'-end of one or both strands of the double stranded nucleic acid molecule. For example, a double stranded nucleic acid molecule of the invention can comprise a nucleotide or non-nucleotide overhang at the 3'-end of the guide strand or antisense strand/region, the 3'-end of the passenger strand or sense strand/region, or both the guide strand or antisense strand/region and the passenger strand or sense strand/region of the double stranded nucleic acid molecule. In another embodiment, the nucleotide overhang portion of a double stranded nucleic acid (siNA) molecule of the invention comprises 2'-O-methyl, 2'-deoxy, 2'-deoxy-2'-fluoro, 2'-deoxy-2'-fluoroarabino (FANA), 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, universal base, acyclic, or 5-C-methyl nucleotides. In another embodiment, the non-nucleotide overhang portion of a double stranded nucleic acid (siNA) molecule of the invention comprises glyceryl, abasic, or inverted deoxy abasic non-nucleotides.

[0044] In one embodiment, the nucleotides comprising the overhang portions of a double stranded nucleic acid (e.g.,

siNA) molecule of the invention correspond to the nucleotides comprising the PCSK9 target polynucleotide sequence of the siNA molecule. Accordingly, in such embodiments, the nucleotides comprising the overhang portion of a siNA molecule of the invention comprise sequence based on the PCSK9 target polynucleotide sequence in which nucleotides comprising the overhang portion of the guide strand or antisense strand/region of a siNA molecule of the invention can be complementary to nucleotides in the PCSK9 target polynucleotide sequence and nucleotides comprising the overhang portion of the passenger strand or sense strand/region of a siNA molecule of the invention can comprise the nucleotides in the PCSK9 target polynucleotide sequence. Such nucleotide overhangs comprise sequence that would result from Dicer processing of a native dsRNA into siRNA.

[0045] In one embodiment, the nucleotides comprising the overhang portion of a double stranded nucleic acid (e.g., siNA) molecule of the invention are complementary to the PCSK9 target polynucleotide sequence and are optionally chemically modified as described herein. As such, in one embodiment, the nucleotides comprising the overhang portion of the guide strand or antisense strand/region of a siNA molecule of the invention can be complementary to nucleotides in the PCSK9 target polynucleotide sequence, i.e. those nucleotide positions in the PCSK9 target polynucleotide sequence that are complementary to the nucleotide positions of the overhang nucleotides in the guide strand or antisense strand/region of a siNA molecule. In another embodiment, the nucleotides comprising the overhang portion of the passenger strand or sense strand/region of a siNA molecule of the invention can comprise the nucleotides in the PCSK9 target polynucleotide sequence, i.e. those nucleotide positions in the PCSK9 target polynucleotide sequence that correspond to the same nucleotide positions of the overhang nucleotides in the passenger strand or sense strand/region of a siNA molecule. In one embodiment, the overhang comprises a two nucleotide (e.g., 3'-GA; 3'-GU; 3'-GG; 3'-GC; 3'-CA; 3'-CU; 3'-CG; 3'-CC; 3'-UA; 3'-UU; 3'-UG; 3'-UC; 3'-AA; 3'-AU; 3'-AG; 3'-AC; 3'-TA; 3'-TC; 3'-TU; 3'-TG; 3'-TC; 3'-AT; 3'-UT; 3'-GT; 3'-CT) overhang that is complementary to a portion of the PCSK9 target polynucleotide sequence. In one embodiment, the overhang comprises a two nucleotide (e.g., 3'-GA; 3'-GU; 3'-GG; 3'-GC; 3'-CA; 3'-CU; 3'-CG; 3'-CC; 3'-UA; 3'-UU; 3'-UG; 3'-UC; 3'-AA; 3'-AU; 3'-AG; 3'-AC; 3'-TA; 3'-TU; 3'-TG; 3'-TC; 3'-AT; 3'-UT; 3'-GT; 3'-CT) overhang that is not complementary to a portion of the PCSK9 target polynucleotide sequence. In another embodiment, the overhang nucleotides of a siNA molecule of the invention are 2'-O-methyl nucleotides, 2'-deoxy-2'-fluoroarabino, and/or 2'-deoxy-2'-fluoro nucleotides. In another embodiment, the overhang nucleotides of a siNA molecule of the invention are 2'-O-methyl nucleotides in the event the overhang nucleotides are purine nucleotides and/or 2'-deoxy-2'-fluoro nucleotides or 2'-deoxy-2'-fluoroarabino nucleotides in the event the overhang nucleotides are pyrimidines nucleotides. In another embodiment, the purine nucleotide (when present) in an overhang of siNA molecule of the invention is 2'-O-methyl nucleotides. In another embodiment, the pyrimidine nucleotide (when present) in an overhang of siNA molecule of the invention are 2'-deoxy-2'-fluoro or 2'-deoxy-2'-fluoroarabino nucleotides.

[0046] In one embodiment, the nucleotides comprising the overhang portion of a double stranded nucleic acid (e.g., siNA) molecule of the invention are not complementary to the

PCSK9 target polynucleotide sequence and are optionally chemically modified as described herein. In one embodiment, the overhang comprises a 3'-UU overhang that is not complementary to a portion of the PCSK9 target polynucleotide sequence. In another embodiment, the nucleotides comprising the overhanging portion of a siNA molecule of the invention are 2'-O-methyl nucleotides, 2'-deoxy-2'-fluoroarabino and/or 2'-deoxy-2'-fluoro nucleotides.

[0047] In one embodiment, the double stranded nucleic molecule (e.g. siNA) of the invention comprises a two or three nucleotide overhang, wherein the nucleotides in the overhang are the same or different. In one embodiment, the double stranded nucleic molecule (e.g. siNA) of the invention comprises a two or three nucleotide overhang, wherein the nucleotides in the overhang are the same or different and wherein one or more nucleotides in the overhang are chemically modified at the base, sugar and/or phosphate backbone.

[0048] In one embodiment, the invention features one or more chemically-modified siNA constructs having specificity for PCSK9 target nucleic acid molecules, such as DNA, or RNA encoding a protein or non-coding RNA associated with the expression of PCSK9 target genes. In one embodiment, the invention features a RNA based siNA molecule (e.g., a siNA comprising 2'-OH nucleotides) having specificity for nucleic acid molecules that includes one or more chemical modifications described herein. Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, 4'-thio ribonucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides (see for example U.S. Ser. No. 10/981,966 filed Nov. 5, 2004, incorporated by reference herein), "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, 2'-deoxy-2'-fluoroarabino (FANA, see for example Dowler et al., 2006, Nucleic Acids Research, 34, 1669-1675) and terminal glyceryl and/or inverted deoxy abasic residue incorporation. These chemical modifications, when used in various siNA constructs, (e.g., RNA based siNA constructs), are shown to preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds.

[0049] In one embodiment, a siNA molecule of the invention comprises chemical modifications described herein (e.g., 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, 4'-thio ribonucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides, LNA) at the internal positions of the siNA molecule. By "internal position" is meant the base paired positions of a siNA duplex.

[0050] In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve in vitro or in vivo characteristics such as stability, activity, toxicity, immune response, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). For example, in one embodiment, between about 5% to about 100% (e.g., about 5%, 10%, 15%, 20%,

25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides) of the nucleotide positions in a siNA molecule of the invention comprise a nucleic acid sugar modification, such as a 2'-sugar modification, e.g., 2'-O-methyl nucleotides, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-fluoroarabino, 2'-O-methoxyethyl nucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxyethoxy nucleotides, or 2'-deoxy nucleotides. In another embodiment, between about 5% to about 100% (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides) of the nucleotide positions in a siNA molecule of the invention comprise a nucleic acid base modification, such as inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2,4,6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (e.g., 5-methylcytidine), 5-alkyluridines (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6-methyluridine), or propyne modifications. In another embodiment, between about 5% to about 100% (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides) of the nucleotide positions in a siNA molecule of the invention comprise a nucleic acid backbone modification, such as a backbone modification having Formula I herein. In another embodiment, between about 5% to about 100% (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides) of the nucleotide positions in a siNA molecule of the invention comprise a nucleic acid sugar, base, or backbone modification or any combination thereof (e.g., any combination of nucleic acid sugar, base, backbone or non-nucleotide modifications herein). In one embodiment, a siNA molecule of the invention comprises at least about 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides. The actual percentage of modified nucleotides present in a given siNA molecule will depend on the total number of nucleotides present in the siNA. If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands.

[0051] A siNA molecule of the invention can comprise modified nucleotides at various locations within the siNA molecule. In one embodiment, a double stranded siNA molecule of the invention comprises modified nucleotides at internal base paired positions within the siNA duplex. For example, internal positions can comprise positions from about 3 to about 19 nucleotides from the 5'-end of either sense or antisense strand or region of a 21 nucleotide siNA duplex having 19 base pairs and two nucleotide 3'-overhangs. In another embodiment, a double stranded siNA molecule of the invention comprises modified nucleotides at non-base paired or overhang regions of the siNA molecule. By "non-base paired" is meant, the nucleotides are not base paired between the sense strand or sense region and the antisense strand or antisense region or the siNA molecule. The overhang nucleotides can be complementary or base paired to a corresponding PCSK9 target polynucleotide sequence (see for example

FIG. 6C). For example, overhang positions can comprise positions from about 20 to about 21 nucleotides from the 5'-end of either sense or antisense strand or region of a 21 nucleotide siNA duplex having 19 base pairs and two nucleotide 3'-overhangs. In another embodiment, a double stranded siNA molecule of the invention comprises modified nucleotides at terminal positions of the siNA molecule. For example, such terminal regions include the 3'-position, 5'-position, for both 3' and 5'-positions of the sense and/or antisense strand or region of the siNA molecule. In another embodiment, a double stranded siNA molecule of the invention comprises modified nucleotides at base-paired or internal positions, non-base paired or overhang regions, and/or terminal regions, or any combination thereof.

[0052] One aspect of the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA. In one embodiment, the double stranded siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is about 21 nucleotides long. In one embodiment, the double-stranded siNA molecule does not contain any ribonucleotides. In another embodiment, the double-stranded siNA molecule comprises one or more ribonucleotides. In one embodiment, each strand of the double-stranded siNA molecule independently comprises about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein each strand comprises about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides that are complementary to the nucleotides of the other strand. In one embodiment, one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof of the PCSK9 target gene, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence of the PCSK9 target gene or a portion thereof.

[0053] In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, comprising an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of the PCSK9 target gene or a portion thereof, and a sense region, wherein the sense region comprises a nucleotide sequence substantially similar to the nucleotide sequence of the PCSK9 target gene or a portion thereof. In one embodiment, the antisense region and the sense region independently comprise about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, wherein the antisense region comprises about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides that are complementary to nucleotides of the sense region.

[0054] In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the PCSK9

target gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region.

[0055] In one embodiment, a siNA molecule of the invention comprises blunt ends, i.e., ends that do not include any overhanging nucleotides. For example, a siNA molecule comprising modifications described herein (e.g., comprising nucleotides having Formulae I-VII or siNA constructs comprising "Stab 00"- "Stab 36" or "Stab 3F"- "Stab 36F" (Table IV) or any combination thereof (see Table IV)) and/or any length described herein can comprise blunt ends or ends with no overhanging nucleotides.

[0056] In one embodiment, any siNA molecule of the invention can comprise one or more blunt ends, i.e. where a blunt end does not have any overhanging nucleotides. In one embodiment, the blunt ended siNA molecule has a number of base pairs equal to the number of nucleotides present in each strand of the siNA molecule. In another embodiment, the siNA molecule comprises one blunt end, for example wherein the 5'-end of the antisense strand and the 3'-end of the sense strand do not have any overhanging nucleotides. In another example, the siNA molecule comprises one blunt end, for example, wherein the 3'-end of the antisense strand and the 5'-end of the sense strand do not have any overhanging nucleotides. In another example, a siNA molecule comprises two blunt ends, for example, wherein the 3'-end of the antisense strand and the 5'-end of the sense strand as well as the 5'-end of the antisense strand and 3'-end of the sense strand do not have any overhanging nucleotides. A blunt ended siNA molecule can comprise, for example, from about 15 to about 30 nucleotides (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides). Other nucleotides present in a blunt ended siNA molecule can comprise, for example, mismatches, bulges, loops, or wobble base pairs to modulate the activity of the siNA molecule to mediate RNA interference.

[0057] By "blunt ends" is meant symmetric termini or termini of a double stranded siNA molecule having no overhanging nucleotides. The two strands of a double stranded siNA molecule align with each other without over-hanging nucleotides at the termini. For example, a blunt ended siNA construct comprises terminal nucleotides that are complementary between the sense and antisense regions of the siNA molecule.

[0058] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. The sense region can be connected to the antisense region via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker.

[0059] In one embodiment, a double stranded nucleic acid molecule (e.g., siNA) molecule of the invention comprises ribonucleotides at positions that maintain or enhance RNAi activity. In one embodiment, ribonucleotides are present in the sense strand or sense region of the siNA molecule, which can provide for RNAi activity by allowing cleavage of the sense strand or sense region by an enzyme within the RISC (e.g., ribonucleotides present at the position of passenger strand, sense strand, or sense region cleavage, such as position 9 of the passenger strand of a 19 base-pair duplex, which

is cleaved in the RISC by AGO2 enzyme, see, for example, Matranga et al., 2005, *Cell*, 123:1-114 and Rand et al., 2005, *Cell*, 123:621-629). In another embodiment, one or more (for example 1, 2, 3, 4 or 5) nucleotides at the 5'-end of the guide strand or guide region (also known as antisense strand or antisense region) of the siNA molecule are ribonucleotides.

[0060] In one embodiment, a double stranded nucleic acid molecule (e.g., siNA) molecule of the invention comprises one or more ribonucleotides at positions within the passenger strand or passenger region (also known as the sense strand or sense region) that allows cleavage of the passenger strand or passenger region by an enzyme in the RISC complex, (e.g., ribonucleotides present at the position of passenger strand, such as position 9 of the passenger strand of a 19 base-pair duplex that is cleaved in the RISC, see, for example, Matranga et al., 2005, *Cell*, 123:1-114 and Rand et al., 2005, *Cell*, 123:621-629).

[0061] In one embodiment, a siNA molecule of the invention contains at least 2, 3, 4, 5, or more chemical modifications that can be the same or different. In one embodiment, a siNA molecule of the invention contains at least 2, 3, 4, 5, or more different chemical modifications.

[0062] In one embodiment, a siNA molecule of the invention is a double-stranded short interfering nucleic acid (siNA), wherein the double stranded nucleic acid molecule comprises about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs, and wherein one or more (e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) of the nucleotide positions in each strand of the siNA molecule comprises a chemical modification. In another embodiment, the siNA contains at least 2, 3, 4, 5, or more different chemical modifications.

[0063] In one embodiment, the invention features double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, wherein the siNA molecule comprises about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs, and wherein each strand of the siNA molecule comprises one or more chemical modifications. In one embodiment, each strand of the double stranded siNA molecule comprises at least two (e.g., 2, 3, 4, 5, or more) different chemical modifications, e.g., different nucleotide sugar, base, or backbone modifications. In another embodiment, one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence of a PCSK9 target gene or a portion thereof, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence or a portion thereof of the PCSK9 target gene. In another embodiment, one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence of a PCSK9 target gene or portion thereof, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence or portion thereof of the PCSK9 target gene. In another embodiment, each strand of the siNA molecule comprises about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides, and each strand comprises at least about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides that are complementary to the nucleotides of the other strand. The

PCSK9 target gene can comprise, for example, sequences referred to herein or incorporated herein by reference. The PCSK9 gene can comprise, for example, sequences referred to in Table I.

[0064] In one embodiment, each strand of a double stranded siNA molecule of the invention comprises a different pattern of chemical modifications, such as any "Stab 00"- "Stab 36" or "Stab 3F"- "Stab 36F" (Table IV) modification patterns herein or any combination thereof (see Table IV). Non-limiting examples of sense and antisense strands of such siNA molecules having various modification patterns are shown in Table III and FIGS. 4 and 5.

[0065] In one embodiment, a siNA molecule of the invention comprises no ribonucleotides. In another embodiment, a siNA molecule of the invention comprises one or more ribonucleotides (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more ribonucleotides).

[0066] In one embodiment, a siNA molecule of the invention comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence of a PCSK9 target gene or a portion thereof, and the siNA further comprises a sense region comprising a nucleotide sequence substantially similar to the nucleotide sequence of the PCSK9 target gene or a portion thereof. In another embodiment, the antisense region and the sense region each comprise about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides and the antisense region comprises at least about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides that are complementary to nucleotides of the sense region. In one embodiment, each strand of the double stranded siNA molecule comprises at least two (e.g., 2, 3, 4, 5, or more) different chemical modifications, e.g., different nucleotide sugar, base, or backbone modifications. The PCSK9 target gene can comprise, for example, sequences referred to herein or incorporated by reference herein. In another embodiment, the siNA is a double stranded nucleic acid molecule, where each of the two strands of the siNA molecule independently comprise about 15 to about 40 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40) nucleotides, and where one of the strands of the siNA molecule comprises at least about 15 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 or more) nucleotides that are complementary to the nucleic acid sequence of the PCSK9 target gene or a portion thereof.

[0067] In one embodiment, a siNA molecule of the invention comprises a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by a PCSK9 target gene, or a portion thereof, and the sense region comprises a nucleotide sequence that is complementary to the antisense region. In one embodiment, the siNA molecule is assembled from two separate oligonucleotide fragments, wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. In another embodiment, the sense region is connected to the antisense region via a linker molecule. In another embodiment, the sense region is connected to the antisense region via a linker molecule, such as a nucleotide or non-nucleotide linker. In one embodiment, each strand of the double stranded siNA molecule comprises at least two (e.g., 2, 3, 4, 5, or more) different chemical modifications, e.g., different nucleotide sugar, base, or backbone

modifications. The PCSK9 target gene can comprise, for example, sequences referred to herein or incorporated by reference herein.

[0068] In one embodiment, a siNA molecule of the invention comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) 2'-deoxy-2'-fluoro pyrimidine modifications (e.g., where one or more or all pyrimidine (e.g., U or C) positions of the siNA are modified with 2'-deoxy-2'-fluoro nucleotides). In one embodiment, the 2'-deoxy-2'-fluoro pyrimidine modifications are present in the sense strand. In one embodiment, the 2'-deoxy-2'-fluoro pyrimidine modifications are present in the antisense strand. In one embodiment, the 2'-deoxy-2'-fluoro pyrimidine modifications are present in both the sense strand and the antisense strand of the siNA molecule.

[0069] In one embodiment, a siNA molecule of the invention comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) 2'-O-methyl purine modifications (e.g., where one or more or all purine (e.g., A or G) positions of the siNA are modified with 2'-O-methyl nucleotides). In one embodiment, the 2'-O-methyl purine modifications are present in the sense strand. In one embodiment, the 2'-O-methyl purine modifications are present in the antisense strand. In one embodiment, the 2'-O-methyl purine modifications are present in both the sense strand and the antisense strand of the siNA molecule.

[0070] In one embodiment, a siNA molecule of the invention comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) 2'-deoxy purine modifications (e.g., where one or more or all purine (e.g., A or G) positions of the siNA are modified with 2'-deoxy nucleotides). In one embodiment, the 2'-deoxy purine modifications are present in the sense strand. In one embodiment, the 2'-deoxy purine modifications are present in the antisense strand. In one embodiment, the 2'-deoxy purine modifications are present in both the sense strand and the antisense strand of the siNA molecule.

[0071] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the PCSK9 target gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the siNA molecule has one or more modified pyrimidine and/or purine nucleotides. In one embodiment, each strand of the double stranded siNA molecule comprises at least two (e.g., 2, 3, 4, 5, or more) different chemical modifications, e.g., different nucleotide sugar, base, or backbone modifications. In one embodiment, the pyrimidine nucleotides in the sense region are 2'-O-methylpyrimidine nucleotides or 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In one embodiment, the pyrimidine nucleotides in the antisense region are 2'-deoxy-2'-

fluoro pyrimidine nucleotides and the purine nucleotides present in the antisense region are 2'- β -methyl or 2'-deoxy purine nucleotides. In another embodiment of any of the above-described siNA molecules, any nucleotides present in a non-complementary region of the sense strand (e.g. overhang region) are 2'-deoxy nucleotides.

[0072] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule, and wherein the fragment comprising the sense region includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the fragment. In one embodiment, the terminal cap moiety is an inverted deoxy abasic moiety or glycerol moiety. In one embodiment, each of the two fragments of the siNA molecule independently comprise about 15 to about 30 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides. In another embodiment, each of the two fragments of the siNA molecule independently comprise about 15 to about 40 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 23, 33, 34, 35, 36, 37, 38, 39, or 40) nucleotides. In a non-limiting example, each of the two fragments of the siNA molecule comprise about 21 nucleotides.

[0073] In one embodiment, the invention features a siNA molecule comprising at least one modified nucleotide, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy-2'-fluoroarabino, 2'-O-trifluoromethyl nucleotide, 2'-O-ethyl-trifluoromethoxy nucleotide, or 2'-O-difluoromethoxy-ethoxy nucleotide or any other modified nucleoside/nucleotide described herein and in U.S. Ser. No. 10/981,966, filed Nov. 5, 2004, incorporated by reference herein. In one embodiment, the invention features a siNA molecule comprising at least two (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) modified nucleotides, wherein the modified nucleotide is selected from the group consisting of 2'-deoxy-2'-fluoro nucleotide, 2'-deoxy-2'-fluoroarabino, 2'-O-trifluoromethyl nucleotide, 2'-O-ethyl-trifluoromethoxy nucleotide, or 2'-O-difluoromethoxy-ethoxy nucleotide or any other modified nucleoside/nucleotide described herein and in U.S. Ser. No. 10/981,966, filed Nov. 5, 2004, incorporated by reference herein. The modified nucleotide/nucleoside can be the same or different. The siNA can be, for example, about 15 to about 40 nucleotides in length. In one embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro, 2'-deoxy-2'-fluoroarabino, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy, 4'-thio pyrimidine nucleotides. In one embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In one embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In one embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In one embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro adenosine nucleotides. In one embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as a phosphorothioate linkage. In one embodiment, the 2'-deoxy-2'-fluoroarabinonucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

one modified internucleotidic linkage, such as phosphorothioate linkage. In one embodiment, the 2'-deoxy-2'-fluoroarabinonucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

[0074] In one embodiment, the invention features a method of increasing the stability of a siNA molecule against cleavage by ribonucleases comprising introducing at least one modified nucleotide into the siNA molecule, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide. In one embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In one embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In one embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In one embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In one embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro adenosine nucleotides. In one embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as a phosphorothioate linkage. In one embodiment, the 2'-deoxy-2'-fluoroarabinonucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

[0075] In one embodiment, the invention features a method of increasing the stability of a siNA molecule against cleavage by ribonucleases comprising introducing at least one modified nucleotide into the siNA molecule, wherein the modified nucleotide is a 2'-deoxy-2'-fluoroarabino nucleotide. In one embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoroarabino pyrimidine nucleotides. In one embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoroarabino cytidine or 2'-deoxy-2'-fluoroarabino uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoroarabino uridine nucleotides. In one embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoroarabino uridine nucleotides. In one embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoroarabino cytidine nucleotides. In one embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoroarabino adenosine nucleotides. In one embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoroarabino guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as a phosphorothioate linkage. In one embodiment, the 2'-deoxy-2'-fluoroarabinonucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

[0076] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the PCSK9 target

gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the purine nucleotides present in the antisense region comprise 2'-deoxy-purine nucleotides. In an alternative embodiment, the purine nucleotides present in the antisense region comprise 2'-O-methyl purine nucleotides. In either of the above embodiments, the antisense region can comprise a phosphorothioate internucleotide linkage at the 3' end of the antisense region. Alternatively, in either of the above embodiments, the antisense region can comprise a glyceryl modification at the 3' end of the antisense region. In another embodiment of any of the above-described siNA molecules, any nucleotides present in a non-complementary region of the antisense strand (e.g. overhang region) are 2'-deoxy nucleotides.

[0077] In one embodiment, the antisense region of a siNA molecule of the invention comprises sequence complementary to a portion of an endogenous transcript having sequence unique to a particular disease or trait related allele in a subject or organism, such as sequence comprising a single nucleotide polymorphism (SNP) associated with the disease or trait specific allele. As such, the antisense region of a siNA molecule of the invention can comprise sequence complementary to sequences that are unique to a particular allele to provide specificity in mediating selective RNAi against the disease, condition, or trait related allele.

[0078] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a PCSK9 target gene or that directs cleavage of a PCSK9 target RNA, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. In one embodiment, each strand of the double stranded siNA molecule is about 21 nucleotides long where about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule, wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule. In another embodiment, the siNA molecule is a double stranded nucleic acid molecule, where each strand is about 19 nucleotide long and where the nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule to form at least about 15 (e.g., 15, 16, 17, 18, or 19) base pairs, wherein one or both ends of the siNA molecule are blunt ends. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine nucleotide, such as a 2'-deoxy-thymidine. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-O-methylpyrimidine nucleotide, such as a 2'-O-methyl uridine, cytidine, or thymidine. In another embodiment, all nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule. In another embodiment, the siNA molecule is a double stranded nucleic acid molecule of about 19 to about 25 base pairs having a sense region and an antisense region, where about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the PCSK9 target gene. In another embodiment, about 21 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the

RNA encoded by the PCSK9 target gene. In any of the above embodiments, the 5'-end of the fragment comprising said antisense region can optionally include a phosphate group.

[0079] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of a PCSK9 target RNA sequence, wherein the siNA molecule does not contain any ribonucleotides and wherein each strand of the double-stranded siNA molecule is about 15 to about 30 nucleotides. In one embodiment, the siNA molecule is 21 nucleotides in length. Examples of non-ribonucleotide containing siNA constructs are combinations of stabilization chemistries shown in Table IV in any combination of Sense/Antisense chemistries, such as Stab 7/8, Stab 7/11, Stab 8/8, Stab 18/8, Stab 18/11, Stab 12/13, Stab 7/13, Stab 18/13, Stab 7/19, Stab 8/19, Stab 18/19, Stab 7/20, Stab 8/20, Stab 18/20, Stab 7/32, Stab 8/32, or Stab 18/32 (e.g., any siNA having Stab 7, 8, 11, 12, 13, 14, 15, 17, 18, 19, 20, or 32 sense or antisense strands or any combination thereof). Herein, numeric Stab chemistries can include both 2'-fluoro and 2'-OCF₃ versions of the chemistries shown in Table IV. For example, "Stab 7/8" refers to both Stab 7/8 and Stab 7F/8F etc. In one embodiment, the invention features a chemically synthesized double stranded RNA molecule that directs cleavage of a PCSK9 target RNA via RNA interference, wherein each strand of said RNA molecule is about 15 to about 30 nucleotides in length; one strand of the RNA molecule comprises nucleotide sequence having sufficient complementarity to the PCSK9 target RNA for the RNA molecule to direct cleavage of the PCSK9 target RNA via RNA interference; and wherein at least one strand of the RNA molecule optionally comprises one or more chemically modified nucleotides described herein, such as without limitation deoxynucleotides, 2'-O-methyl nucleotides, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-fluoroarabino, 2'-O-methoxyethyl nucleotides, 4'-thio nucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides, etc. or any combination thereof.

[0080] In one embodiment, a PCSK9 target RNA of the invention comprises sequence encoding a protein.

[0081] In one embodiment, PCSK9 target RNA of the invention comprises non-coding RNA sequence (e.g., miRNA, snRNA, siRNA etc.), see for example Mattick, 2005, *Science*, 309, 1527-1528; Clayerie, 2005, *Science*, 309, 1529-1530; Sethupathy et al., 2006, *RNA*, 12, 192-197; and Czech, 2006 *NEJM*, 354, 11: 1194-1195.

[0082] In one embodiment, the invention features a medicament comprising a siNA molecule of the invention.

[0083] In one embodiment, the invention features an active ingredient comprising a siNA molecule of the invention.

[0084] In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule to inhibit, down-regulate, or reduce expression of a PCSK9 target gene, wherein the siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is independently about 15 to about 30 or more (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 or more) nucleotides long. In one embodiment, the siNA molecule of the invention is a double stranded nucleic acid molecule comprising one or more chemical modifications, where each of the two fragments of the siNA molecule independently comprise about 15 to about 40 (e.g. about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40) nucleotides and

where one of the strands comprises at least 15 nucleotides that are complementary to nucleotide sequence of PCSK9 target encoding RNA or a portion thereof. In a non-limiting example, each of the two fragments of the siNA molecule comprise about 21 nucleotides. In another embodiment, the siNA molecule is a double stranded nucleic acid molecule comprising one or more chemical modifications, where each strand is about 21 nucleotide long and where about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule, wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule. In another embodiment, the siNA molecule is a double stranded nucleic acid molecule comprising one or more chemical modifications, where each strand is about 19 nucleotide long and where the nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule to form at least about 15 (e.g., 15, 16, 17, 18, or 19) base pairs, wherein one or both ends of the siNA molecule are blunt ends. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine nucleotide, such as a 2'-deoxy-thymidine. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-O-methylpyrimidine nucleotide, such as a 2'-O-methyl uridine, cytidine, or thymidine. In another embodiment, all nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule. In another embodiment, the siNA molecule is a double stranded nucleic acid molecule of about 19 to about 25 base pairs having a sense region and an antisense region and comprising one or more chemical modifications, where about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the PCSK9 target gene. In another embodiment, about 21 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the PCSK9 target gene. In any of the above embodiments, the 5'-end of the fragment comprising said antisense region can optionally include a phosphate group.

[0085] In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule that inhibits, down-regulates, or reduces expression of a PCSK9 target gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of PCSK9 target RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand. In one embodiment, each strand has at least two (e.g., 2, 3, 4, 5, or more) chemical modifications, which can be the same or different, such as nucleotide, sugar, base, or backbone modifications. In one embodiment, a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, a majority of the purine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

[0086] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits, down-regulates, or reduces expression of a PCSK9 target gene, wherein one of the strands of the double-stranded

siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of PCSK9 target RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand. In one embodiment, each strand has at least two (e.g., 2, 3, 4, 5, or more) chemical modifications, which can be the same or different, such as nucleotide, sugar, base, or backbone modifications. In one embodiment, a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, a majority of the purine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

[0087] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits, down-regulates, or reduces expression of a PCSK9 target gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of PCSK9 target RNA that encodes a protein or portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, each strand of the siNA molecule comprises about 15 to about 30 or more (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 or more) nucleotides, wherein each strand comprises at least about 15 nucleotides that are complementary to the nucleotides of the other strand. In one embodiment, the siNA molecule is assembled from two oligonucleotide fragments, wherein one fragment comprises the nucleotide sequence of the antisense strand of the siNA molecule and a second fragment comprises nucleotide sequence of the sense region of the siNA molecule. In one embodiment, the sense strand is connected to the antisense strand via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker. In a further embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2' fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2' fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In still another embodiment, the pyrimidine nucleotides present in the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-O-methyl purine nucleotides. In a further embodiment the sense strand comprises a 3'-end and a 5'-end, wherein a terminal cap moiety (e.g., an inverted deoxy abasic moiety or inverted deoxy nucleotide moiety such as inverted thymidine) is present at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the sense strand. In another embodiment, the antisense strand comprises a phosphorothioate internucleotide linkage at the 3' end of the antisense strand. In another embodiment, the antisense strand comprises a glycerol modification at the

3' end. In another embodiment, the 5'-end of the antisense strand optionally includes a phosphate group.

[0088] In any of the above-described embodiments of a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a PCSK9 target gene, wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, each of the two strands of the siNA molecule can comprise about 15 to about 30 or more (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 or more) nucleotides. In one embodiment, about 15 to about 30 or more (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 or more) nucleotides of each strand of the siNA molecule are base-paired to the complementary nucleotides of the other strand of the siNA molecule. In another embodiment, about 15 to about 30 or more (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 or more) nucleotides of each strand of the siNA molecule are base-paired to the complementary nucleotides of the other strand of the siNA molecule, wherein at least two 3' terminal nucleotides of each strand of the siNA molecule are not base-paired to the nucleotides of the other strand of the siNA molecule. In another embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine, such as 2'-deoxy-thymidine. In one embodiment, each strand of the siNA molecule is base-paired to the complementary nucleotides of the other strand of the siNA molecule. In one embodiment, about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides of the antisense strand are base-paired to the nucleotide sequence of the PCSK9 target RNA or a portion thereof. In one embodiment, about 18 to about 25 (e.g., about 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides of the antisense strand are base-paired to the nucleotide sequence of the PCSK9 target RNA or a portion thereof.

[0089] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a PCSK9 target gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of PCSK9 target RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand. In one embodiment, each strand has at least two (e.g., 2, 3, 4, 5, or more) different chemical modifications, such as nucleotide sugar, base, or backbone modifications. In one embodiment, a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, a majority of the purine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, the 5'-end of the antisense strand optionally includes a phosphate group.

[0090] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a PCSK9 target gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of PCSK9 target RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modifica-

tion, and wherein the nucleotide sequence or a portion thereof of the antisense strand is complementary to a nucleotide sequence of the untranslated region or a portion thereof of the PCSK9 target RNA.

[0091] In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a PCSK9 target gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of PCSK9 target RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand, wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein the nucleotide sequence of the antisense strand is complementary to a nucleotide sequence of the PCSK9 target RNA or a portion thereof that is present in the PCSK9 target RNA.

[0092] In one embodiment, the invention features a composition comprising a siNA molecule of the invention and a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features two or more differing siNA molecules of the invention (e.g. siNA molecules that target different regions of PCSK9 target RNA or siNA molecules that target PCSK9 pathway RNA) and a pharmaceutically acceptable carrier or diluent.

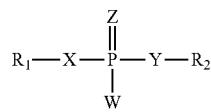
[0093] In a non-limiting example, the introduction of chemically-modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of in vivo stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically-modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically-modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by PCSK9 targeting particular cells or tissues and/or improving cellular uptake of the nucleic acid molecule. Therefore, even if the activity of a chemically-modified nucleic acid molecule is reduced as compared to a native nucleic acid molecule, for example, when compared to an all-RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than that of the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siNA, chemically-modified siNA can also minimize the possibility of activating interferon activity or immunostimulation in humans.

[0094] In any of the embodiments of siNA molecules described herein, the antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the antisense region can comprise about one to about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. In any of the embodiments of

siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

[0095] One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding a PCSK9 target and the sense region can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

[0096] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein the chemical modification comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:

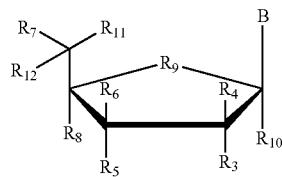


[0097] wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified and which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or acetyl and wherein W, X, Y, and Z are optionally not all O. In another embodiment, a backbone modification of the invention comprises a phosphonoacetate and/or thiophosphonoacetate internucleotide linkage (see for example Sheehan et al., 2003, Nucleic Acids Research, 31, 4109-4118).

[0098] The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulphur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting

example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide or non-nucleotide having any of Formulae I-VII.

[0099] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein the chemical modification comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula II:

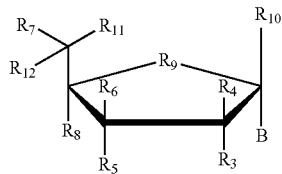


wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCH3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-5-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having any of Formula I, II, III, IV, V, VI and/or VII, any of which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA. In one embodiment, R3 and/or R7 comprises a conjugate moiety and a linker (e.g., a nucleotide or non-nucleotide linker as described herein or otherwise known in the art). Non-limiting examples of conjugate moieties include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylglucosamine; polymers, such as polyethylene glycol (PEG); phospholipids; cholesterol; steroids, and polyamines, such as PEI, spermine or spermidine. In one embodiment, a nucleotide of the invention having Formula II is a 2'-deoxy-2'-fluoro nucleotide. In one embodiment, a nucleotide of the invention having Formula II is a 2'-O-methyl nucleotide. In one embodiment, a nucleotide of the invention having Formula II is a 2'-deoxy nucleotide.

[0100] The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucle-

otide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end of the sense strand, the antisense strand, or both strands.

[0101] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein the chemical modification comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula III:



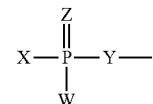
wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCH₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-O SH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-5-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having any of Formula I, II, III, IV, V, VI and/or VII, any of which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule; R9 is O, S, CH₂, S=O, CHF, or CF₂, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA. In one embodiment, R3 and/or R7 comprises a conjugate moiety and a linker (e.g., a nucleotide or non-nucleotide linker as described herein or otherwise known in the art). Non-limiting examples of conjugate moieties include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as

polyethyleneglycol (PEG); phospholipids; cholesterol; steroids, and polyamines, such as PEI, spermine or spermidine.

[0102] The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotides or non-nucleotides of Formula III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

[0103] In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3',3'-2',2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

[0104] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, alkylhalo, or acetyl; and wherein W, X, Y and Z are optionally not all 0 and Y serves as a point of attachment to the siNA molecule.

[0105] In one embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the PCSK9 target-complementary strand, for example, a strand complementary to a PCSK9 target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the PCSK9 target-complementary strand wherein the siNA molecule also comprises about 1 to about 3 (e.g., about 1, 2, or 3) nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (e.g., about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the PCSK9 target-complementary strand of a siNA molecule of the invention, for example a siNA molecule having chemical modifications having any of Formulae I-VII.

[0106] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For example, in a non-limiting example, the invention features a chemically-modified short interfering nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA strands. The phosphorothioate internucleotide linkages can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (e.g., about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands.

[0107] Each strand of the double stranded siNA molecule can have one or more chemical modifications such that each strand comprises a different pattern of chemical modifications. Several non-limiting examples of modification schemes that could give rise to different patterns of modifications are provided herein.

[0108] In one embodiment, the invention features a siNA molecule, wherein the sense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy and/or about one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

romethoxy-ethoxy, 4'-thio and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

[0109] In another embodiment, the invention features a siNA molecule, wherein the sense strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

[0110] In one embodiment, the invention features a siNA molecule, wherein the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or about one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate inter-

nucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

[0111] In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy, 4'-thio and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

[0112] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule having about 1 to about 5 or more (specifically about 1, 2, 3, 4, 5 or more) phosphorothioate internucleotide linkages in each strand of the siNA molecule.

[0113] In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the 2'-5' internucleotide linkage(s) can be present at various other positions within one or both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

[0114] In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified, wherein each strand is independently about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length, wherein the duplex has about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs, and wherein the chemical modification comprises a structure having any of Formulae I-VII. For example, an exemplary chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-

modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (e.g., about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 42 to about 50 (e.g., about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 to about 21 (e.g., 19, 20, or 21) base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

[0115] In another embodiment, a siNA molecule of the invention comprises a hairpin structure, wherein the siNA is about 25 to about 50 (e.g., about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (e.g., about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In one embodiment, a linear hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

[0116] In another embodiment, a siNA molecule of the invention comprises an asymmetric hairpin structure, wherein the siNA is about 25 to about 50 (e.g., about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary

chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (e.g., about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms an asymmetric hairpin structure having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In one embodiment, an asymmetric hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, an asymmetric hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

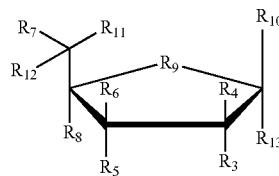
[0117] In another embodiment, a siNA molecule of the invention comprises an asymmetric double stranded structure having separate polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length, wherein the sense region is about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides in length, wherein the sense region and the anti-sense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises an asymmetric double stranded structure having separate polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 18 to about 23 (e.g., about 18, 19, 20, 21, 22, or 23) nucleotides in length and wherein the sense region is about 3 to about 15 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15) nucleotides in length, wherein the sense region and the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. In another embodiment, the asymmetric double stranded siNA molecule can also have a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV).

[0118] In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (e.g., about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a circular oligonucleotide having about 42 to about 50 (e.g., about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19 base pairs and 2 loops.

[0119] In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both

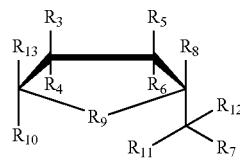
loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

[0120] In one embodiment, a siNA molecule of the invention comprises at least one (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCH₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-5-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having any of Formula I, II, III, IV, V, VI and/or VII, any of which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule; R9 is O, S, CH₂, S=O, CHF, or CF₂. In one embodiment, R3 and/or R7 comprises a conjugate moiety and a linker (e.g., a nucleotide or non-nucleotide linker as described herein or otherwise known in the art). Non-limiting examples of conjugate moieties include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylglucosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; cholesterol; steroids, and polyamines, such as PEI, spermine or spermidine.

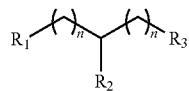
[0121] In one embodiment, a siNA molecule of the invention comprises at least one (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a compound having Formula VI:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCH₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-5-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having any of Formula I, II, III, IV, V, VI and/or VII, any of which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule; R9 is O, S, CH₂, S=O, CHF, or CF₂.

noalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having any of Formula I, II, III, IV, V, VI and/or VII, any of which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule; R9 is O, S, CH₂, S=O, CHF, or CF₂, and either R2, R3, R8 or R13 serve as points of attachment to the siNA molecule of the invention. In one embodiment, R3 and/or R7 comprises a conjugate moiety and a linker (e.g., a nucleotide or non-nucleotide linker as described herein or otherwise known in the art). Non-limiting examples of conjugate moieties include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; cholesterol; steroids, and polyamines, such as PEI, spermine or spermidine.

[0122] In another embodiment, a siNA molecule of the invention comprises at least one (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) substituted polyalkyl moieties, for example a compound having Formula VII:



wherein each n is independently an integer from 1 to 12, each R₁, R₂ and R₃ is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCH₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-O-SH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-5'-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having any of Formula I, II, III, IV, V, VI and/or VII, any of which can be included in the structure of the siNA molecule or serve as a point of attachment to the siNA molecule. In one embodiment, R3 and/or R1 comprises a conjugate moiety and a linker (e.g., a nucleotide or non-nucleotide linker as described herein or otherwise known in the art). Non-limiting examples of conjugate moieties include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; cholesterol; steroids, and polyamines, such as PEI, spermine or spermidine.

[0123] By "ZIP code" sequences is meant, any peptide or protein sequence that is involved in cellular topogenic signaling mediated transport (see for example Ray et al., 2004, *Science*, 306(1501): 1505).

[0124] Each nucleotide within the double stranded siNA molecule can independently have a chemical modification comprising the structure of any of Formulae I-VIII. Thus, in one embodiment, one or more nucleotide positions of a siNA molecule of the invention comprises a chemical modification having structure of any of Formulae I-VII or any other modi-

fication herein. In one embodiment, each nucleotide position of a siNA molecule of the invention comprises a chemical modification having structure of any of Formulae I-VII or any other modification herein.

[0125] In one embodiment, one or more nucleotide positions of one or both strands of a double stranded siNA molecule of the invention comprises a chemical modification having structure of any of Formulae I-VII or any other modification herein. In one embodiment, each nucleotide position of one or both strands of a double stranded siNA molecule of the invention comprises a chemical modification having structure of any of Formulae I-VII or any other modification herein.

[0126] In another embodiment, the invention features a compound having Formula VII, wherein R₁ and R₂ are hydroxyl (OH) groups, n=1, and R₃ comprises O and is the point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA molecule of the invention. This modification is referred to herein as "glyceryl" (for example modification 6 in FIG. 10).

[0127] In another embodiment, a chemically modified nucleoside or non-nucleoside (e.g. a moiety having any of Formula V, VI or VII) of the invention is at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of a siNA molecule of the invention. For example, chemically modified nucleoside or non-nucleoside (e.g., a moiety having Formula V, VI or VII) can be present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense strand, the sense strand, or both antisense and sense strands of the siNA molecule. In one embodiment, the chemically modified nucleoside or non-nucleoside (e.g., a moiety having Formula V, VI or VII) is present at the 5'-end and 3'-end of the sense strand and the 3'-end of the antisense strand of a double stranded siNA molecule of the invention. In one embodiment, the chemically modified nucleoside or non-nucleoside (e.g., a moiety having Formula V, VI or VII) is present at the terminal position of the 5'-end and 3'-end of the sense strand and the 3'-end of the antisense strand of a double stranded siNA molecule of the invention. In one embodiment, the chemically modified nucleoside or non-nucleoside (e.g., a moiety having Formula V, VI or VII) is present at the two terminal positions of the 5'-end and 3'-end of the sense strand and the 3'-end of the antisense strand of a double stranded siNA molecule of the invention. In one embodiment, the chemically modified nucleoside or non-nucleoside (e.g., a moiety having Formula V, VI or VII) is present at the penultimate position of the 5'-end and 3'-end of the sense strand and the 3'-end of the antisense strand of a double stranded siNA molecule of the invention. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.

[0128] In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3',3'-2',2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

[0129] In one embodiment, a siNA molecule of the invention comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for example, at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

[0130] In one embodiment, a siNA molecule of the invention comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9,

10, or more) 4'-thio nucleotides, for example, at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

[0131] In another embodiment, a siNA molecule of the invention comprises one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example, at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

[0132] In one embodiment, a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprises a sense strand or sense region having one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more) 2'-O-alkyl (e.g. 2'-O-methyl), 2'-deoxy-2'-fluoro, 2'-deoxy, FANA, or abasic chemical modifications or any combination thereof.

[0133] In one embodiment, a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprises an antisense strand or antisense region having one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more) 2'-O-alkyl (e.g. 2'-O-methyl), 2'-deoxy-2'-fluoro, 2'-deoxy, FANA, or abasic chemical modifications or any combination thereof.

[0134] In one embodiment, a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprises a sense strand or sense region and an antisense strand or antisense region, each having one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more) 2'-O-alkyl (e.g. 2'-O-methyl), 2'-deoxy-2'-fluoro, 2'-deoxy, FANA, or abasic chemical modifications or any combination thereof.

[0135] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides).

[0136] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the sense region are FANA pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are FANA pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are FANA pyrimidine nucleotides).

[0137] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides).

[0138] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region and an antisense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the sense region and the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro

pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides).

[0139] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (e.g., one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-deoxy purine nucleotides).

[0140] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (e.g., one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-O-methyl purine nucleotides).

[0141] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (e.g., one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-deoxy purine nucleotides).

[0142] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxyethoxy pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxyethoxy pyrimidine nucleotides), and wherein any (e.g., one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-deoxy purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

[0143] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxyethoxy pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxyethoxy pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides).

are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides).

[0149] In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system comprising a sense region, wherein one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides), and one or more purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-deoxy purine nucleotides), and an antisense region, wherein one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides or alternately a plurality (i.e. more than one) of pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides), and one or more purine nucleotides present in the antisense region are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides). The sense region and/or the antisense region can have a terminal cap modification, such as any modification described herein or shown in FIG. 10, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense and/or antisense sequence. The sense and/or antisense region can optionally further comprise a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides. The overhang nucleotides can further comprise one or more (e.g., about 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in FIGS. 4 and 5 and Table III herein. In any of these described embodiments, the purine nucleotides present in the sense region are alternatively 2'-O-methyl, 4'-thio, 2'- β -trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides).

otides) and one or more purine nucleotides present in the antisense region are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl, 4'-thio, 2'- β -trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides). Also, in any of these embodiments, one or more purine nucleotides present in the sense region are alternatively purine ribonucleotides (e.g., wherein all purine nucleotides are purine ribonucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are purine ribonucleotides) and any purine nucleotides present in the antisense region are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides). Additionally, in any of these embodiments, one or more purine nucleotides present in the sense region and/or present in the antisense region are alternatively selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides and 2'-O-methyl nucleotides or alternately a plurality (i.e. more than one) of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides and 2'-O-methyl nucleotides).

[0150] In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984) otherwise known as a "ribo-like" or "A-form helix" configuration. As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-C-methylene-(D-ribofuranosyl)

nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides, 4'-thio nucleotides and 2'-O-methyl nucleotides.

[0151] In one embodiment, the sense strand of a double stranded siNA molecule of the invention comprises a terminal cap moiety, (see for example FIG. 10) such as an inverted deoxyabasic moiety, at the 3'-end, 5'-end, or both 3' and 5'-ends of the sense strand.

[0152] In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein the chemical modification comprises a conjugate covalently attached to the chemically-modified siNA molecule. Non-limiting examples of conjugates contemplated by the invention include conjugates and ligands described in Vargeese et al., U.S. Ser. No. 10/427,160, filed Apr. 30, 2003, incorporated by reference herein in its entirety, including the drawings. In another embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule into a biological system, such as a cell. In another embodiment, the conjugate molecule attached to the chemically-modified siNA molecule is a ligand for a cellular receptor, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethylene-glycol (PEG); phospholipids; cholesterol; steroids, and polyamines, such as PEI, spermine or spermidine. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese et al., U.S. Ser. No. 10/201,394, filed Jul. 22, 2002 incorporated by reference herein. The type of conjugates used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified with various conjugates to determine whether the siNA conjugate complex possesses improved properties while maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

[0153] In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the siNA to the antisense region of the

siNA. In one embodiment, a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker is used, for example, to attach a conjugate moiety to the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of 2 nucleotides in length, for example about 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a PCSK9 target molecule wherein the nucleic acid molecule has sequence that comprises a sequence recognized by the PCSK9 target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a PCSK9 target molecule where the PCSK9 target molecule does not naturally bind to a nucleic acid. The PCSK9 target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold et al., 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.*, 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628.)

[0154] In yet another embodiment, a non-nucleotide linker of the invention comprises abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those having between 2 and 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma et al., *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand et al., *Nucleic Acids Res.* 1990, 18:6353; McCurdy et al., *Nucleosides & Nucleotides* 1991, 10:287; Jschke et al., *Tetrahedron Lett.* 1993, 34:301; Ono et al., *Biochemistry* 1991, 30:9914; Arnold et al., International Publication No. WO 89/02439; Usman et al., International Publication No. WO 95/06731; Dudycz et al., International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000, all hereby incorporated by reference herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

[0155] In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled from two separate oligonucleotides do not comprise any ribonucleotides. For example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA comprise separate oligonucleotides that do not have any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotides. In another example, a siNA molecule can

be assembled from a single oligonucleotide where the sense and antisense regions of the siNA are linked or circularized by a nucleotide or non-nucleotide linker as described herein, wherein the oligonucleotide does not have any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotide. Applicant has surprisingly found that the presence of ribonucleotides (e.g., nucleotides having a 2'-hydroxyl group) within the siNA molecule is not required or essential to support RNAi activity. As such, in one embodiment, all positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and/or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

[0156] In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system comprising a single stranded polynucleotide having complementarity to a PCSK9 target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group and a 3'-terminal phosphate group (e.g., a 2',3'-cyclic phosphate). In another embodiment, the single stranded siNA molecule of the invention comprises about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

[0157] In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity or that alternately modulates RNAi activity in a cell or reconstituted in vitro system comprising a single stranded polynucleotide having complementarity to a PCSK9 target nucleic acid sequence, wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, or 2'-O-difluoromethoxy-ethoxy purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in FIG. 10, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense

sequence. The siNA optionally further comprises about 1 to about 4 or more (e.g., about 1, 2, 3, 4 or more) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group. In any of these embodiments, any purine nucleotides present in the antisense region are alternatively 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA (i.e., purine nucleotides present in the sense and/or antisense region) can alternatively be locked nucleic acid (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine nucleotides are LNA nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA are alternatively 2'-methoxyethyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides). In another embodiment, any modified nucleotides present in the single stranded siNA molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

[0158] In one embodiment, a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprises a sense strand or sense region having two or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more) 2'-O-alkyl (e.g. 2'-O-methyl) modifications or any combination thereof. In another embodiment, the 2'-O-alkyl modification is at alternating position in the sense strand or sense region of the siNA, such as position 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 etc. or position 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 etc.

[0159] In one embodiment, a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprises an antisense strand or antisense region having two or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more) 2'-O-alkyl (e.g. 2'-O-methyl) modifications or any combination thereof. In another embodiment, the 2'-O-alkyl modification is at alternating position in the antisense strand or antisense region of the siNA, such as position 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 etc. or position 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 etc.

[0160] In one embodiment, a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprises a sense strand or sense region and an antisense strand or antisense region, each having two or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more) 2'-O-alkyl (e.g. 2'-O-methyl), 2'-deoxy-2'-fluoro, 2'-deoxy, or abasic chemical

modifications or any combination thereof. In another embodiment, the 2'-O-alkyl modification is at alternating position in the sense strand or sense region of the siNA, such as position 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 etc. or position 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 etc. In another embodiment, the 2'-O-alkyl modification is at alternating position in the antisense strand or antisense region of the siNA, such as position 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21 etc. or position 2, 4, 6, 8, 10, 12, 14, 16, 18, 20 etc.

[0161] In one embodiment, a siNA molecule of the invention comprises chemically modified nucleotides or non-nucleotides (e.g., having any of Formulae I-VII, such as 2'-deoxy, 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy or 2'-O-methyl nucleotides) at alternating positions within one or more strands or regions of the siNA molecule. For example, such chemical modifications can be introduced at every other position of a RNA based siNA molecule, starting at either the first or second nucleotide from the 3'-end or 5'-end of the siNA. In a non-limiting example, a double stranded siNA molecule of the invention in which each strand of the siNA is 21 nucleotides in length is featured wherein positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21 of each strand are chemically modified (e.g., with compounds having any of Formulae I-VII, such as such as 2'-deoxy, 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy or 2'-O-methyl nucleotides). In another non-limiting example, a double stranded siNA molecule of the invention in which each strand of the siNA is 21 nucleotides in length is featured wherein positions 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20 of each strand are chemically modified (e.g., with compounds having any of Formulae I-VII, such as such as 2'-deoxy, 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy or 2'-O-methyl nucleotides). In one embodiment, one strand of the double stranded siNA molecule comprises chemical modifications at positions 2, 4, 6, 8, 10, 12, 14, 16, 18, and 20 and chemical modifications at positions 1, 3, 5, 7, 9, 11, 13, 15, 17, 19 and 21. Such siNA molecules can further comprise terminal cap moieties and/or backbone modifications as described herein.

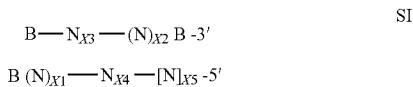
[0162] In one embodiment, a siNA molecule of the invention comprises the following features: if purine nucleotides are present at the 5'-end (e.g., at any of terminal nucleotide positions 1, 2, 3, 4, 5, or 6 from the 5'-end) of the antisense strand or antisense region (otherwise referred to as the guide sequence or guide strand) of the siNA molecule then such purine nucleosides are ribonucleotides. In another embodiment, the purine ribonucleotides, when present, are base paired to nucleotides of the sense strand or sense region (otherwise referred to as the passenger strand) of the siNA molecule. Such purine ribonucleotides can be present in a siNA stabilization motif that otherwise comprises modified nucleotides.

[0163] In one embodiment, a siNA molecule of the invention comprises the following features: if pyrimidine nucleotides are present at the 5'-end (e.g., at any of terminal nucleotide positions 1, 2, 3, 4, 5, or 6 from the 5'-end) of the antisense strand or antisense region (otherwise referred to as the guide sequence or guide strand) of the siNA molecule then such pyrimidine nucleosides are ribonucleotides. In another embodiment, the pyrimidine ribonucleotides, when present, are base paired to nucleotides of the sense strand or sense region (otherwise referred to as the passenger strand) of the

siNA molecule. Such pyrimidine ribonucleotides can be present in a siNA stabilization motif that otherwise comprises modified nucleotides.

[0164] In one embodiment, a siNA molecule of the invention comprises the following features: if pyrimidine nucleotides are present at the 5'-end (e.g., at any of terminal nucleotide positions 1, 2, 3, 4, 5, or 6 from the 5'-end) of the antisense strand or antisense region (otherwise referred to as the guide sequence or guide strand) of the siNA molecule then such pyrimidine nucleosides are modified nucleotides. In another embodiment, the modified pyrimidine nucleotides, when present, are base paired to nucleotides of the sense strand or sense region (otherwise referred to as the passenger strand) of the siNA molecule. Non-limiting examples of modified pyrimidine nucleotides include those having any of Formulae I-VII, such as such as 2'-deoxy, 2'-deoxy-2'-fluoro, 4'-thio, 2'-O-trifluoromethyl, 2'-O-ethyl-trifluoromethoxy, 2'-O-difluoromethoxy-ethoxy or 2'-O-methyl nucleotides.

[0165] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SI:



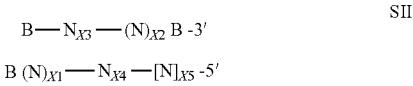
[0166] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions wherein any purine nucleotides when present are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0167] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are independently 2'-O-methyl nucleotides, 2'-deoxyribonucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides;

[0168] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are independently 2'-deoxyribonucleotides, 2'-O-methyl nucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides; and

[0169] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0170] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SII:



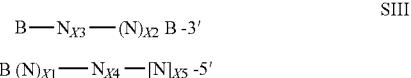
[0171] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions wherein any purine nucleotides when present are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0172] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0173] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are ribonucleotides; any purine nucleotides present in the sense strand (upper strand) are ribonucleotides; and

[0174] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0175] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SIII:



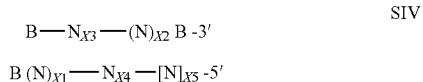
[0176] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions wherein any purine nucleotides when present are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0177] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0178] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are ribonucleotides; and

[0179] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0180] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SIV:



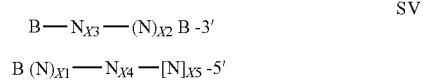
[0181] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions wherein any purine nucleotides when present are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0182] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0183] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are deoxyribonucleotides; and

[0184] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0185] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SV:



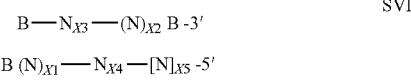
[0186] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions wherein any purine nucleotides when present are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0187] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are nucleotides having a ribo-like configuration (e.g., Northern or A-form helix configuration); any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0188] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are nucleotides having a ribo-like configuration (e.g., Northern or A-form helix configuration); any purine nucleotides present in the sense strand (upper strand) are 2'-O-methyl nucleotides; and

[0189] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0190] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SVI:



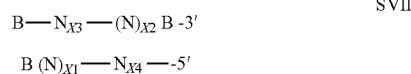
[0191] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions comprising sequence that renders the 5'-end of the antisense strand (lower strand) less thermally stable than the 5'-end of the sense strand (upper strand); X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0192] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the anti-sense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are independently 2'-O-methyl nucleotides, 2'-deoxyribonucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides;

[0193] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are independently 2'-deoxyribonucleotides, 2'-O-methyl nucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides; and

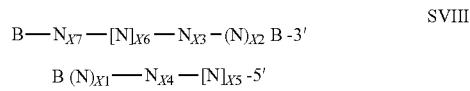
[0194] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0195] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SVII:



[0196] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30; NX3 is complementary to NX4, and any (N) nucleotides are 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides.

[0197] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SVIII:



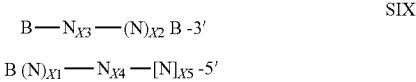
[0198] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions comprising sequence that renders the 5'-end of the antisense strand (lower strand) less thermally stable than the 5'-end of the sense strand (upper strand); [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 15; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; X6 is an integer from about 1 to about 4; X7 is an integer from about 9 to about 15; NX7, NX6, and NX3 are complementary to NX4 and NX5, and

[0199] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the anti-sense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are independently 2'-O-methyl nucleotides, 2'-deoxyribonucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides;

[0200] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides other than [N] nucleotides; any purine nucleotides present in the sense strand (upper strand) are independently 2'-deoxyribonucleotides, 2'-O-methyl nucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides other than [N] nucleotides; and

[0201] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0202] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SIX:



[0203] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

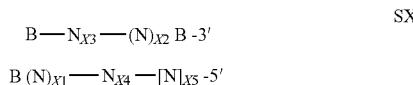
[0204] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the anti-sense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are independently

2'-O-methyl nucleotides, 2'-deoxyribonucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides;

[0205] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are independently 2'-deoxyribonucleotides, 2'-O-methyl nucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides; and

[0206] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0207] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SX:



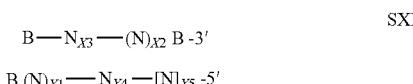
[0208] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0209] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0210] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are ribonucleotides; any purine nucleotides present in the sense strand (upper strand) are ribonucleotides; and

[0211] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0212] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SXI:



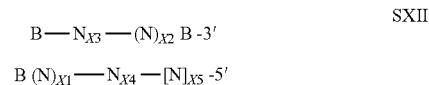
[0213] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0214] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0215] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are ribonucleotides; and

[0216] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0217] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SXII:



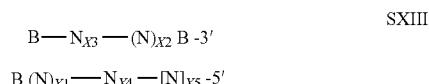
[0218] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0219] (a) any pyridimidine nucleotides present in the antisense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0220] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the sense strand (upper strand) are deoxyribonucleotides; and

[0221] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0222] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SXIII:



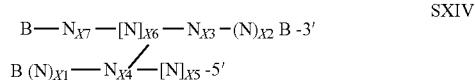
[0223] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 30; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; NX3 is complementary to NX4 and NX5, and

[0224] (a) any pyrimidine nucleotides present in the anti-sense strand (lower strand) are nucleotides having a ribo-like configuration (e.g., Northern or A-form helix configuration); any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are 2'-O-methyl nucleotides;

[0225] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are nucleotides having a ribo-like configuration (e.g., Northern or A-form helix configuration); any purine nucleotides present in the sense strand (upper strand) are 2'-O-methyl nucleotides; and

[0226] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0227] In one embodiment, the invention features a double stranded nucleic acid molecule having structure SXIV:



[0228] wherein each N is independently a nucleotide; each B is a terminal cap moiety that can be present or absent; (N) represents non-base paired or overhanging nucleotides which can be unmodified or chemically modified; [N] represents nucleotide positions that are ribonucleotides; [N] represents nucleotide positions that are ribonucleotides; X1 and X2 are independently integers from about 0 to about 4; X3 is an integer from about 9 to about 15; X4 is an integer from about 11 to about 30, provided that the sum of X4 and X5 is between 17-36; X5 is an integer from about 1 to about 6; X6 is an integer from about 1 to about 4; X7 is an integer from about 9 to about 15; NX7, NX6, and NX3 are complementary to NX4 and NX5, and

[0229] (a) any pyrimidine nucleotides present in the anti-sense strand (lower strand) are 2'-deoxy-2'-fluoro nucleotides; any purine nucleotides present in the antisense strand (lower strand) other than the purines nucleotides in the [N] nucleotide positions, are independently 2'-O-methyl nucleotides, 2'-deoxyribonucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides;

[0230] (b) any pyrimidine nucleotides present in the sense strand (upper strand) are 2'-deoxy-2'-fluoro nucleotides other than [N] nucleotides; any purine nucleotides present in the sense strand (upper strand) are independently 2'-deoxyribonucleotides, 2'-O-methyl nucleotides or a combination of 2'-deoxyribonucleotides and 2'-O-methyl nucleotides other than [N] nucleotides; and

[0231] (c) any (N) nucleotides are optionally 2'-O-methyl, 2'-deoxy-2'-fluoro, or deoxyribonucleotides.

[0232] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises a terminal phosphate group at the 5'-end of the antisense strand or antisense region of the nucleic acid molecule.

[0233] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIR, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises X5=1, 2, or 3; each X1 and X2=1 or 2; X3=12, 13, 14, 15, 16, 17, 18,

19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30, and X4=15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30.

[0234] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises X5=1; each X1 and X2=2; X3=19, and X4=18.

[0235] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises X5=2; each X1 and X2=2; X3=19, and X4=17

[0236] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises X5=3; each X1 and X2=2; X3=19, and X4=16.

[0237] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises B at the 3' and 5' ends of the sense strand or sense region.

[0238] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises B at the 3'-end of the antisense strand or antisense region.

[0239] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises B at the 3' and 5' ends of the sense strand or sense region and B at the 3'-end of the antisense strand or antisense region.

[0240] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV further comprises one or more phosphorothioate internucleotide linkages at the first terminal (N) on the 3' end of the sense strand, antisense strand, or both sense strand and antisense strands of the nucleic acid molecule. For example, a double stranded nucleic acid molecule can comprise X1 and/or X2=2 having overhanging nucleotide positions with a phosphorothioate internucleotide linkage, e.g., (NsN) where "s" indicates phosphorothioate.

[0241] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises (N) nucleotides that are 2'-O-methyl nucleotides.

[0242] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises (N) nucleotides that are 2'-O-methyl nucleotides.

[0243] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises (N) nucleotides in the antisense strand (lower strand) that are complementary to nucleotides in a PCSK9 target polynucleotide sequence having complementary to the N and [N] nucleotides of the antisense (lower) strand.

[0244] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises (N) nucleotides in the sense strand (upper strand) that comprise a contiguous nucleotide sequence of about 15 to about 30 nucleotides of a PCSK9 target polynucleotide sequence.

[0245] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV comprises (N) nucleotides in the sense strand (upper strand) that comprise nucleotide sequence corresponding a PCSK9 target poly-

nucleotide sequence having complementary to the antisense (lower) strand such that the contiguous (N) and N nucleotide sequence of the sense strand comprises nucleotide sequence of the PCSK9 target nucleic acid sequence.

[0246] In one embodiment, a double stranded nucleic acid molecule having any of structure SVIII or SXIV comprises B only at the 5'-end of the sense (upper) strand of the double stranded nucleic acid molecule.

[0247] In one embodiment, a double stranded nucleic acid molecule having any of structure SI, SII, SIII, SIV, SV, SVI, SVII, SVIII, SIX, SX, SXII, SXIII, or SXIV further comprises an unpaired terminal nucleotide at the 5'-end of the antisense (lower) strand. The unpaired nucleotide is not complementary to the sense (upper) strand. In one embodiment, the unpaired terminal nucleotide is complementary to a PCSK9 target polynucleotide sequence having complementary to the N and [N] nucleotides of the antisense (lower) strand. In another embodiment, the unpaired terminal nucleotide is not complementary to a PCSK9 target polynucleotide sequence having complementary to the N and [N] nucleotides of the antisense (lower) strand.

[0248] In one embodiment, a double stranded nucleic acid molecule having any of structure SVIII or SXIV comprises X6=1 and X3=10.

[0249] In one embodiment, a double stranded nucleic acid molecule having any of structure SVIII or SXIV comprises X6=2 and X3=9.

[0250] In one embodiment, the invention features a composition comprising a siNA molecule or double stranded nucleic acid molecule or RNAi inhibitor formulated as any of formulation LNP-051; LNP-053; LNP-054; LNP-069; LNP-073; LNP-077; LNP-080; LNP-082; LNP-083; LNP-060; LNP-061; LNP-086; LNP-097; LNP-098; LNP-099; LNP-100; LNP-101; LNP-102; LNP-103; or LNP-104 (see Table VI).

[0251] In one embodiment, the invention features a composition comprising a first double stranded nucleic acid and a second double stranded nucleic acid molecule each having a first strand and a second strand that are complementary to each other, wherein the second strand of the first double stranded nucleic acid molecule comprises sequence complementary to a first PCSK9 target sequence and the second strand of the second double stranded nucleic acid molecule comprises sequence complementary to a second PCSK9 target or PCSK9 pathway target sequence (e.g., H6PD). In one embodiment, the composition further comprises a cationic lipid, a neutral lipid, and a polyethyleneglycol-conjugate. In one embodiment, the composition further comprises a cationic lipid, a neutral lipid, a polyethyleneglycol-conjugate, and a cholesterol. In one embodiment, the composition further comprises a polyethyleneglycol-conjugate, a cholesterol, and a surfactant. In one embodiment, the cationic lipid is selected from the group consisting of CLinDMA, pCLinDMA, eCLinDMA, DMOBA, and DMLBA. In one embodiment, the neutral lipid is selected from the group consisting of DSPC, DOBA, and cholesterol. In one embodiment, the polyethyleneglycol-conjugate is selected from the group consisting of a PEG-dimyristoyl glycerol and PEG-cholesterol. In one embodiment, the PEG is 2 KPEG. In one embodiment, the surfactant is selected from the group consisting of palmityl alcohol, stearyl alcohol, oleyl alcohol and linoleyl alcohol. In one embodiment, the cationic lipid is CLinDMA, the neutral lipid is DSPC, the polyethylene glycol conjugate is 2 KPEG-DMG, the cholesterol is cholesterol,

and the surfactant is linoleyl alcohol. In one embodiment, the CLinDMA, the DSPC, the 2 KPEG-DMG, the cholesterol, and the linoleyl alcohol are present in molar ratio of 43:38:10:2:7 respectively.

[0252] In any of the embodiments herein, the siNA molecule of the invention modulates expression of one or more PCSK9 targets via RNA interference or the inhibition of RNA interference. In one embodiment, the RNA interference is RISC mediated cleavage of the PCSK9 target (e.g., siRNA mediated RNA interference). In one embodiment, the RNA interference is translational inhibition of the PCSK9 target (e.g., miRNA mediated RNA interference). In one embodiment, the RNA interference is transcriptional inhibition of the PCSK9 target (e.g., siRNA mediated transcriptional silencing). In one embodiment, the RNA interference takes place in the cytoplasm. In one embodiment, the RNA interference takes place in the nucleus.

[0253] In any of the embodiments herein, the siNA molecule of the invention modulates expression of one or more PCSK9 targets via inhibition of an endogenous PCSK9 RNA, such as an endogenous PCSK9 mRNA, PCSK9 siRNA, PCSK9 miRNA, or alternately through inhibition of RISC.

[0254] In one embodiment, the invention features one or more RNAi inhibitors that modulate the expression of one or more PCSK9 gene targets by miRNA inhibition, siRNA inhibition, or RISC inhibition.

[0255] In one embodiment, a RNAi inhibitor of the invention is a siNA molecule as described herein that has one or more strands that are complementary to one or more target miRNA or siRNA molecules.

[0256] In one embodiment, the RNAi inhibitor of the invention is an antisense molecule that is complementary to a target miRNA or siRNA molecule or a portion thereof. An antisense RNAi inhibitor of the invention can be of length of about 10 to about 40 nucleotides in length (e.g., 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 nucleotides in length). An antisense RNAi inhibitor of the invention can comprise one or more modified nucleotides or non-nucleotides as described herein (see for example molecules having any of Formulae I-VII herein or any combination thereof). In one embodiment, an antisense RNAi inhibitor of the invention can comprise one or more or all 2'-O-methyl nucleotides. In one embodiment, an antisense RNAi inhibitor of the invention can comprise one or more or all 2'-deoxy-2'-fluoro nucleotides. In one embodiment, an antisense RNAi inhibitor of the invention can comprise one or more or all 2'-O-methoxy-ethyl (also known as 2'-methoxyethoxy or MOE) nucleotides. In one embodiment, an antisense RNAi inhibitor of the invention can comprise one or more or all phosphorothioate internucleotide linkages. In one embodiment, an antisense RNA inhibitor or the invention can comprise a terminal cap moiety at the 3'-end, the 5'-end, or both the 5' and 3' ends of the antisense RNA inhibitor.

[0257] In one embodiment, a RNAi inhibitor of the invention is a nucleic acid aptamer having binding affinity for RISC, such as a regulatable aptamer (see for example An et al., 2006, *RNA*, 12:710-716). An aptamer RNAi inhibitor of the invention can be of length of about 10 to about 50 nucleotides in length (e.g., 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides in length). An aptamer RNAi inhibitor of the invention can comprise one or more modified nucleotides or non-nucle-

otides as described herein (see for example molecules having any of Formulae I-VII herein or any combination thereof). In one embodiment, an aptamer RNAi inhibitor of the invention can comprise one or more or all 2'-O-methyl nucleotides. In one embodiment, an aptamer RNAi inhibitor of the invention can comprise one or more or all 2'-deoxy-2'-fluoro nucleotides. In one embodiment, an aptamer RNAi inhibitor of the invention can comprise one or more or all 2'-O-methoxyethyl (also known as 2'-methoxyethoxy or MOE) nucleotides. In one embodiment, an aptamer RNAi inhibitor of the invention can comprise one or more or all phosphorothioate internucleotide linkages. In one embodiment, an aptamer RNA inhibitor or the invention can comprise a terminal cap moiety at the 3'-end, the 5'-end, or both the 5' and 3' ends of the aptamer RNA inhibitor.

[0258] In one embodiment, the invention features a method for modulating the expression of a PCSK9 target gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified or unmodified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the cell.

[0259] In one embodiment, the invention features a method for modulating the expression of a PCSK9 target gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified or unmodified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the PCSK9 target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the cell.

[0260] In another embodiment, the invention features a method for modulating the expression of more than one PCSK9 target gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified or unmodified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target genes; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the cell.

[0261] In another embodiment, the invention features a method for modulating the expression of two or more PCSK9 target genes within a cell comprising: (a) synthesizing one or more siNA molecules of the invention, which can be chemically-modified or unmodified, wherein the siNA strands comprise sequences complementary to RNA of the PCSK9 target genes and wherein the sense strand sequences of the siNAs comprise sequences identical or substantially similar to the sequences of the PCSK9 target RNAs; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the cell.

[0262] In another embodiment, the invention features a method for modulating the expression of more than one PCSK9 target gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified or unmodified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the

sequences of the PCSK9 target RNAs; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the cell.

[0263] In another embodiment, the invention features a method for modulating the expression of a PCSK9 target gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified or unmodified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene, wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequences of the PCSK9 target RNA; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the cell.

[0264] In one embodiment, siNA molecules of the invention are used as reagents in ex vivo applications. For example, siNA reagents are introduced into tissue or cells that are transplanted into a subject for therapeutic effect. The cells and/or tissue can be derived from an organism or subject that later receives the explant, or can be derived from another organism or subject prior to transplantation. The siNA molecules can be used to modulate the expression of one or more genes in the cells or tissue, such that the cells or tissue obtain a desired phenotype or are able to perform a function when transplanted in vivo. In one embodiment, certain PCSK9 target cells from a patient are extracted. These extracted cells are contacted with siNAs PCSK9 targeting a specific nucleotide sequence within the cells under conditions suitable for uptake of the siNAs by these cells (e.g. using delivery reagents such as cationic lipids, liposomes and the like or using techniques such as electroporation to facilitate the delivery of siNAs into cells). The cells are then reintroduced back into the same patient or other patients.

[0265] In one embodiment, the invention features a method of modulating the expression of a PCSK9 target gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in that organism.

[0266] In one embodiment, the invention features a method of modulating the expression of a PCSK9 target gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the PCSK9 target RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived

from or into another organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in that organism.

[0267] In another embodiment, the invention features a method of modulating the expression of more than one PCSK9 target gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target genes; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in that organism.

[0268] In one embodiment, the invention features a method of modulating the expression of a PCSK9 target gene in a subject or organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target gene; and (b) introducing the siNA molecule into the subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the subject or organism. The level of PCSK9 target protein or RNA can be determined using various methods well-known in the art.

[0269] In another embodiment, the invention features a method of modulating the expression of more than one PCSK9 target gene in a subject or organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the PCSK9 target genes; and (b) introducing the siNA molecules into the subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the subject or organism. The level of PCSK9 target protein or RNA can be determined as is known in the art.

[0270] In one embodiment, the invention features a method for modulating the expression of a PCSK9 target gene within a cell (e.g., a liver or adipose tissue cell) comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PCSK9 target gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the cell.

[0271] In another embodiment, the invention features a method for modulating the expression of more than one PCSK9 target gene within a cell (e.g., a liver or adipose tissue cell) comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PCSK9 target gene; and (b) contacting the cell in vitro or in vivo with the siNA molecule under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the cell.

[0272] In one embodiment, the invention features a method of modulating the expression of a PCSK9 target gene in a tissue explant ((e.g., liver or any other organ, tissue or cell as can be transplanted from one organism to another or back to the same organism from which the organ, tissue or cell is

derived) comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PCSK9 target gene; and (b) contacting a cell of the tissue explant derived from a particular subject or organism with the siNA molecule under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the subject or organism the tissue was derived from or into another subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in that subject or organism.

[0273] In another embodiment, the invention features a method of modulating the expression of more than one PCSK9 target gene in a tissue explant (e.g., liver or any other organ, tissue or cell as can be transplanted from one organism to another or back to the same organism from which the organ, tissue or cell is derived) comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PCSK9 target gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the subject or organism the tissue was derived from or into another subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in that subject or organism.

[0274] In one embodiment, the invention features a method of modulating the expression of a PCSK9 target gene in a subject or organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PCSK9 target gene; and (b) introducing the siNA molecule into the subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the subject or organism.

[0275] In another embodiment, the invention features a method of modulating the expression of more than one PCSK9 target gene in a subject or organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the PCSK9 target gene; and (b) introducing the siNA molecules into the subject or organism under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the subject or organism.

[0276] In one embodiment, the invention features a method of modulating the expression of a PCSK9 target gene in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target gene in the subject or organism.

[0277] In one embodiment, the invention features a method for treating or preventing a disease, disorder, trait or condition related to PCSK9 gene expression or PCSK9 activity in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the PCSK9

target gene in the subject or organism. The reduction of gene expression and thus reduction in the level of the respective protein/RNA relieves, to some extent, the symptoms of the disease, disorder, trait or condition.

[0278] In one embodiment, the invention features a method for treating or preventing one or more metabolic diseases, traits, or conditions in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the PCSK9 target gene in the subject or organism whereby the treatment or prevention of the metabolic disease(s), trait(s), or condition(s) can be achieved. In one embodiment, the invention features contacting the subject or organism with a siNA molecule of the invention via local administration to relevant tissues or cells. In one embodiment, the invention features contacting the subject or organism with a siNA molecule of the invention via systemic administration (such as via intravenous, intramuscular, subcutaneous, or GI administration of siNA) to relevant tissues or cells, such as tissues or cells involved in the maintenance or development of the metabolic disease, trait, or condition in a subject or organism (e.g., liver, pancreas, small intestine, adipose tissue or cells). The siNA molecule of the invention can be formulated or conjugated as described herein or otherwise known in the art to target appropriate tissues or cells in the subject or organism (e.g., liver, pancreas, small intestine, adipose tissue or cells). The siNA molecule can be combined with other therapeutic treatments and modalities as are known in the art for the treatment of or prevention of metabolic diseases, traits, or conditions in a subject or organism. In one embodiment, the metabolic disease is selected from the group consisting of diabetes (e.g., type I and/or type II diabetes), insulin resistance, obesity, or related conditions, including but not limited to sleep apnea, hiatal hernia, reflux esophagitis, osteoarthritis, gout, cancers associated with weight gain, gallstones, kidney stones, pulmonary hypertension, infertility, cardiovascular disease, above normal weight, and above normal lipid levels, uric acid levels, or oxalate levels.

[0279] In one embodiment, the invention features a method for treating or preventing one or more metabolic diseases, traits, or conditions in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate (e.g., inhibit) the expression of an inhibitor of PCSK9 gene expression in the subject or organism. In one embodiment, the inhibitor of PCSK9 gene expression is a miRNA.

[0280] In one embodiment, the invention features a method for treating or preventing one or more cardiovascular diseases, traits, or conditions in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the PCSK9 target gene in the subject or organism whereby the treatment or prevention of the cardiovascular disease(s), trait(s), or condition(s) can be achieved. In one embodiment, the invention features contacting the subject or organism with a siNA molecule of the invention via local administration to relevant tissues or cells, e.g., liver, pancreas, small intestine, adipose tissue or cells tissues or cells. In one embodiment, the invention features contacting the subject or organism with a siNA molecule of the invention via systemic administration (such as via intravenous, intramuscular, subcutaneous, or GI administration of siNA) to relevant tissues or cells, such as tissues or cells involved in the maintenance or development of the cardiovascular disease, trait, or condition

in a subject or organism. The siNA molecule of the invention can be formulated or conjugated as described herein or otherwise known in the art to target appropriate tissues or cells in the subject or organism. The siNA molecule can be combined with other therapeutic treatments and modalities as are known in the art for the treatment of or prevention of cardiovascular diseases, traits, or conditions in a subject or organism. In one embodiment the cardiovascular disease is selected from the group consisting of hypertension, coronary thrombosis, stroke, lipid syndromes, hyperglycemia, hypertriglyceridemia, hyperlipidemia, ischemia, congestive heart failure, and myocardial infarction.

[0281] In one embodiment, the invention features a method for treating or preventing one or more cardiovascular diseases, traits, or conditions in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate (e.g., inhibit) the expression of an inhibitor of PCSK9 gene expression in the subject or organism. In one embodiment, the inhibitor of PCSK9 gene expression is a miRNA.

[0282] In one embodiment, the invention features a method for weight loss in a subject or organism comprising contacting the subject or organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the PCSK9 target gene in the subject or organism whereby the weight loss can be achieved. In one embodiment, the invention features contacting the subject or organism with a siNA molecule of the invention via local administration to relevant tissues or cells, e.g., liver, pancreas, small intestine, adipose tissue or cells. In one embodiment, the invention features contacting the subject or organism with a siNA molecule of the invention via systemic administration (such as via intravenous, intramuscular, subcutaneous, or GI administration of siNA) to relevant tissues or cells. The siNA molecule of the invention can be formulated or conjugated as described herein or otherwise known in the art to target appropriate tissues or cells in the subject or organism. The siNA molecule can be combined with other therapeutic treatments and modalities as are known in the art for weight loss in a subject or organism.

[0283] In one embodiment, the siNA molecule or double stranded nucleic acid molecule of the invention is formulated as a composition described in U.S. Provisional patent application No. 60/678,531 and in related U.S. Provisional patent application No. 60/703,946, filed Jul. 29, 2005, and U.S. Provisional patent application No. 60/737,024, filed Nov. 15, 2005 (Vargeese et al.).

[0284] In any of the methods herein for modulating the expression of one or more PCSK9 targets or for treating or preventing PCSK9 related diseases, traits, conditions, or phenotypes in a cell, subject, or organism, the siNA molecule of the invention modulates expression of one or more PCSK9 targets via RNA interference. In one embodiment, the RNA interference is RISC mediated cleavage of the PCSK9 target (e.g., siRNA mediated RNA interference). In one embodiment, the RNA interference is translational inhibition of the PCSK9 target (e.g., miRNA mediated RNA interference). In one embodiment, the RNA interference is transcriptional inhibition of the PCSK9 target (e.g., siRNA mediated transcriptional silencing). In one embodiment, the RNA interference takes place in the cytoplasm. In one embodiment, the RNA interference takes place in the nucleus.

[0285] In any of the methods of treatment of the invention, the siNA can be administered to the subject as a course of

treatment, for example administration at various time intervals, such as once per day over the course of treatment, once every two days over the course of treatment, once every three days over the course of treatment, once every four days over the course of treatment, once every five days over the course of treatment, once every six days over the course of treatment, once per week over the course of treatment, once every other week over the course of treatment, once per month over the course of treatment, etc. In one embodiment, the course of treatment is once every 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 weeks. In one embodiment, the course of treatment is from about one to about 52 weeks or longer (e.g., indefinitely). In one embodiment, the course of treatment is from about one to about 48 months or longer (e.g., indefinitely).

[0286] In one embodiment, a course of treatment involves an initial course of treatment, such as once every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more weeks for a fixed interval (e.g., 1x, 2x, 3x, 4x, 5x, 6x, 7x, 8x, 9x, 10x or more) followed by a maintenance course of treatment, such as once every 4, 6, 8, 10, 15, 20, 25, 30, 35, 40, or more weeks for an additional fixed interval (e.g., 1x, 2x, 3x, 4x, 5x, 6x, 7x, 8x, 9x, 10x or more).

[0287] In any of the methods of treatment of the invention, the siNA can be administered to the subject systemically as described herein or otherwise known in the art, either alone as a monotherapy or in combination with additional therapies described herein or as are known in the art. Systemic administration can include, for example, pulmonary (inhalation, nebulization etc.) intravenous, subcutaneous, intramuscular, catheterization, nasopharangeal, transdermal, or oral/gastrointestinal administration as is generally known in the art.

[0288] In one embodiment, in any of the methods of treatment or prevention of the invention, the siNA can be administered to the subject locally or to local tissues as described herein or otherwise known in the art, either alone as a monotherapy or in combination with additional therapies as are known in the art. Local administration can include, for example, inhalation, nebulization, catheterization, implantation, direct injection, dermal/transdermal application, stenting, ear/eye drops, or portal vein administration to relevant tissues, or any other local administration technique, method or procedure, as is generally known in the art.

[0289] In another embodiment, the invention features a method of modulating the expression of more than one PCSK9 target gene in a subject or organism comprising contacting the subject or organism with one or more siNA molecules of the invention under conditions suitable to modulate (e.g., inhibit) the expression of the PCSK9 target genes in the subject or organism.

[0290] The siNA molecules of the invention can be designed to down regulate or inhibit target gene expression through RNAi targeting of a variety of nucleic acid molecules. In one embodiment, the siNA molecules of the invention are used to target various DNA corresponding to a target gene, for example via heterochromatic silencing or transcriptional inhibition. In one embodiment, the siNA molecules of the invention are used to target various RNAs corresponding to a target gene, for example via RNA target cleavage or translational inhibition. Non-limiting examples of such RNAs include messenger RNA (mRNA), non-coding RNA (ncRNA) or regulatory elements (see for example Mattick, 2005, Science, 309, 1527-1528 and Clayerie, 2005, Science, 309, 1529-1530) which includes miRNA and other small RNAs, alternate RNA splice variants of target gene(s), post-transcriptionally modified RNA of target gene(s), pre-mRNA

of target gene(s), and/or RNA templates. If alternate splicing produces a family of transcripts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of the membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, cosmetic applications, veterinary applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

[0291] In another embodiment, the siNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families such as PCSK9 family genes (e.g., all known PCSK9 isotypes, or select groupings of PCSK9 isotypes). As such, siNA molecules targeting multiple PCSK9 targets can provide increased therapeutic effect. In addition, by avoiding other PCSK9 isotypes, toxicity may be avoided.

[0292] In one embodiment, siNA molecules can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example metabolic and/or cardiovascular diseases, disorders, traits and conditions.

[0293] In one embodiment, siNA molecule(s) and/or methods of the invention are used to down regulate the expression of gene(s) that encode RNA referred to by Genbank Accession, for example, target genes encoding RNA sequence(s) referred to herein by Genbank Accession number, for example, Genbank Accession Nos. shown herein (e.g. in Table I) and in U.S. Ser. No. 10/923,536 and PCT/US03/05028, both incorporated by reference herein.

[0294] In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In one embodiment, the siNA molecules of (a) have strands of a fixed length, for example, about 23 nucleotides in length. In another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length. In one embodiment, the assay can comprise a reconstituted in vitro siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for

detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

[0295] In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of 4N, where N represents the number of base paired nucleotides in each of the siNA construct strands (e.g. for a siNA construct having 21 nucleotide sense and antisense strands with 19 base pairs, the complexity would be 4¹⁹); and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target target RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 6 herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example, by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target target RNA sequence. The target target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

[0296] In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In one embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 15 to about 30 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

[0297] By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

[0298] By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the back-

ground of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

[0299] In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a method for diagnosing a disease, trait, or condition in a subject comprising administering to the subject a composition of the invention under conditions suitable for the diagnosis of the disease, trait, or condition in the subject. In another embodiment, the invention features a method for treating or preventing a disease, trait, or condition, such as metabolic and/or cardiovascular diseases, traits, conditions, or disorders in a subject, comprising administering to the subject a composition of the invention under conditions suitable for the treatment or prevention of the disease, trait, or condition in the subject, alone or in conjunction with one or more other therapeutic compounds.

[0300] In another embodiment, the invention features a method for validating a target gene target, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a target gene; (b) introducing the siNA molecule into a cell, tissue, subject, or organism under conditions suitable for modulating expression of the target gene in the cell, tissue, subject, or organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, subject, or organism.

[0301] In another embodiment, the invention features a method for validating a target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of the target gene in the biological system; and (c) determining the function of the gene by assaying for any phenotypic change in the biological system.

[0302] By "biological system" is meant, material, in a purified or unpurified form, from biological sources, including but not limited to human or animal, wherein the system comprises the components required for RNAi activity. The term "biological system" includes, for example, a cell, tissue, subject, or organism, or extract thereof. The term biological system also includes reconstituted RNAi systems that can be used in an *in vitro* setting.

[0303] By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g., siNA). Such detectable changes include, but are not limited to, changes in shape, size, proliferation, motility, protein expression or RNA expression or other physical or chemical changes as can be assayed by methods known in the art. The detectable change can also include expression of reporter genes/molecules such as Green Fluorescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

[0304] In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a target gene in a biological system, including, for example, in a cell, tissue, subject, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one target gene in a biological system, including, for example, in a cell, tissue, subject, or organism.

[0305] In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

[0306] In one embodiment, the synthesis of a siNA molecule of the invention, which can be chemically-modified, comprises: (a) synthesis of two complementary strands of the siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide synthesis. In yet another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase tandem oligonucleotide synthesis.

[0307] In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of the second oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety than can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand.

[0308] In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example, under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place concomitantly. In another embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic conditions.

[0309] In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis

wherein both strands of the siNA duplex are synthesized in tandem using a cleavable linker attached to the first sequence which acts a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions suitable for hybridization of the separate siNA sequence strands results in formation of the double-stranded siNA molecule.

[0310] In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b) synthesizing a second oligonucleotide sequence having complementarity to the first sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety than can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second oligonucleotide sequence strand under conditions suitable for isolating the full-length sequence comprising both siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example, under hydrolysis conditions. In another embodiment, cleavage of the linker molecule in (c) above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

[0311] In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an oligonucleotide having a first and a second sequence, wherein the first sequence is complementary to the second sequence, and the first oligonucleotide sequence is linked to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group, for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the deprotection results in the cleavage of the linker joining the two oligonucleotide sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as described herein.

[0312] In another embodiment, the method of synthesis of siNA molecules of the invention comprises the teachings of Scaringe et al., U.S. Pat. Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

[0313] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide (e.g., RNA or DNA target), wherein the siNA construct comprises one or more chemical modifications, for example, one

or more chemical modifications having any of Formulae I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

[0314] In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

[0315] In another embodiment, the invention features a method for generating siNA molecules with improved toxicologic profiles (e.g., having attenuated or no immunostimulatory properties) comprising (a) introducing nucleotides having any of Formula I-VII (e.g., siNA motifs referred to in Table IV) or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved toxicologic profiles.

[0316] In another embodiment, the invention features a method for generating siNA formulations with improved toxicologic profiles (e.g., having attenuated or no immunostimulatory properties) comprising (a) generating a siNA formulation comprising a siNA molecule of the invention and a delivery vehicle or delivery particle as described herein or as otherwise known in the art, and (b) assaying the siNA formulation of step (a) under conditions suitable for isolating siNA formulations having improved toxicologic profiles.

[0317] In another embodiment, the invention features a method for generating siNA molecules that do not stimulate an interferon response (e.g., no interferon response or attenuated interferon response) in a cell, subject, or organism, comprising (a) introducing nucleotides having any of Formula I-VII (e.g., siNA motifs referred to in Table IV) or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules that do not stimulate an interferon response.

[0318] In another embodiment, the invention features a method for generating siNA formulations that do not stimulate an interferon response (e.g., no interferon response or attenuated interferon response) in a cell, subject, or organism, comprising (a) generating a siNA formulation comprising a siNA molecule of the invention and a delivery vehicle or delivery particle as described herein or as otherwise known in the art, and (b) assaying the siNA formulation of step (a) under conditions suitable for isolating siNA formulations that do not stimulate an interferon response. In one embodiment, the interferon comprises interferon alpha.

[0319] In another embodiment, the invention features a method for generating siNA molecules that do not stimulate an inflammatory or proinflammatory cytokine response (e.g., no cytokine response or attenuated cytokine response) in a cell, subject, or organism, comprising (a) introducing nucleotides having any of Formula I-VII (e.g., siNA motifs referred to in Table IV) or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules that do not stimulate a cytokine response. In one embodiment, the cytokine comprises an interleukin such as interleukin-6 (IL-6) and/or tumor necrosis alpha (TNF- α).

[0320] In another embodiment, the invention features a method for generating siNA formulations that do not stimulate an inflammatory or proinflammatory cytokine response

(e.g., no cytokine response or attenuated cytokine response) in a cell, subject, or organism, comprising (a) generating a siNA formulation comprising a siNA molecule of the invention and a delivery vehicle or delivery particle as described herein or as otherwise known in the art, and (b) assaying the siNA formulation of step (a) under conditions suitable for isolating siNA formulations that do not stimulate a cytokine response. In one embodiment, the cytokine comprises an interleukin such as interleukin-6 (IL-6) and/or tumor necrosis alpha (TNF- α).

[0321] In another embodiment, the invention features a method for generating siNA molecules that do not stimulate Toll-like Receptor (TLR) response (e.g., no TLR response or attenuated TLR response) in a cell, subject, or organism, comprising (a) introducing nucleotides having any of Formula I-VII (e.g., siNA motifs referred to in Table IV) or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules that do not stimulate a TLR response. In one embodiment, the TLR comprises TLR3, TLR7, TLR8 and/or TLR9.

[0322] In another embodiment, the invention features a method for generating siNA formulations that do not stimulate a Toll-like Receptor (TLR) response (e.g., no TLR response or attenuated TLR response) in a cell, subject, or organism, comprising (a) generating a siNA formulation comprising a siNA molecule of the invention and a delivery vehicle or delivery particle as described herein or as otherwise known in the art, and (b) assaying the siNA formulation of step (a) under conditions suitable for isolating siNA formulations that do not stimulate a TLR response. In one embodiment, the TLR comprises TLR3, TLR7, TLR8 and/or TLR9.

[0323] In one embodiment, the invention features a chemically synthesized double stranded short interfering nucleic acid (siNA) molecule that directs cleavage of a target RNA via RNA interference (RNAi), wherein: (a) each strand of said siNA molecule is about 18 to about 38 nucleotides in length; (b) one strand of said siNA molecule comprises nucleotide sequence having sufficient complementarity to said target RNA for the siNA molecule to direct cleavage of the target RNA via RNA interference; and (c) wherein the nucleotide positions within said siNA molecule are chemically modified to reduce the immunostimulatory properties of the siNA molecule to a level below that of a corresponding unmodified siRNA molecule. Such siNA molecules are said to have an improved toxicologic profile compared to an unmodified or minimally modified siNA.

[0324] By "improved toxicologic profile", is meant that the chemically modified or formulated siNA construct exhibits decreased toxicity in a cell, subject, or organism compared to an unmodified or unformulated siNA, or siNA molecule having fewer modifications or modifications that are less effective in imparting improved toxicology. In a non-limiting example, siNA molecules and formulations with improved toxicologic profiles are associated with reduced immunostimulatory properties, such as a reduced, decreased or attenuated immunostimulatory response in a cell, subject, or organism compared to an unmodified or unformulated siNA, or siNA molecule having fewer modifications or modifications that are less effective in imparting improved toxicology. Such an improved toxicologic profile is characterized by abrogated or reduced immunostimulation, such as reduction or abrogation of induction of interferons (e.g., interferon

alpha), inflammatory cytokines (e.g., interleukins such as IL-6, and/or TNF-alpha), and/or toll like receptors (e.g., TLR-3, TLR-7, TLR-8, and/or TLR-9). In one embodiment, a siNA molecule or formulation with an improved toxicological profile comprises no ribonucleotides. In one embodiment, a siNA molecule or formulation with an improved toxicological profile comprises less than 5 ribonucleotides (e.g., 1, 2, 3, or 4 ribonucleotides). In one embodiment, a siNA molecule or formulation with an improved toxicological profile comprises Stab 7, Stab 8, Stab 11, Stab 12, Stab 13, Stab 16, Stab 17, Stab 18, Stab 19, Stab 20, Stab 23, Stab 24, Stab 25, Stab 26, Stab 27, Stab 28, Stab 29, Stab 30, Stab 31, Stab 32, Stab 33, Stab 34, Stab 35, Stab 36 or any combination thereof (see Table IV). Herein, numeric Stab chemistries include both 2'-fluoro and 2'-OCF₃ versions of the chemistries shown in Table IV. For example, "Stab 7/8" refers to both Stab 7/8 and Stab 7F/8F etc. In one embodiment, a siNA molecule or formulation with an improved toxicological profile comprises a siNA molecule of the invention and a formulation as described in United States Patent Application Publication No. 20030077829, incorporated by reference herein in its entirety including the drawings.

[0325] In one embodiment, the level of immunostimulatory response associated with a given siNA molecule can be measured as is described herein or as is otherwise known in the art, for example by determining the level of PKR/interferon response, proliferation, B-cell activation, and/or cytokine production in assays to quantitate the immunostimulatory response of particular siNA molecules (see, for example, Leifer et al., 2003, *J. Immunother.* 26, 313-9; and U.S. Pat. No. 5,968,909, incorporated in its entirety by reference). In one embodiment, the reduced immunostimulatory response is between about 10% and about 100% compared to an unmodified or minimally modified siRNA molecule, e.g., about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% reduced immunostimulatory response. In one embodiment, the immunostimulatory response associated with a siNA molecule can be modulated by the degree of chemical modification. For example, a siNA molecule having between about 10% and about 100%, e.g., about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% or at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% of the nucleotide positions in the siNA molecule modified can be selected to have a corresponding degree of immunostimulatory properties as described herein.

[0326] In one embodiment, the degree of reduced immunostimulatory response is selected for optimized RNAi activity. For example, retaining a certain degree of immunostimulation can be preferred to treat viral infection, where less than 100% reduction in immunostimulation may be preferred for maximal antiviral activity (e.g., about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% reduction in immunostimulation) whereas the inhibition of expression of an endogenous gene target may be preferred with siNA molecules that possess minimal immunostimulatory properties to prevent non-specific toxicity or off target effects (e.g., about 90% to about 100% reduction in immunostimulation).

[0327] In one embodiment, the invention features a chemically synthesized double stranded siNA molecule that directs cleavage of a target RNA via RNA interference (RNAi), wherein (a) each strand of said siNA molecule is about 18 to about 38 nucleotides in length; (b) one strand of said siNA molecule comprises nucleotide sequence having sufficient complementarity to said target RNA for the siNA molecule to

direct cleavage of the target RNA via RNA interference; and (c) wherein one or more nucleotides of said siNA molecule are chemically modified to reduce the immunostimulatory properties of the siNA molecule to a level below that of a corresponding unmodified siNA molecule. In one embodiment, each strand comprises at least about 18 nucleotides that are complementary to the nucleotides of the other strand.

[0328] In another embodiment, the siNA molecule comprising modified nucleotides to reduce the immunostimulatory properties of the siNA molecule comprises an antisense region having nucleotide sequence that is complementary to a nucleotide sequence of a target gene or a portion thereof and further comprises a sense region, wherein said sense region comprises a nucleotide sequence substantially similar to the nucleotide sequence of said target gene or portion thereof. In one embodiment thereof, the antisense region and the sense region comprise about 18 to about 38 nucleotides, wherein said antisense region comprises at least about 18 nucleotides that are complementary to nucleotides of the sense region. In one embodiment thereof, the pyrimidine nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides. In another embodiment thereof, the purine nucleotides in the sense region are 2'-deoxy purine nucleotides. In yet another embodiment thereof, the pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In another embodiment thereof, the pyrimidine nucleotides of said antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In yet another embodiment thereof, the purine nucleotides of said antisense region are 2'-O-methyl purine nucleotides. In still another embodiment thereof, the purine nucleotides present in said antisense region comprise 2'-deoxypurine nucleotides. In another embodiment, the antisense region comprises a phosphorothioate internucleotide linkage at the 3' end of said antisense region. In another embodiment, the antisense region comprises a glyceryl modification at a 3' end of said antisense region.

[0329] In other embodiments, the siNA molecule comprising modified nucleotides to reduce the immunostimulatory properties of the siNA molecule can comprise any of the structural features of siNA molecules described herein. In other embodiments, the siNA molecule comprising modified nucleotides to reduce the immunostimulatory properties of the siNA molecule can comprise any of the chemical modifications of siNA molecules described herein.

[0330] In one embodiment, the invention features a method for generating a chemically synthesized double stranded siNA molecule having chemically modified nucleotides to reduce the immunostimulatory properties of the siNA molecule, comprising (a) introducing one or more modified nucleotides in the siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating an siNA molecule having reduced immunostimulatory properties compared to a corresponding siNA molecule having unmodified nucleotides. Each strand of the siNA molecule is about 18 to about 38 nucleotides in length. One strand of the siNA molecule comprises nucleotide sequence having sufficient complementarity to the target RNA for the siNA molecule to direct cleavage of the target RNA via RNA interference. In one embodiment, the reduced immunostimulatory properties comprise an abrogated or reduced induction of inflammatory or proinflammatory cytokines, such as interleukin-6 (IL-6) or tumor necrosis alpha (TNF- α), in response to the siNA being introduced in a cell, tissue, or organism. In another embodiment, the reduced immunostimulatory prop-

erties comprise an abrogated or reduced induction of Toll Like Receptors (TLRs), such as TLR3, TLR7, TLR8 or TLR9, in response to the siNA being introduced in a cell, tissue, or organism. In another embodiment, the reduced immunostimulatory properties comprise an abrogated or reduced induction of interferons, such as interferon alpha, in response to the siNA being introduced in a cell, tissue, or organism.

[0331] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the sense and antisense strands of the siNA construct.

[0332] In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

[0333] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

[0334] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

[0335] In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence.

[0336] In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

[0337] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide, wherein the siNA construct comprises one or more chemical modifications described herein that modulate the polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

[0338] In another embodiment, the invention features a method for generating siNA molecules capable of mediating

increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to a chemically-modified siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA molecule.

[0339] In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi against a target polynucleotide in a cell, wherein the chemical modifications do not significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a manner that would decrease the efficacy of RNAi mediated by such siNA constructs.

[0340] In another embodiment, the invention features a method for generating siNA molecules with improved RNAi specificity against polynucleotide targets comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi specificity. In one embodiment, improved specificity comprises having reduced off target effects compared to an unmodified siNA molecule. For example, introduction of terminal cap moieties at the 3'-end, 5'-end, or both 3' and 5'-ends of the sense strand or region of a siNA molecule of the invention can direct the siNA to have improved specificity by preventing the sense strand or sense region from acting as a template for RNAi activity against a corresponding target having complementarity to the sense strand or sense region.

[0341] In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a target polynucleotide comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity.

[0342] In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a target RNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target RNA.

[0343] In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a target DNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target DNA.

[0344] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the cellular uptake of the siNA construct, such as cholesterol conjugation of the siNA.

[0345] In another embodiment, the invention features a method for generating siNA molecules against a target polynucleotide with improved cellular uptake comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

[0346] In one embodiment, the invention features siNA constructs that mediate RNAi against a target polynucleotide, wherein the siNA construct comprises one or more chemical modifications described herein that increases the bioavailability of the siNA construct, for example, by attaching polymeric conjugates such as polyethyleneglycol or equivalent conjugates that improve the pharmacokinetics of the siNA construct, or by attaching conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples of such conjugates are described in Vargeese et al., U.S. Ser. No. 10/201,394 incorporated by reference herein.

[0347] In one embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing a conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such conjugates can include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; cholesterol; cholesterol derivatives, polyamines, such as spermine or spermidine; and others.

[0348] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence is chemically modified in a manner that it can no longer act as a guide sequence for efficiently mediating RNA interference and/or be recognized by cellular proteins that facilitate RNAi. In one embodiment, the first nucleotide sequence of the siNA is chemically modified as described herein. In one embodiment, the first nucleotide sequence of the siNA is not modified (e.g., is all RNA).

[0349] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein the second sequence is designed or modified in a manner that prevents its entry into the RNAi pathway as a guide sequence or as a sequence that is complementary to a target nucleic acid (e.g., RNA) sequence. In one embodiment, the first nucleotide sequence of the siNA is chemically modified as described herein. In one embodiment, the first nucleotide sequence of the siNA is not modified (e.g., is all RNA). Such design or modifications are expected to enhance the activity of siNA and/or improve the specificity of siNA molecules of the invention. These modifications are also expected to minimize any off-target effects and/or associated toxicity.

[0350] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second

sequence having complementarity to said first sequence, wherein said second sequence is incapable of acting as a guide sequence for mediating RNA interference. In one embodiment, the first nucleotide sequence of the siNA is chemically modified as described herein. In one embodiment, the first nucleotide sequence of the siNA is not modified (e.g., is all RNA).

[0351] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence does not have a terminal 5'-hydroxyl (5'-OH) or 5'-phosphate group.

[0352] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence comprises a terminal cap moiety at the 5'-end of said second sequence. In one embodiment, the terminal cap moiety comprises an inverted abasic, inverted deoxy abasic, inverted nucleotide moiety, a group shown in FIG. 10, an alkyl or cycloalkyl group, a heterocycle, or any other group that prevents RNAi activity in which the second sequence serves as a guide sequence or template for RNAi.

[0353] In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence comprises a terminal cap moiety at the 5'-end and 3'-end of said second sequence. In one embodiment, each terminal cap moiety individually comprises an inverted abasic, inverted deoxy abasic, inverted nucleotide moiety, a group shown in FIG. 10, an alkyl or cycloalkyl group, a heterocycle, or any other group that prevents RNAi activity in which the second sequence serves as a guide sequence or template for RNAi.

[0354] In one embodiment, the invention features a method for generating siNA molecules of the invention with improved specificity for down regulating or inhibiting the expression of a target nucleic acid (e.g., a DNA or RNA such as a gene or its corresponding RNA), comprising (a) introducing one or more chemical modifications into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved specificity. In another embodiment, the chemical modification used to improve specificity comprises terminal cap modifications at the 5'-end, 3'-end, or both 5' and 3'-ends of the siNA molecule. The terminal cap modifications can comprise, for example, structures shown in FIG. 10 (e.g. inverted deoxyabasic moieties) or any other chemical modification that renders a portion of the siNA molecule (e.g. the sense strand) incapable of mediating RNA interference against an off target nucleic acid sequence. In a non-limiting example, a siNA molecule is designed such that only the antisense sequence of the siNA molecule can serve as a guide sequence for RISC mediated degradation of a corresponding target RNA sequence. This can be accomplished by rendering the sense sequence of the siNA inactive by introducing chemical modifications to the sense strand that preclude recognition of the sense strand as a guide sequence by RNAi

machinery. In one embodiment, such chemical modifications comprise any chemical group at the 5'-end of the sense strand of the siNA, or any other group that serves to render the sense strand inactive as a guide sequence for mediating RNA interference. These modifications, for example, can result in a molecule where the 5'-end of the sense strand no longer has a free 5'-hydroxyl (5'-OH) or a free 5'-phosphate group (e.g., phosphate, diphosphate, triphosphate, cyclic phosphate etc.). Non-limiting examples of such siNA constructs are described herein, such as "Stab 9/10", "Stab 7/8", "Stab 7/19", "Stab 17/22", "Stab 23/24", "Stab 24/25", and "Stab 24/26" (e.g., any siNA having Stab 7, 9, 17, 23, or 24 sense strands) chemistries and variants thereof (see Table IV) wherein the 5'-end and 3'-end of the sense strand of the siNA do not comprise a hydroxyl group or phosphate group. Herein, numeric Stab chemistries include both 2'-fluoro and 2'-OCF₃ versions of the chemistries shown in Table IV. For example, "Stab 7/8" refers to both Stab 7/8 and Stab 7F/8F etc.

[0355] In one embodiment, the invention features a method for generating siNA molecules of the invention with improved specificity for down regulating or inhibiting the expression of a PCSK9 target nucleic acid (e.g., a DNA or RNA such as a gene or its corresponding RNA), comprising introducing one or more chemical modifications into the structure of a siNA molecule that prevent a strand or portion of the siNA molecule from acting as a template or guide sequence for RNAi activity. In one embodiment, the inactive strand or sense region of the siNA molecule is the sense strand or sense region of the siNA molecule, i.e. the strand or region of the siNA that does not have complementarity to the target nucleic acid sequence. In one embodiment, such chemical modifications comprise any chemical group at the 5'-end of the sense strand or region of the siNA that does not comprise a 5'-hydroxyl (5'-OH) or 5'-phosphate group, or any other group that serves to render the sense strand or sense region inactive as a guide sequence for mediating RNA interference. Non-limiting examples of such siNA constructs are described herein, such as "Stab 9/10", "Stab 7/8", "Stab 7/19", "Stab 17/22", "Stab 23/24", "Stab 24/25", and "Stab 24/26" (e.g., any siNA having Stab 7, 9, 17, 23, or 24 sense strands) chemistries and variants thereof (see Table IV) wherein the 5'-end and 3'-end of the sense strand of the siNA do not comprise a hydroxyl group or phosphate group. Herein, numeric Stab chemistries include both 2'-fluoro and 2'-OCF₃ versions of the chemistries shown in Table IV. For example, "Stab 7/8" refers to both Stab 7/8 and Stab 7F/8F etc.

[0356] In one embodiment, the invention features a method for screening siNA molecules that are active in mediating RNA interference against a target nucleic acid sequence comprising (a) generating a plurality of unmodified siNA molecules, (b) screening the siNA molecules of step (a) under conditions suitable for isolating siNA molecules that are active in mediating RNA interference against the target nucleic acid sequence, and (c) introducing chemical modifications (e.g. chemical modifications as described herein or as otherwise known in the art) into the active siNA molecules of (b). In one embodiment, the method further comprises re-screening the chemically modified siNA molecules of step (c) under conditions suitable for isolating chemically modified siNA molecules that are active in mediating RNA interference against the target nucleic acid sequence.

[0357] In one embodiment, the invention features a method for screening chemically modified siNA molecules that are active in mediating RNA interference against a target nucleic

acid sequence comprising (a) generating a plurality of chemically modified siNA molecules (e.g. siNA molecules as described herein or as otherwise known in the art), and (b) screening the siNA molecules of step (a) under conditions suitable for isolating chemically modified siNA molecules that are active in mediating RNA interference against the target nucleic acid sequence.

[0358] The term "ligand" refers to any compound or molecule, such as a drug, peptide, hormone, or neurotransmitter, that is capable of interacting with another compound, such as a receptor, either directly or indirectly. The receptor that interacts with a ligand can be present on the surface of a cell or can alternately be an intercellular receptor. Interaction of the ligand with the receptor can result in a biochemical reaction, or can simply be a physical interaction or association.

[0359] In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing an excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such excipients include polymers such as cyclodextrins, lipids, cationic lipids, polyamines, phospholipids, nanoparticles, receptors, ligands, and others.

[0360] In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

[0361] In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 100 to about 50,000 daltons (Da).

[0362] The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to test samples and/or subjects. For example, preferred components of the kit include a siNA molecule of the invention and a vehicle that promotes introduction of the siNA into cells of interest as described herein (e.g., using lipids and other methods of transfection known in the art, see for example Beigelman et al, U.S. Pat. No. 6,395,713). The kit can be used for target validation, such as in determining gene function and/or activity, or in drug optimization, and in drug discovery (see for example Usman et al., U.S. Ser. No. 60/402,996). Such a kit can also include instructions to allow a user of the kit to practice the invention.

[0363] The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used herein refers to any nucleic acid molecule capable of inhibiting or down regulating gene expression or viral replication by mediating RNA interference "RNAi" or gene silencing in a sequence-specific manner. These terms can refer to both individual nucleic acid molecules, a plurality of such nucleic acid molecules, or pools of such nucleic acid molecules. The siNA can be a double-stranded nucleic acid molecule comprising self-complementary sense and antisense regions, wherein the anti-sense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid

molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e., each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double stranded structure, for example wherein the double stranded region is about 15 to about 30, e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 base pairs; the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof (e.g., about 15 to about 25 or more nucleotides of the siNA molecule are complementary to the target nucleic acid or a portion thereof). Alternatively, the siNA is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either in vivo or in vitro to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez et al., 2002, *Cell*, 110, 563-574 and Schwarz et al., 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiments, the siNA molecule of the invention comprises separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linkers molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der waals interactions, hydrophobic interactions, and/or stacking interactions. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target

gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the invention lack 2'-hydroxy(2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the presence of ribonucleotides within the siNA molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. Non limiting examples of siNA molecules of the invention are shown in FIGS. 4-6, and Tables II and III herein. Such siNA molecules are distinct from other nucleic acid technologies known in the art that mediate inhibition of gene expression, such as ribozymes, antisense, triplex forming, aptamer, 2,5-A chimera, or decoy oligonucleotides.

[0364] By "RNA interference" or "RNAi" is meant a biological process of inhibiting or down regulating gene expression in a cell as is generally known in the art and which is mediated by short interfering nucleic acid molecules, see for example Zamore and Haley, 2005, *Science*, 309, 1519-1524; Vaughn and Martienssen, 2005, *Science*, 309, 1525-1526; Zamore et al., 2000, *Cell*, 101, 25-33; Bass, 2001, *Nature*, 411, 428-429; Elbashir et al., 2001, *Nature*, 411, 494-498; and Kreutzer et al., International PCT Publication No. WO 00/44895; Zernicka-Goetz et al., International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck et al., International PCT Publication No. WO 00/01846; Mello and Fire, International PCT Publication No. WO 01/29058; Deschamps-Depailliette, International PCT Publication No. WO 99/07409; and Li et al., International PCT Publication No. WO 00/44914; Allshire, 2002, *Science*, 297, 1818-1819; Volpe et al., 2002, *Science*, 297, 1833-1837; Jennewein, 2002, *Science*, 297, 2215-2218; and Hall et al., 2002, *Science*, 297, 2232-2237; Hutvagner and Zamore, 2002, *Science*, 297, 2056-60; McManus et al., 2002, *RNA*, 8, 842-850; Reinhart et al., 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, transcriptional inhibition, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional

level. In a non-limiting example, epigenetic modulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure or methylation patterns to alter gene expression (see, for example, Verdel et al., 2004, *Science*, 303, 672-676; Pal-Bhadra et al., 2004, *Science*, 303, 669-672; Allshire, 2002, *Science*, 297, 1818-1819; Volpe et al., 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall et al., 2002, *Science*, 297, 2232-2237). In another non-limiting example, modulation of gene expression by siNA molecules of the invention can result from siNA mediated cleavage of RNA (either coding or non-coding RNA) via RISC, or alternately, translational inhibition as is known in the art. In another embodiment, modulation of gene expression by siNA molecules of the invention can result from transcriptional inhibition (see for example Janowski et al., 2005, *Nature Chemical Biology*, 1, 216-222).

[0365] In one embodiment, a siNA molecule of the invention is a duplex forming oligonucleotide “DFO”, (see for example FIGS. 14-15 and Vaish et al., U.S. Ser. No. 10/727, 780 filed Dec. 3, 2003 and International PCT Application No. US04/16390, filed May 24, 2004).

[0366] In one embodiment, a siNA molecule of the invention is a multifunctional siNA, (see for example FIGS. 16-28 and Jadhav et al., U.S. Ser. No. 60/543,480 filed Feb. 10, 2004 and International PCT Application No. US04/16390, filed May 24, 2004). In one embodiment, the multifunctional siNA of the invention can comprise sequence targeting, for example, two or more regions of PCSK9 RNA (see for example target sequences in Tables II and III). In one embodiment, the multifunctional siNA of the invention can comprise sequence targeting one or more different PCSK9 targets, including coding regions and non-coding regions of PCSK9.

[0367] By “asymmetric hairpin” as used herein is meant a linear siNA molecule comprising an antisense region, a loop portion that can comprise nucleotides or non-nucleotides, and a sense region that comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex with loop. For example, an asymmetric hairpin siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 15 to about 30, or about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides) and a loop region comprising about 4 to about 12 (e.g., about 4, 5, 6, 7, 8, 9, 10, 11, or 12) nucleotides, and a sense region having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides that are complementary to the antisense region. The asymmetric hairpin siNA molecule can also comprise a 5'-terminal phosphate group that can be chemically modified. The loop portion of the asymmetric hairpin siNA molecule can comprise nucleotides, non-nucleotides, linker molecules, or conjugate molecules as described herein.

[0368] By “asymmetric duplex” as used herein is meant a siNA molecule having two separate strands comprising a sense region and an antisense region, wherein the sense region comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex. For example, an asymmetric duplex siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g., about 15 to about 30, or about 15, 16, 17, 18, 19, 20, 21,

22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides) and a sense region having about 3 to about 25 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides that are complementary to the antisense region.

[0369] By “RNAi inhibitor” is meant any molecule that can down regulate, reduce or inhibit RNA interference function or activity in a cell or organism. An RNAi inhibitor can down regulate, reduce or inhibit RNAi (e.g., RNAi mediated cleavage of a target polynucleotide, translational inhibition, or transcriptional silencing) by interaction with or interfering the function of any component of the RNAi pathway, including protein components such as RISC, or nucleic acid components such as miRNAs or siRNAs. A RNAi inhibitor can be a siNA molecule, an antisense molecule, an aptamer, or a small molecule that interacts with or interferes with the function of RISC, a miRNA, or a siRNA or any other component of the RNAi pathway in a cell or organism. By inhibiting RNAi (e.g., RNAi mediated cleavage of a target polynucleotide, translational inhibition, or transcriptional silencing), a RNAi inhibitor of the invention can be used to modulate (e.g., up-regulate or down regulate) the expression of a target gene. In one embodiment, a RNA inhibitor of the invention is used to up-regulate gene expression by interfering with (e.g., reducing or preventing) endogenous down-regulation or inhibition of gene expression through translational inhibition, transcriptional silencing, or RISC mediated cleavage of a polynucleotide (e.g., mRNA). By interfering with mechanisms of endogenous repression, silencing, or inhibition of gene expression, RNAi inhibitors of the invention can therefore be used to up-regulate gene expression for the treatment of diseases, traits, or conditions resulting from a loss of function.

[0370] By “aptamer” or “nucleic acid aptamer” as used herein is meant a polynucleotide that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that is distinct from sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art, see for example Gold et al., 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.*, 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628. Aptamer molecules of the invention can be chemically modified as is generally known in the art or as described herein.

[0371] The term “antisense nucleic acid”, as used herein, refers to a nucleic acid molecule that binds to target RNA by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm et al., 1993 *Nature* 365, 566) interactions and alters the activity of the target RNA (for a review, see Stein and Cheng, 1993 *Science* 261, 1004 and Woolf et al., U.S. Pat. No. 5,849,902) by steric interaction or by RNase H mediated target recognition. Typically, antisense molecules are complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in cer-

tain embodiments, an antisense molecule can bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule can bind such that the antisense molecule forms a loop. Thus, the antisense molecule can be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule can be complementary to a target sequence or both. For a review of current antisense strategies, see Schmajuk et al., 1999, *J. Biol. Chem.*, 274, 21783-21789; Delihas et al., 1997, *Nature*, 385, 751-753; Stein et al., 1997, *Antisense N. A. Drug Dev.*, 7, 151; Crooke, 2000, *Methods Enzymol.*, 313, 3-45; Crooke, 1998, *Biotech. Genet. Eng. Rev.*, 15, 121-157; Crooke, 1997, *Ad. Pharmacol.*, 40, 1-49. In addition, antisense DNA or antisense modified with 2'-MOE and other modifications as are known in the art can be used to target RNA by means of DNA-RNA interactions, thereby activating RNase H, which digests the target RNA in the duplex. The antisense oligonucleotides can comprise one or more RNase H activating region, which is capable of activating RNase H cleavage of a target RNA. Antisense DNA can be synthesized chemically or expressed via the use of a single stranded DNA expression vector or equivalent thereof. Antisense molecules of the invention can be chemically modified as is generally known in the art or as described herein.

[0372] By "modulate" is meant that the expression of the gene, or level of a RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the use of the word "modulate" is not limited to this definition.

[0373] By "inhibit", "down-regulate", or "reduce", it is meant that the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, is reduced below that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. In one embodiment, inhibition, down-regulation or reduction with an siNA molecule is below that level observed in the presence of an inactive or attenuated molecule. In another embodiment, inhibition, down-regulation, or reduction with siNA molecules is below that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In another embodiment, inhibition, down-regulation, or reduction of gene expression with a nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence. In one embodiment, inhibition, down regulation, or reduction of gene expression is associated with post transcriptional silencing, such as RNAi mediated cleavage of a target nucleic acid molecule (e.g. RNA) or inhibition of translation. In one embodiment, inhibition, down regulation, or reduction of gene expression is associated with pretranscriptional silencing, such as by alterations in DNA methylation patterns and DNA chromatin structure.

[0374] By "up-regulate", or "promote", it is meant that the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, is increased above that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. In one

embodiment, up-regulation or promotion of gene expression with an siNA molecule is above that level observed in the presence of an inactive or attenuated molecule. In another embodiment, up-regulation or promotion of gene expression with siNA molecules is above that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In another embodiment, up-regulation or promotion of gene expression with a nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence. In one embodiment, up-regulation or promotion of gene expression is associated with inhibition of RNA mediated gene silencing, such as RNAi mediated cleavage or silencing of a coding or non-coding RNA target that down regulates, inhibits, or silences the expression of the gene of interest to be up-regulated. The down regulation of gene expression can, for example, be induced by a coding RNA or its encoded protein, such as through negative feedback or antagonistic effects. The down regulation of gene expression can, for example, be induced by a non-coding RNA having regulatory control over a gene of interest, for example by silencing expression of the gene via translational inhibition, chromatin structure, methylation, RISC mediated RNA cleavage, or translational inhibition. As such, inhibition or down regulation of targets that down regulate, suppress, or silence a gene of interest can be used to up-regulate or promote expression of the gene of interest toward therapeutic use.

[0375] By "gene", or "target gene" or "target DNA", is meant a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding a polypeptide. A gene or target gene can also encode a functional RNA (fRNA) or non-coding RNA (ncRNA), such as small temporal RNA (stRNA), micro RNA (miRNA), small nuclear RNA (snRNA), short interfering RNA (siRNA), small nucleolar RNA (snRNA), ribosomal RNA (rRNA), transfer RNA (tRNA) and precursor RNAs thereof. Such non-coding RNAs can serve as target nucleic acid molecules for siNA mediated RNA interference in modulating the activity of fRNA or ncRNA involved in functional or regulatory cellular processes. Aberrant fRNA or ncRNA activity leading to disease can therefore be modulated by siNA molecules of the invention. siNA molecules targeting fRNA and ncRNA can also be used to manipulate or alter the genotype or phenotype of a subject, organism or cell, by intervening in cellular processes such as genetic imprinting, transcription, translation, or nucleic acid processing (e.g., transamination, methylation etc.). The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts. For a review, see for example Snyder and Gerstein, 2003, *Science*, 300, 258-260.

[0376] By "non-canonical base pair" is meant any non-Watson Crick base pair, such as mismatches and/or wobble base pairs, including flipped mismatches, single hydrogen bond mismatches, trans-type mismatches, triple base interactions, and quadruple base interactions. Non-limiting examples of such non-canonical base pairs include, but are

not limited to, AC reverse Hoogsteen, AC wobble, AU reverse Hoogsteen, GU wobble, AA N7 amino, CC 2-carbonyl-amino(H1)-N-3-amino(H2), GA sheared, UC 4-carbonyl-amino, UU imino-carbonyl, AC reverse wobble, AU Hoogsteen, AU reverse Watson Crick, CG reverse Watson Crick, GC N3-amino-amino N3, AA N1-amino symmetric, AA N7-amino symmetric, GA N7-N1 amino-carbonyl, GA+ carbonyl-amino N7-N1, GG N1-carbonyl symmetric, GG N3-amino symmetric, CC carbonyl-amino symmetric, CC N3-amino symmetric, UU 2-carbonyl-imino symmetric, UU 4-carbonyl-imino symmetric, AA amino-N3, AA N1-amino, AC amino 2-carbonyl, AC N3-amino, AC N7-amino, AU amino-4-carbonyl, AU N1-imino, AU N3-imino, AU N7-imino, CC carbonyl-amino, GA amino-N1, GA amino-N7, GA carbonyl-amino, GA N3-amino, GC amino-N3, GC carbonyl-amino, GC N3-amino, GC N7-amino, GG amino-N7, GG carbonyl-imino, GG N7-amino, GU amino-2-carbonyl, GU carbonyl-imino, GU imino-2-carbonyl, GU N7-imino, psiU imino-2-carbonyl, UC 4-carbonyl-amino, UC imino-carbonyl, UU imino-4-carbonyl, AC C2-H—N3, GA carbonyl-C2-H, UU imino-4-carbonyl 2 carbonyl-C5-H, AC amino(A) N3(C)-carbonyl, GC imino amino-carbonyl, Gpsi imino-2-carbonyl amino-2-carbonyl, and GU imino amino-2-carbonyl base pairs.

[0377] By "PCSK9" as used herein is meant, any Proprotein Convertase Subtilisin Kexin 9 or PCSK9 protein, peptide, or polypeptide having PCSK9 activity, such as encoded by PCSK9 Genbank Accession Nos. shown in Table I. The term PCSK9 also refers to nucleic acid sequences encoding or regulating the expression of any PCSK9 protein, peptide, or polypeptide having PCSK9 activity. The term "PCSK9" is also meant to include other PCSK9 encoding sequence, such as PCSK9 sequences derived from various subjects or organisms, including other PCSK9 isoforms, mutant PCSK9 genes, splice variants of PCSK9 genes, and PCSK9 gene polymorphisms.

[0378] By "PCSK9 pathway target" is meant any target involved in PCSK9 pathways of gene expression or activity, including such targets as ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9), LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and F-box-only protein 3.

[0379] By "target" as used herein is meant, any target protein, peptide, or polypeptide, such as encoded by Genbank Accession Nos. herein (see Table I) and in U.S. Ser. No. 10/923,536 and PCT/US03/05028, both incorporated by reference herein. The term "target" also refers to nucleic acid sequences or target polynucleotide sequence encoding any target protein, peptide, or polypeptide, such as proteins, peptides, or polypeptides encoded by sequences having Genbank Accession Nos. shown herein or in US Ser. No. 10/923,536 and PCT/US03/05028. The target of interest can include target polynucleotide sequences, such as target DNA or target RNA. The term "target" is also meant to include other sequences, such as differing isoforms, mutant target genes, splice variants of target polynucleotides, target polymorphisms, and non-coding (e.g., ncRNA, miRNA, stRNA) or other regulatory polynucleotide sequences as described herein. Therefore, in various embodiments of the invention, a double stranded nucleic acid molecule of the invention (e.g., siNA) having complementarity to a target RNA can be used to inhibit or down regulate miRNA or other ncRNA activity. In one embodiment, inhibition of miRNA or ncRNA activity can

be used to down regulate or inhibit gene expression (e.g., gene targets described herein or otherwise known in the art) that is dependent on miRNA or ncRNA activity. In another embodiment, inhibition of miRNA or ncRNA activity by double stranded nucleic acid molecules of the invention (e.g. siNA) having complementarity to the miRNA or ncRNA can be used to up regulate or promote target gene expression (e.g., gene targets described herein or otherwise known in the art) where the expression of such genes is down regulated, suppressed, or silenced by the miRNA or ncRNA. Such up-regulation of gene expression can be used to treat diseases and conditions associated with a loss of function or haploinsufficiency as are generally known in the art.

[0380] In one embodiment, the target is any of PCSK9 RNA or a portion thereof.

[0381] In one embodiment, the target is any of PCSK9 DNA or a portion thereof.

[0382] In one embodiment, the target is any of PCSK9 mRNA or a portion thereof.

[0383] In one embodiment, the target is any of PCSK9 miRNA or a portion thereof.

[0384] In one embodiment, the target is any of PCSK9 siRNA or a portion thereof.

[0385] In one embodiment, the target is any of PCSK9 stRNA or a portion thereof.

[0386] In one embodiment, the target is a PCSK9 target and/or PCSK9 pathway target or a portion thereof.

[0387] In one embodiment, the target is any (e.g., one or more) of target sequences shown in Table I or a portion thereof. In one embodiment, the target is any (e.g., one or more) of target sequences shown in Table II and III or a portion thereof. In another embodiment, the target is a siRNA, miRNA, or stRNA corresponding to any (e.g., one or more) target, upper strand, or lower strand sequence shown in Table II or III or a portion thereof. In another embodiment, the target is any siRNA, miRNA, or stRNA corresponding any (e.g., one or more) sequence shown in Table I or a portion thereof.

[0388] By "homologous sequence" is meant, a nucleotide sequence that is shared by one or more polynucleotide sequences, such as genes, gene transcripts and/or non-coding polynucleotides. For example, a homologous sequence can be a nucleotide sequence that is shared by two or more genes encoding related but different proteins, such as different members of a gene family, different protein epitopes, different protein isoforms or completely divergent genes, such as a cytokine and its corresponding receptors. A homologous sequence can be a nucleotide sequence that is shared by two or more non-coding polynucleotides, such as noncoding DNA or RNA, regulatory sequences, introns, and sites of transcriptional control or regulation. Homologous sequences can also include conserved sequence regions shared by more than one polynucleotide sequence. Homology does not need to be perfect homology (e.g., 100%), as partially homologous sequences are also contemplated by the instant invention (e.g., 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80% etc.).

[0389] By "conserved sequence region" is meant, a nucleotide sequence of one or more regions in a polynucleotide does not vary significantly between generations or from one biological system, subject, or organism to another biological system, subject, or organism. The polynucleotide can include both coding and non-coding DNA and RNA.

[0390] By "sense region" is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence. In one embodiment, the sense region of the siNA molecule is referred to as the sense strand or passenger strand.

[0391] By "antisense region" is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule. In one embodiment, the antisense region of the siNA molecule is referred to as the antisense strand or guide strand.

[0392] By "target nucleic acid" or "target polynucleotide" is meant any nucleic acid sequence (e.g., any PCSK9 and/or PCSK9 pathway sequence) whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA. In one embodiment, a target nucleic acid of the invention is target RNA or DNA.

[0393] By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types as described herein. In one embodiment, a double stranded nucleic acid molecule of the invention, such as an siNA molecule, wherein each strand is between 15 and 30 nucleotides in length, comprises between about 10% and about 100% (e.g., about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%) complementarity between the two strands of the double stranded nucleic acid molecule. In another embodiment, a double stranded nucleic acid molecule of the invention, such as an siNA molecule, where one strand is the sense strand and the other stand is the antisense strand, wherein each strand is between 15 and 30 nucleotides in length, comprises between at least about 10% and about 100% (e.g., at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%) complementarity between the nucleotide sequence in the antisense strand of the double stranded nucleic acid molecule and the nucleotide sequence of its corresponding target nucleic acid molecule, such as a target RNA or target mRNA or viral RNA. In one embodiment, a double stranded nucleic acid molecule of the invention, such as an siNA molecule, where one strand comprises nucleotide sequence that is referred to as the sense region and the other strand comprises a nucleotide sequence that is referred to as the antisense region, wherein each strand is between 15 and 30 nucleotides in length, comprises between about 10% and about 100% (e.g., about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100%) complementarity between the sense region and the antisense region of the double stranded nucleic acid molecule. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner et al., 1987, *CSH Symp. Quant. Biol. LII* pp. 123-133; Frier et al., 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner et al., 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g.,

5, 6, 7, 8, 9, or 10 nucleotides out of a total of 10 nucleotides in the first oligonucleotide being based paired to a second nucleic acid sequence having 10 nucleotides represents 50%, 60%, 70%, 80%, 90%, and 100% complementary respectively). In one embodiment, a siNA molecule of the invention has perfect complementarity between the sense strand or sense region and the antisense strand or antisense region of the siNA molecule. In one embodiment, a siNA molecule of the invention is perfectly complementary to a corresponding target nucleic acid molecule. "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. In one embodiment, a siNA molecule of the invention comprises about 15 to about 30 or more (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 or more) nucleotides that are complementary to one or more target nucleic acid molecules or a portion thereof. In one embodiment, a siNA molecule of the invention has partial complementarity (i.e., less than 100% complementarity) between the sense strand or sense region and the antisense strand or antisense region of the siNA molecule or between the antisense strand or antisense region of the siNA molecule and a corresponding target nucleic acid molecule. For example, partial complementarity can include various mismatches or non-based paired nucleotides (e.g., 1, 2, 3, 4, 5 or more mismatches or non-based paired nucleotides) within the siNA structure which can result in bulges, loops, or overhangs that result between the between the sense strand or sense region and the antisense strand or antisense region of the siNA molecule or between the antisense strand or antisense region of the siNA molecule and a corresponding target nucleic acid molecule.

[0394] In one embodiment, a double stranded nucleic acid molecule of the invention, such as siNA molecule, has perfect complementarity between the sense strand or sense region and the antisense strand or antisense region of the nucleic acid molecule. In one embodiment, double stranded nucleic acid molecule of the invention, such as siNA molecule, is perfectly complementary to a corresponding target nucleic acid molecule.

[0395] In one embodiment, double stranded nucleic acid molecule of the invention, such as siNA molecule, has partial complementarity (i.e., less than 100% complementarity) between the sense strand or sense region and the antisense strand or antisense region of the double stranded nucleic acid molecule or between the antisense strand or antisense region of the nucleic acid molecule and a corresponding target nucleic acid molecule. For example, partial complementarity can include various mismatches or non-base paired nucleotides (e.g., 1, 2, 3, 4, 5 or more mismatches or non-based paired nucleotides, such as nucleotide bulges) within the double stranded nucleic acid molecule, structure which can result in bulges, loops, or overhangs that result between the sense strand or sense region and the antisense strand or antisense region of the double stranded nucleic acid molecule or between the antisense strand or antisense region of the double stranded nucleic acid molecule and a corresponding target nucleic acid molecule.

[0396] In one embodiment, double stranded nucleic acid molecule of the invention is a microRNA (miRNA). By "microRNA" or "miRNA" is meant, a small double stranded RNA that regulates the expression of target messenger RNAs either by mRNA cleavage, translational repression/inhibition or heterochromatic silencing (see for example Ambros, 2004,

Quant. Biol. LII pp. 123-133; Frier et al., 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner et al., 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g.,

Nature, 431, 350-355; Bartel, 2004, Cell, 116, 281-297; Cullen, 2004, Virus Research., 102, 3-9; He et al., 2004, Nat. Rev. Genet., 5, 522-531; Ying et al., 2004, Gene, 342, 25-28; and Sethupathy et al., 2006, RNA, 12:192-197). In one embodiment, the microRNA of the invention, has partial complementarity (i.e., less than 100% complementarity) between the sense strand or sense region and the antisense strand or antisense region of the miRNA molecule or between the antisense strand or antisense region of the miRNA and a corresponding target nucleic acid molecule. For example, partial complementarity can include various mismatches or non-base paired nucleotides (e.g., 1, 2, 3, 4, 5 or more mismatches or non-based paired nucleotides, such as nucleotide bulges) within the double stranded nucleic acid molecule, structure which can result in bulges, loops, or overhangs that result between the sense strand or sense region and the anti-sense strand or antisense region of the miRNA or between the antisense strand or antisense region of the miRNA and a corresponding target nucleic acid molecule.

[0397] In one embodiment, siNA molecules of the invention that down regulate or reduce PCSK9 gene expression are used for preventing or treating metabolic and/or cardiovascular and related diseases, disorders, conditions, or traits in a subject or organism as described herein or otherwise known in the art.

[0398] By "metabolic disease" is meant any disease or condition affecting metabolic pathways as is known in the art. Metabolic disease can result in an abnormal metabolic process, either congenital due to inherited enzyme abnormality (inborn errors of metabolism) or acquired due to disease of an endocrine organ or failure of a metabolically important organ such as the liver. In one embodiment, metabolic disease includes hyperlipidemia, hypercholesterolemia, cardiovascular disease, atherosclerosis, hypertension, diabetes (e.g., type I and/or type II diabetes), insulin resistance, and/or obesity.

[0399] By "cardiovascular disease" is meant and disease or condition affecting the heart and vasculature, including but not limited to, coronary heart disease (CHD), cerebrovascular disease (CVD), aortic stenosis, peripheral vascular disease, atherosclerosis, arteriosclerosis, myocardial infarction (heart attack), cerebrovascular diseases (stroke), transient ischaemic attacks (TIA), angina (stable and unstable), atrial fibrillation, arrhythmia, valvular disease, congestive heart failure, hypercholesterolemia, type I hyperlipoproteinemia, type II hyperlipoproteinemia, type III hyperlipoproteinemia, type IV hyperlipoproteinemia, type V hyperlipoproteinemia, secondary hypertriglyceridemia, and familial lecithin cholesterol acyltransferase deficiency.

[0400] In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 15 to about 30 nucleotides in length, in specific embodiments about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 15 to about 30 base pairs (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30). In another embodiment, one or more strands of the siNA molecule of the invention independently comprises about 15 to about 30 nucleotides (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30) that are complementary to a target nucleic acid molecule. In yet another embodiment, siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (e.g., about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44 (e.g., about 38,

39, 40, 41, 42, 43, or 44) nucleotides in length and comprising about 15 to about 25 (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs. Exemplary siNA molecules of the invention are shown in Tables II and III and/or FIGS. 4-5.

[0401] As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell can be present in an organism, e.g., birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

[0402] The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues ex vivo, or in vivo through local delivery to the lung, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in Tables II-III and/or FIGS. 4-5. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemically modified constructs described in Table IV and the lipid nanoparticle (LNP) formulations shown in Table VI can be applied to any siNA sequence or group of siNA sequences of the invention.

[0403] In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites within a target polynucleotide of the invention.

[0404] By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β -D-ribofuranose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

[0405] By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid molecules of the invention can be administered. A subject can be a mammal or mammalian cells, including a human or human cells. In one embodiment, the subject is an infant (e.g., subjects that are less than 1 month old, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 months old). In one embodiment, the subject is a toddler (e.g., 1, 2, 3, 4, 5 or 6 years old). In one embodiment, the subject is a senior (e.g., anyone over the age of about 65 years of age).

[0406] By "chemical modification" as used herein is meant any modification of chemical structure of the nucleotides that differs from nucleotides of native siRNA or RNA. The term "chemical modification" encompasses the addition, substitution, or modification of native siRNA or RNA nucleosides and nucleotides with modified nucleosides and modified nucleotides as described herein or as is otherwise known in the art. Non-limiting examples of such chemical modifications include without limitation compositions having any of Formulae I, II, III, IV, V, VI, or VII herein, phosphorothioate internucleotide linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, 4'-thio ribonucleotides, 2'-O-trifluoromethyl nucleotides, 2'-O-ethyl-trifluoromethoxy nucleotides, 2'-O-difluoromethoxy-ethoxy nucleotides (see for example U.S. Ser. No. 10/981,966 filed Nov. 5, 2004, incorporated by reference herein), FANA, "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, terminal glyceryl and/or inverted deoxy abasic residue incorporation, or a modification having any of Formulae I-VH herein. In one embodiment, the nucleic acid molecules of the invention (e.g., dsRNA, siNA etc.) are partially modified (e.g., about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% modified) with chemical modifications. In another embodiment, the nucleic acid molecules of the invention (e.g., dsRNA, siNA etc.) are completely modified (e.g., about 100% modified) with chemical modifications.

[0407] The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

[0408] The term "phosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise an acetyl or protected acetyl group.

[0409] The term "thiophosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z comprises an acetyl or protected acetyl group and W comprises a sulfur atom or alternately W comprises an acetyl or protected acetyl group and Z comprises a sulfur atom.

[0410] The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitopyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example Loakes, 2001, Nucleic Acids Research, 29, 2437-2447).

[0411] The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or C5), are independently or in combination absent from the nucleotide.

[0412] The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to for preventing or treating diseases, disorders, conditions, and traits described herein or otherwise known in the art, in a subject or organism.

[0413] In one embodiment, the siNA molecules of the invention can be administered to a subject or can be administered to other appropriate cells evident to those skilled in the

art, individually or in combination with one or more drugs under conditions suitable for the treatment.

[0414] In a further embodiment, the siNA molecules can be used in combination with other known treatments to prevent or treat respiratory diseases, disorders, or conditions in a subject or organism. For example, the described molecules could be used in combination with one or more known compounds, treatments, or procedures to prevent or treat diseases, disorders, conditions, and traits described herein in a subject or organism as are known in the art.

[0415] In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector can also contain sequence(s) encoding a single nucleic acid molecule that is self-complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul et al., 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee et al., 2002, *Nature Biotechnology*, 19, 500; and Novina et al., 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

[0416] In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

[0417] In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown herein (Table I) or in PCT/US03/05028 and U.S. Ser. No. 10/923,536, both incorporated by reference herein.

[0418] In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

[0419] In another aspect of the invention, siNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession numbers herein) are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecules bind and down-regulate gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell.

[0420] By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

[0421] Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0422] FIG. 1 shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary

siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group, remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

[0423] FIG. 2 shows a MALDI-TOF mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

[0424] FIG. 3 shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

[0425] FIG. 4A-F shows non-limiting examples of chemically-modified siNA constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be substituted in the overhanging regions designated by parenthesis (N N)). Various modifications are shown for the sense and antisense strands of the siNA constructs. The (N N) nucleotide positions can be chemically modified as described herein (e.g., 2'-O-methyl, 2'-deoxy-2'-fluoro etc.) and can be either derived from a corresponding target nucleic acid sequence or not (see for example FIG. 6C). Furthermore, the sequences shown in FIG. 4 can optionally include a ribonucleotide at the 9th position from the 5'-end of the sense strand or the 11th position based on the 5'-end of the guide strand by counting 11 nucleotide positions in from the 5'-terminus of the guide strand (see FIG. 6C).

[0426] FIG. 4A: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise

ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the antisense strand.

[0427] FIG. 4B: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the sense and antisense strand.

[0428] FIG. 4C: The sense strand comprises 21 nucleotides having 5'- and 3'-terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the antisense strand.

[0429] FIG. 4D: The sense strand comprises 21 nucleotides having 5'- and 3'-terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified inter-

nucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the antisense strand.

[0430] FIG. 4E: The sense strand comprises 21 nucleotides having 5'- and 3'-terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the antisense strand.

[0431] FIG. 4F: The sense strand comprises 21 nucleotides having 5'- and 3'-terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-deoxy nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the antisense strand. The antisense strand of constructs A-F comprise sequence complementary to any target nucleic acid sequence of the invention. Furthermore, when a glyceryl moiety (L) is present at the 3'-end of the antisense strand for any construct shown in FIG. 4 A-F, the modified internucleotide linkage is optional.

[0432] FIG. 5A-F shows non-limiting examples of specific chemically-modified siNA sequences of the invention. A-F applies the chemical modifications described in FIG. 4A-F to an exemplary PCSK9 siNA sequence. Such chemical modifications can be applied to any PCSK9 sequence. Furthermore, the sequences shown in FIG. 5 can optionally include a ribonucleotide at the 9th position from the 5'-end of the sense strand or the 11th position based on the 5'-end of the guide strand by counting 11 nucleotide positions in from the 5'-terminus of the guide strand (see FIG. 6C). In addition, the sequences shown in FIG. 5 can optionally include terminal

ribonucleotides at up to about 4 positions at the 5'-end of the antisense strand (e.g., about 1, 2, 3, or 4 terminal ribonucleotides at the 5'-end of the antisense strand).

[0433] FIG. 6A-C shows non-limiting examples of different siNA constructs of the invention.

[0434] The examples shown in FIG. 6A (constructs 1, 2, and 3) have 19 representative base pairs; however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example, comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 in vivo and/or in vitro. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 in vivo and/or in vitro, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 in vivo and/or in vitro. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use in vivo or in vitro and/or in vitro.

[0435] The examples shown in FIG. 6B represent different variations of double stranded nucleic acid molecule of the invention, such as microRNA, that can include overhangs, bulges, loops, and stem-loops resulting from partial complementarity. Such motifs having bulges, loops, and stem-loops are generally characteristics of miRNA. The bulges, loops, and stem-loops can result from any degree of partial complementarity, such as mismatches or bulges of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides in one or both strands of the double stranded nucleic acid molecule of the invention.

[0436] The example shown in FIG. 6C represents a model double stranded nucleic acid molecule of the invention comprising a 19 base pair duplex of two 21 nucleotide sequences having dinucleotide 3'-overhangs. The top strand (1) represents the sense strand (passenger strand), the middle strand (2) represents the antisense (guide strand), and the lower strand (3) represents a target polynucleotide sequence. The dinucleotide overhangs (NN) can comprise sequence derived from the target polynucleotide. For example, the 3'-(NN) sequence in the guide strand can be complementary to the 5'-[NN] sequence of the target polynucleotide. In addition, the 5'-(NN) sequence of the passenger strand can comprise the same sequence as the 5'-[NN] sequence of the target polynucleotide sequence. In other embodiments, the overhangs (NN) are not derived from the target polynucleotide sequence, for example where the 3'-(NN) sequence in the guide strand are not complementary to the 5'-[NN] sequence of the target polynucleotide and the 5'-(NN) sequence of the passenger strand can comprise different sequence from the 5'-[NN] sequence of the target polynucleotide sequence. In additional embodiments, any (NN) nucleotides are chemically modified, e.g., as 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or other modifications herein. Furthermore, the passenger strand can comprise a ribonucleotide position N of the passenger strand. For the representative 19 base pair 21 mer duplex shown, position N can be 9 nucleotides in from the 3' end of the passenger strand. However, in duplexes of differing length, the position N is determined based on the 5'-end of the guide strand by counting 11 nucleotide positions in from the

5'-terminus of the guide strand and picking the corresponding base paired nucleotide in the passenger strand. Cleavage by Ago2 takes place between positions 10 and 11 as indicated by the arrow. In additional embodiments, there are two ribonucleotides, NN, at positions 10 and 11 based on the 5'-end of the guide strand by counting 10 and 11 nucleotide positions from the 5'-terminus of the guide strand and picking the corresponding base paired nucleotides in the passenger strand.

[0437] FIG. 7A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate siNA hairpin constructs.

[0438] FIG. 7A: A DNA oligomer is synthesized with a 5'-restriction site (R1) sequence followed by a region having sequence identical (sense region of siNA) to a predetermined target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, which is followed by a loop sequence of defined sequence (X), comprising, for example, about 3 to about 10 nucleotides.

[0439] FIG. 7B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence that will result in a siNA transcript having specificity for a target sequence and having self-complementary sense and antisense regions.

[0440] FIG. 7C: The construct is heated (for example to about 95° C.) to linearize the sequence, thus allowing extension of a complementary second DNA strand using a primer to the 3'-restriction sequence of the first strand. The double-stranded DNA is then inserted into an appropriate vector for expression in cells. The construct can be designed such that a 3'-terminal nucleotide overhang results from the transcription, for example, by engineering restriction sites and/or utilizing a poly-U termination region as described in Paul et al., 2002, *Nature Biotechnology*, 29, 505-508.

[0441] FIG. 8A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate double-stranded siNA constructs.

[0442] FIG. 8A: A DNA oligomer is synthesized with a 5'-restriction (R1) site sequence followed by a region having sequence identical (sense region of siNA) to a predetermined target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, and which is followed by a 3'-restriction site (R2) which is adjacent to a loop sequence of defined sequence (X).

[0443] FIG. 8B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence.

[0444] FIG. 8C: The construct is processed by restriction enzymes specific to R1 and R2 to generate a double-stranded DNA which is then inserted into an appropriate vector for expression in cells. The transcription cassette is designed such that a U6 promoter region flanks each side of the dsDNA which generates the separate sense and antisense strands of the siNA. Poly T termination sequences can be added to the constructs to generate U overhangs in the resulting transcript.

[0445] FIG. 9A-E is a diagrammatic representation of a method used to determine target sites for siNA mediated RNAi within a particular target nucleic acid sequence, such as messenger RNA.

[0446] FIG. 9A: A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic

acid sequence, and wherein the sense region comprises sequence complementary to the antisense region of the siNA.

[0447] FIGS. 9B&C: (FIG. 9B) The sequences are pooled and are inserted into vectors such that (FIG. 9C) transfection of a vector into cells results in the expression of the siNA.

[0448] FIG. 9D: Cells are sorted based on phenotypic change that is associated with modulation of the target nucleic acid sequence.

[0449] FIG. 9E: The siNA is isolated from the sorted cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

[0450] FIG. 10 shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including (1) [3'-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5'-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

[0451] FIG. 11 shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistant while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-mofications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g. human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

[0452] FIG. 12 shows non-limiting examples of phosphorylated siNA molecules of the invention, including linear and duplex constructs and asymmetric derivatives thereof.

[0453] FIG. 13 shows non-limiting examples of chemically modified terminal phosphate groups of the invention.

[0454] FIG. 14A shows a non-limiting example of methodology used to design self complementary DFO constructs utilizing palindrome and/or repeat nucleic acid sequences that are identified in a target nucleic acid sequence. (i) A palindrome or repeat sequence is identified in a nucleic acid target sequence. (ii) A sequence is designed that is complementary to the target nucleic acid sequence and the palindrome sequence. (iii) An inverse repeat sequence of the non-palindrome/repeat portion of the complementary sequence is appended to the 3'-end of the complementary sequence to generate a self complementary DFO molecule comprising sequence complementary to the nucleic acid target. (iv) The DFO molecule can self-assemble to form a double stranded

oligonucleotide. FIG. 14B shows a non-limiting representative example of a duplex forming oligonucleotide sequence. FIG. 14C shows a non-limiting example of the self assembly schematic of a representative duplex forming oligonucleotide sequence. FIG. 14D shows a non-limiting example of the self assembly schematic of a representative duplex forming oligonucleotide sequence followed by interaction with a target nucleic acid sequence resulting in modulation of gene expression.

[0455] FIG. 15 shows a non-limiting example of the design of self complementary DFO constructs utilizing palindrome and/or repeat nucleic acid sequences that are incorporated into the DFO constructs that have sequence complementary to any target nucleic acid sequence of interest. Incorporation of these palindrome/repeat sequences allow the design of DFO constructs that form duplexes in which each strand is capable of mediating modulation of target gene expression, for example by RNAi. First, the target sequence is identified. A complementary sequence is then generated in which nucleotide or non-nucleotide modifications (shown as X or Y) are introduced into the complementary sequence that generate an artificial palindrome (shown as XYXYXY in the Figure). An inverse repeat of the non-palindrome/repeat complementary sequence is appended to the 3'-end of the complementary sequence to generate a self complementary DFO comprising sequence complementary to the nucleic acid target. The DFO can self-assemble to form a double stranded oligonucleotide.

[0456] FIG. 16 shows non-limiting examples of multifunctional siNA molecules of the invention comprising two separate polynucleotide sequences that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences. FIG. 16A shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 3'-ends of each polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. FIG. 16B shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 5'-ends of each polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences.

[0457] FIG. 17 shows non-limiting examples of multifunctional siNA molecules of the invention comprising a single polynucleotide sequence comprising distinct regions that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences. FIG. 17A shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid

sequence (complementary region 2), wherein the second complementary region is situated at the 3'-end of the polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. FIG. 17B shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first complementary region is situated at the 5'-end of the polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. In one embodiment, these multifunctional siNA constructs are processed in vivo or in vitro to generate multifunctional siNA constructs as shown in FIG. 16.

[0458] FIG. 18 shows non-limiting examples of multifunctional siNA molecules of the invention comprising two separate polynucleotide sequences that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences and wherein the multifunctional siNA construct further comprises a self complementary, palindrome, or repeat region, thus enabling shorter bifunctional siNA constructs that can mediate RNA interference against differing target nucleic acid sequences. FIG. 18A shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 3'-ends of each polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. FIG. 18B shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 5'-ends of each polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences.

[0459] FIG. 19 shows non-limiting examples of multifunctional siNA molecules of the invention comprising a single polynucleotide sequence comprising distinct regions that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences and wherein the multifunctional siNA construct further comprises a self complementary, palindrome, or repeat region, thus enabling shorter

bifunctional siNA constructs that can mediate RNA interference against differing target nucleic acid sequences. FIG. 19A shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the second complementary region is situated at the 3'-end of the polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. FIG. 19B shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first complementary region is situated at the 5'-end of the polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. In one embodiment, these multifunctional siNA constructs are processed in vivo or in vitro to generate multifunctional siNA constructs as shown in FIG. 18.

[0460] FIG. 20 shows a non-limiting example of how multifunctional siNA molecules of the invention can target two separate target nucleic acid molecules, such as separate RNA molecules encoding differing proteins (e.g., any of PCSK9 targets herein), for example, a cytokine and its corresponding receptor, differing viral strains, a virus and a cellular protein involved in viral infection or replication, or differing proteins involved in a common or divergent biologic pathway that is implicated in the maintenance of progression of disease. Each strand of the multifunctional siNA construct comprises a region having complementarity to separate target nucleic acid molecules. The multifunctional siNA molecule is designed such that each strand of the siNA can be utilized by the RISC complex to initiate RNA interference mediated cleavage of its corresponding target. These design parameters can include destabilization of each end of the siNA construct (see for example Schwarz et al., 2003, *Cell*, 115, 199-208). Such destabilization can be accomplished for example by using guanosine-cytidine base pairs, alternate base pairs (e.g., wobbles), or destabilizing chemically modified nucleotides at terminal nucleotide positions as is known in the art.

[0461] FIG. 21 shows a non-limiting example of how multifunctional siNA molecules of the invention can target two separate target nucleic acid sequences within the same target nucleic acid molecule, such as alternate coding regions of a RNA, coding and non-coding regions of a RNA, or alternate splice variant regions of a RNA. Each strand of the multifunctional siNA construct comprises a region having complementarity to the separate regions of the target nucleic acid molecule. The multifunctional siNA molecule is designed such that each strand of the siNA can be utilized by the RISC complex to initiate RNA interference mediated cleavage of its

corresponding target region. These design parameters can include destabilization of each end of the siNA construct (see for example Schwarz et al., 2003, *Cell*, 115, 199-208). Such destabilization can be accomplished for example by using guanosine-cytidine base pairs, alternate base pairs (e.g., wobbles), or destabilizing chemically modified nucleotides at terminal nucleotide positions as is known in the art.

[0462] FIG. 22(A-H) shows non-limiting examples of tethered multifunctional siNA constructs of the invention. In the examples shown, a linker (e.g., nucleotide or non-nucleotide linker) connects two siNA regions (e.g., two sense, two antisense, or alternately a sense and an antisense region together). Separate sense (or sense and antisense) sequences corresponding to a first target sequence and second target sequence are hybridized to their corresponding sense and/or antisense sequences in the multifunctional siNA. In addition, various conjugates, ligands, aptamers, polymers or reporter molecules can be attached to the linker region for selective or improved delivery and/or pharmacokinetic properties.

[0463] FIG. 23 shows a non-limiting example of various dendrimer based multifunctional siNA designs.

[0464] FIG. 24 shows a non-limiting example of various supramolecular multifunctional siNA designs.

[0465] FIG. 25 shows a non-limiting example of a dicer enabled multifunctional siNA design using a 30 nucleotide precursor siNA construct. A 30 base pair duplex is cleaved by Dicer into 22 and 8 base pair products from either end (8 b.p. fragments not shown). For ease of presentation the overhangs generated by dicer are not shown—but can be compensated for. Three targeting sequences are shown. The required sequence identity overlapped is indicated by grey boxes. The N's of the parent 30 b.p. siNA are suggested sites of 2'-OH positions to enable Dicer cleavage if this is tested in stabilized chemistries. Note that processing of a 30 mer duplex by Dicer RNase III does not give a precise 22+8 cleavage, but rather produces a series of closely related products (with 22+8 being the primary site). Therefore, processing by Dicer will yield a series of active siNAs.

[0466] FIG. 26 shows a non-limiting example of a dicer enabled multifunctional siNA design using a 40 nucleotide precursor siNA construct. A 40 base pair duplex is cleaved by Dicer into 20 base pair products from either end. For ease of presentation the overhangs generated by dicer are not shown—but can be compensated for. Four targeting sequences are shown. The target sequences having homology are enclosed by boxes. This design format can be extended to larger RNAs. If chemically stabilized siNAs are bound by Dicer, then strategically located ribonucleotide linkages can enable designer cleavage products that permit our more extensive repertoire of multifunctional designs. For example cleavage products not limited to the Dicer standard of approximately 22-nucleotides can allow multifunctional siNA constructs with a target sequence identity overlap ranging from, for example, about 3 to about 15 nucleotides.

[0467] FIG. 27 shows a non-limiting example of additional multifunctional siNA construct designs of the invention. In one example, a conjugate, ligand, aptamer, label, or other moiety is attached to a region of the multifunctional siNA to enable improved delivery or pharmacokinetic profiling.

[0468] FIG. 28 shows a non-limiting example of additional multifunctional siNA construct designs of the invention. In one example, a conjugate, ligand, aptamer, label, or other moiety is attached to a region of the multifunctional siNA to enable improved delivery or pharmacokinetic profiling.

[0469] FIG. 29 shows a non-limiting example of a cholesterol linked phosphoramidite that can be used to synthesize cholesterol conjugated siNA molecules of the invention. An example is shown with the cholesterol moiety linked to the 5'-end of the sense strand of a siNA molecule.

DETAILED DESCRIPTION OF THE INVENTION

Mechanism of Action of Nucleic Acid Molecules of the Invention

[0470] The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-modified short interfering nucleic acids possess similar or improved capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By "improved capacity to mediate RNAi" or "improved RNAi activity" is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (*i.e.*, less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

[0471] RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire et al., 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire et al., 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response though a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

[0472] The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Berstein et al., 2001, *Nature*, 409, 363). Short interfering RNAs derived from Dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner et al., 2001, *Science*, 293, 834). The RNAi response also features an endonuclease

complex containing a siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir et al., 2001, *Genes Dev.*, 15, 188). In addition, RNA interference can also involve small RNA (*e.g.*, micro-RNA or miRNA) mediated gene silencing, presumably through cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science*, 297, 1818-1819; Volpe et al., 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall et al., 2002, *Science*, 297, 2232-2237). As such, siNA molecules of the invention can be used to mediate gene silencing via interaction with RNA transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-transcriptional level.

[0473] RNAi has been studied in a variety of systems. Fire et al., 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond et al., 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir et al., 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21 nucleotide siRNA duplexes are most active when containing two 2-nucleotide 3'-terminal nucleotide overhangs. Furthermore, substitution of one or both siRNA strands with 2'-deoxy or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of 3'-terminal siRNA nucleotides with deoxy nucleotides was shown to be tolerated. Mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end (Elbashir et al., 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen et al., 2001, *Cell*, 107, 309); however, siRNA molecules lacking a 5'-phosphate are active when introduced exogenously, suggesting that 5'-phosphorylation of siRNA constructs may occur *in vivo*.

Duplex Forming Oligonucleotides (DFO) of the Invention

[0474] In one embodiment, the invention features siNA molecules comprising duplex forming oligonucleotides (DFO) that can self-assemble into double stranded oligonucleotides. The duplex forming oligonucleotides of the invention can be chemically synthesized or expressed from transcription units and/or vectors. The DFO molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, agricultural, veterinary, target validation, genomic discovery, genetic engineering and pharmacogenomic applications.

[0475] Applicant demonstrates herein that certain oligonucleotides, referred to herein for convenience but not limitation as duplex forming oligonucleotides or DFO molecules, are potent mediators of sequence specific regulation of gene expression. The oligonucleotides of the invention are distinct from other nucleic acid sequences known in the art (e.g., siRNA, miRNA, stRNA, shRNA, antisense oligonucleotides etc.) in that they represent a class of linear polynucleotide sequences that are designed to self-assemble into double stranded oligonucleotides, where each strand in the double stranded oligonucleotides comprises a nucleotide sequence that is complementary to a PCSK9 target nucleic acid molecule. Nucleic acid molecules of the invention can thus self assemble into functional duplexes in which each strand of the duplex comprises the same polynucleotide sequence and each strand comprises a nucleotide sequence that is complementary to a PCSK9 target nucleic acid molecule.

[0476] Generally, double stranded oligonucleotides are formed by the assembly of two distinct oligonucleotide sequences where the oligonucleotide sequence of one strand is complementary to the oligonucleotide sequence of the second strand; such double stranded oligonucleotides are assembled from two separate oligonucleotides, or from a single molecule that folds on itself to form a double stranded structure, often referred to in the field as hairpin stem-loop structure (e.g., shRNA or short hairpin RNA). These double stranded oligonucleotides known in the art all have a common feature in that each strand of the duplex has a distinct nucleotide sequence.

[0477] Distinct from the double stranded nucleic acid molecules known in the art, the applicants have developed a novel, potentially cost effective and simplified method of forming a double stranded nucleic acid molecule starting from a single stranded or linear oligonucleotide. The two strands of the double stranded oligonucleotide formed according to the instant invention have the same nucleotide sequence and are not covalently linked to each other. Such double-stranded oligonucleotides molecules can be readily linked post-synthetically by methods and reagents known in the art and are within the scope of the invention. In one embodiment, the single stranded oligonucleotide of the invention (the duplex forming oligonucleotide) that forms a double stranded oligonucleotide comprises a first region and a second region, where the second region includes a nucleotide sequence that is an inverted repeat of the nucleotide sequence in the first region, or a portion thereof, such that the single stranded oligonucleotide self assembles to form a duplex oligonucleotide in which the nucleotide sequence of one strand of the duplex is the same as the nucleotide sequence of the second strand. Non-limiting examples of such duplex forming oligonucleotides are illustrated in FIGS. 14 and 15. These duplex forming oligonucleotides (DFOs) can optionally include certain palindrome or repeat sequences where such palindrome or repeat sequences are present in between the first region and the second region of the DFO.

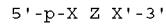
[0478] In one embodiment, the invention features a duplex forming oligonucleotide (DFO) molecule, wherein the DFO comprises a duplex forming self complementary nucleic acid sequence that has nucleotide sequence complementary to a PCSK9 target nucleic acid sequence. The DFO molecule can comprise a single self complementary sequence or a duplex resulting from assembly of such self complementary sequences.

[0479] In one embodiment, a duplex forming oligonucleotide (DFO) of the invention comprises a first region and a second region, wherein the second region comprises a nucleotide sequence comprising an inverted repeat of nucleotide sequence of the first region such that the DFO molecule can assemble into a double stranded oligonucleotide. Such double stranded oligonucleotides can act as a short interfering nucleic acid (siNA) to modulate gene expression. Each strand of the double stranded oligonucleotide duplex formed by DFO molecules of the invention can comprise a nucleotide sequence region that is complementary to the same nucleotide sequence in a PCSK9 target nucleic acid molecule (e.g., PCSK9 target RNA).

[0480] In one embodiment, the invention features a single stranded DFO that can assemble into a double stranded oligonucleotide. The applicant has surprisingly found that a single stranded oligonucleotide with nucleotide regions of self complementarity can readily assemble into duplex oligonucleotide constructs. Such DFOs can assemble into duplexes that can inhibit gene expression in a sequence specific manner. The DFO molecules of the invention comprise a first region with nucleotide sequence that is complementary to the nucleotide sequence of a second region and where the sequence of the first region is complementary to a PCSK9 target nucleic acid (e.g., RNA). The DFO can form a double stranded oligonucleotide wherein a portion of each strand of the double stranded oligonucleotide comprises a sequence complementary to a PCSK9 target nucleic acid sequence.

[0481] In one embodiment, the invention features a double stranded oligonucleotide, wherein the two strands of the double stranded oligonucleotide are not covalently linked to each other, and wherein each strand of the double stranded oligonucleotide comprises a nucleotide sequence that is complementary to the same nucleotide sequence in a PCSK9 target nucleic acid molecule or a portion thereof (e.g., PCSK9 RNA target). In another embodiment, the two strands of the double stranded oligonucleotide share an identical nucleotide sequence of at least about 15, preferably at least about 16, 17, 18, 19, 20, or 21 nucleotides.

[0482] In one embodiment, a DFO molecule of the invention comprises a structure having Formula DFO-I:

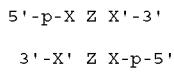


wherein Z comprises a palindromic or repeat nucleic acid sequence optionally with one or more modified nucleotides (e.g., nucleotide with a modified base, such as 2-amino purine, 2-amino-1,6-dihydro purine or a universal base), for example of length about 2 to about 24 nucleotides in even numbers (e.g., about 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, or 22 or 24 nucleotides), X represents a nucleic acid sequence, for example of length of about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotides), X' comprises a nucleic acid sequence, for example of length about 1 and about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 21 nucleotides) having nucleotide sequence complementarity to sequence X or a portion thereof, p comprises a terminal phosphate group that can be present or absent, and wherein sequence X and Z, either independently or together, comprise nucleotide sequence that is complementary to a PCSK9 target nucleic acid sequence or a portion thereof and is of length sufficient to interact (e.g., base pair) with the PCSK9 target nucleic acid sequence or a portion

thereof (e.g., PCSK9 RNA target). For example, X independently can comprise a sequence from about 12 to about 21 or more (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more) nucleotides in length that is complementary to nucleotide sequence in a PCSK9 target RNA or a portion thereof. In another non-limiting example, the length of the nucleotide sequence of X and Z together, when X is present, that is complementary to the PCSK9 target or a portion thereof (e.g., PCSK9 RNA target) is from about 12 to about 21 or more nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more). In yet another non-limiting example, when X is absent, the length of the nucleotide sequence of Z that is complementary to the PCSK9 target or a portion thereof is from about 12 to about 24 or more nucleotides (e.g., about 12, 14, 16, 18, 20, 22, 24, or more). In one embodiment X, Z and X' are independently oligonucleotides, where X and/or Z comprises a nucleotide sequence of length sufficient to interact (e.g., base pair) with a nucleotide sequence in the PCSK9 target or a portion thereof (e.g., PCSK9 RNA target). In one embodiment, the lengths of oligonucleotides X and X' are identical. In another embodiment, the lengths of oligonucleotides X and X' are not identical. In another embodiment, the lengths of oligonucleotides X and Z, or Z and X', or X, Z and X' are either identical or different.

[0483] When a sequence is described in this specification as being of "sufficient" length to interact (i.e., base pair) with another sequence, it is meant that the length is such that the number of bonds (e.g., hydrogen bonds) formed between the two sequences is enough to enable the two sequence to form a duplex under the conditions of interest. Such conditions can be *in vitro* (e.g., for diagnostic or assay purposes) or *in vivo* (e.g., for therapeutic purposes). It is a simple and routine matter to determine such lengths.

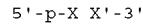
[0484] In one embodiment, the invention features a double stranded oligonucleotide construct having Formula DFO-I (a):



wherein Z comprises a palindromic or repeat nucleic acid sequence or palindromic or repeat-like nucleic acid sequence with one or more modified nucleotides (e.g., nucleotides with a modified base, such as 2-amino purine, 2-amino-1,6-dihydro purine or a universal base), for example of length about 2 to about 24 nucleotides in even numbers (e.g., about 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 or 24 nucleotides), X represents a nucleic acid sequence, for example of length about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotides), X' comprises a nucleic acid sequence, for example of length about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 nucleotides) having nucleotide sequence complementarity to sequence X or a portion thereof, p comprises a terminal phosphate group that can be present or absent, and wherein each X and Z independently comprises a nucleotide sequence that is complementary to a PCSK9 target nucleic acid sequence or a portion thereof (e.g., PCSK9 RNA target) and is of length sufficient to interact with the PCSK9 target nucleic acid sequence of a portion thereof (e.g., PCSK9 RNA target). For example, sequence X independently can comprise a sequence from about 12 to about 21 or more nucleotides (e.g., about 12, 13,

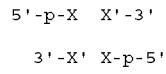
14, 15, 16, 17, 18, 19, 20, 21, or more) in length that is complementary to a nucleotide sequence in a PCSK9 target or a portion thereof (e.g., PCSK9 RNA target). In another non-limiting example, the length of the nucleotide sequence of X and Z together (when X is present) that is complementary to the PCSK9 target or a portion thereof is from about 12 to about 21 or more nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more). In yet another non-limiting example, when X is absent, the length of the nucleotide sequence of Z that is complementary to the PCSK9 target or a portion thereof is from about 12 to about 24 or more nucleotides (e.g., about 12, 14, 16, 18, 20, 22, 24 or more). In one embodiment X, Z and X' are independently oligonucleotides, where X and/or Z comprises a nucleotide sequence of length sufficient to interact (e.g., base pair) with nucleotide sequence in the PCSK9 target or a portion thereof (e.g., PCSK9 RNA target). In one embodiment, the lengths of oligonucleotides X and X' are identical. In another embodiment, the lengths of oligonucleotides X and X' are not identical. In another embodiment, the lengths of oligonucleotides X and Z or Z and X' are either identical or different. In one embodiment, the double stranded oligonucleotide construct of Formula I(a) includes one or more, specifically 1, 2, 3 or 4, mismatches, to the extent such mismatches do not significantly diminish the ability of the double stranded oligonucleotide to inhibit PCSK9 target gene expression.

[0485] In one embodiment, a DFO molecule of the invention comprises structure having Formula DFO-II:



wherein each X and X' are independently oligonucleotides of length about 12 nucleotides to about 21 nucleotides, wherein X comprises, for example, a nucleic acid sequence of length about 12 to about 21 nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 nucleotides), X' comprises a nucleic acid sequence, for example of length about 12 to about 21 nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotides) having nucleotide sequence complementarity to sequence X or a portion thereof, p comprises a terminal phosphate group that can be present or absent, and wherein X comprises a nucleotide sequence that is complementary to a PCSK9 target nucleic acid sequence (e.g., PCSK9 target RNA) or a portion thereof and is of length sufficient to interact (e.g., base pair) with the PCSK9 target nucleic acid sequence of a portion thereof. In one embodiment, the length of oligonucleotides X and X' are identical. In another embodiment the length of oligonucleotides X and X' are not identical. In one embodiment, length of the oligonucleotides X and X' are sufficient to form a relatively stable double stranded oligonucleotide.

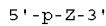
[0486] In one embodiment, the invention features a double stranded oligonucleotide construct having Formula DFO-II (a):



wherein each X and X' are independently oligonucleotides of length about 12 nucleotides to about 21 nucleotides, wherein X comprises a nucleic acid sequence, for example of length about 12 to about 21 nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 nucleotides), X' comprises a nucleic

acid sequence, for example of length about 12 to about 21 nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 nucleotides) having nucleotide sequence complementarity to sequence X or a portion thereof, p comprises a terminal phosphate group that can be present or absent, and wherein X comprises nucleotide sequence that is complementary to a PCSK9 target nucleic acid sequence or a portion thereof (e.g., PCSK9 RNA target) and is of length sufficient to interact (e.g., base pair) with the PCSK9 target nucleic acid sequence (e.g., PCSK9 target RNA) or a portion thereof. In one embodiment, the lengths of oligonucleotides X and X' are identical. In another embodiment, the lengths of oligonucleotides X and X' are not identical. In one embodiment, the lengths of the oligonucleotides X and X' are sufficient to form a relatively stable double stranded oligonucleotide. In one embodiment, the double stranded oligonucleotide construct of Formula II(a) includes one or more, specifically 1, 2, 3 or 4, mismatches, to the extent such mismatches do not significantly diminish the ability of the double stranded oligonucleotide to inhibit PCSK9 target gene expression.

[0487] In one embodiment, the invention features a DFO molecule having Formula DFO-I(b):



where Z comprises a palindromic or repeat nucleic acid sequence optionally including one or more non-standard or modified nucleotides (e.g., nucleotide with a modified base, such as 2-amino purine or a universal base) that can facilitate base-pairing with other nucleotides. Z can be, for example, of length sufficient to interact (e.g., base pair) with nucleotide sequence of a PCSK9 target nucleic acid (e.g., PCSK9 target RNA) molecule, preferably of length of at least 12 nucleotides, specifically about 12 to about 24 nucleotides (e.g., about 12, 14, 16, 18, 20, 22 or 24 nucleotides). p represents a terminal phosphate group that can be present or absent.

[0488] In one embodiment, a DFO molecule having any of Formula DFO-I, DFO-I(a), DFO-I(b), DFO-II(a) or DFO-II can comprise chemical modifications as described herein without limitation, such as, for example, nucleotides having any of Formulae I-VII, stabilization chemistries as described in Table IV, or any other combination of modified nucleotides and non-nucleotides as described in the various embodiments herein.

[0489] In one embodiment, the palindrome or repeat sequence or modified nucleotide (e.g., nucleotide with a modified base, such as 2-amino purine or a universal base) in Z of DFO constructs having Formula DFO-I, DFO-I(a) and DFO-I(b), comprises chemically modified nucleotides that are able to interact with a portion of the PCSK9 target nucleic acid sequence (e.g., modified base analogs that can form Watson Crick base pairs or non-Watson Crick base pairs).

[0490] In one embodiment, a DFO molecule of the invention, for example a DFO having Formula DFO-I or DFO-II, comprises about 15 to about 40 nucleotides (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 nucleotides). In one embodiment, a DFO molecule of the invention comprises one or more chemical modifications. In a non-limiting example, the introduction of chemically modified nucleotides and/or non-nucleotides into nucleic acid molecules of the invention provides a powerful tool in overcoming potential limitations of in vivo stability and bioavailability inherent to unmodified RNA molecules that are delivered exogenously. For example, the

use of chemically modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically modified nucleic acid molecules tend to have a longer half-life in serum or in cells or tissues. Furthermore, certain chemical modifications can improve the bioavailability and/or potency of nucleic acid molecules by not only enhancing half-life but also facilitating the targeting of nucleic acid molecules to particular organs, cells or tissues and/or improving cellular uptake of the nucleic acid molecules. Therefore, even if the activity of a chemically modified nucleic acid molecule is reduced in vitro as compared to a native/unmodified nucleic acid molecule, for example when compared to an unmodified RNA molecule, the overall activity of the modified nucleic acid molecule can be greater than the native or unmodified nucleic acid molecule due to improved stability, potency, duration of effect, bioavailability and/or delivery of the molecule.

Multifunctional or Multi-Targeted siNA Molecules of the Invention

[0491] In one embodiment, the invention features siNA molecules comprising multifunctional short interfering nucleic acid (multifunctional siNA) molecules that modulate the expression of one or more PCSK9 target genes in a biologic system, such as a cell, tissue, or organism. The multifunctional short interfering nucleic acid (multifunctional siNA) molecules of the invention can target more than one region of the PCSK9 target nucleic acid sequence or can target sequences of more than one distinct target nucleic acid molecules (e.g., PCSK9 or PCSK9 pathway RNA and/or DNA targets). The multifunctional siNA molecules of the invention can be chemically synthesized or expressed from transcription units and/or vectors. The multifunctional siNA molecules of the instant invention provide useful reagents and methods for a variety of human applications, therapeutic, diagnostic, agricultural, veterinary, target validation, genomic discovery, genetic engineering and pharmacogenomic applications.

[0492] Applicant demonstrates herein that certain oligonucleotides, referred to herein for convenience but not limitation as multifunctional short interfering nucleic acid or multifunctional siNA molecules, are potent mediators of sequence specific regulation of gene expression. The multifunctional siNA molecules of the invention are distinct from other nucleic acid sequences known in the art (e.g., siRNA, miRNA, siRNA, shRNA, antisense oligonucleotides, etc.) in that they represent a class of polynucleotide molecules that are designed such that each strand in the multifunctional siNA construct comprises a nucleotide sequence that is complementary to a distinct nucleic acid sequence in one or more target nucleic acid molecules. A single multifunctional siNA molecule (generally a double-stranded molecule) of the invention can thus target more than one (e.g., 2, 3, 4, 5, or more) differing target nucleic acid target molecules. Nucleic acid molecules of the invention can also target more than one (e.g., 2, 3, 4, 5, or more) region of the same target nucleic acid sequence. As such multifunctional siNA molecules of the invention are useful in down regulating or inhibiting the expression of one or more target nucleic acid molecules. For example, a multifunctional siNA molecule of the invention can target (e.g., have complementarity to) nucleic acid molecules selected from the group consisting of PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin

9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, F-box-only protein 3 or any combination thereof. By reducing or inhibiting expression of more than one target nucleic acid molecule with one multifunctional siNA construct, multifunctional siNA molecules of the invention represent a class of potent therapeutic agents that can provide simultaneous inhibition of multiple targets within a disease (e.g., angiogenic) related pathway. Such simultaneous inhibition can provide synergistic therapeutic treatment strategies without the need for separate preclinical and clinical development efforts or complex regulatory approval process.

[0493] Use of multifunctional siNA molecules that target more than one region of a target nucleic acid molecule (e.g., PCSK9 target RNA or DNA) is expected to provide potent inhibition of gene expression. For example, a single multifunctional siNA construct of the invention can target both conserved and variable regions of a target nucleic acid molecule (e.g., PCSK9 RNA or DNA), thereby allowing down regulation or inhibition of different PCSK9 isoforms or variants to optimize therapeutic efficacy and minimize toxicity, or allowing for targeting of both coding and non-coding regions of the PCSK9 target nucleic acid molecule.

[0494] Generally, double stranded oligonucleotides are formed by the assembly of two distinct oligonucleotides where the oligonucleotide sequence of one strand is complementary to the oligonucleotide sequence of the second strand; such double stranded oligonucleotides are generally assembled from two separate oligonucleotides (e.g., siRNA). Alternately, a duplex can be formed from a single molecule that folds on itself (e.g., shRNA or short hairpin RNA). These double stranded oligonucleotides are known in the art to mediate RNA interference and all have a common feature wherein only one nucleotide sequence region (guide sequence or the antisense sequence) has complementarity to a target nucleic acid sequence, and the other strand (sense sequence) comprises nucleotide sequence that is homologous to the target nucleic acid sequence. Generally, the antisense sequence is retained in the active RISC complex and guides the RISC to the target nucleotide sequence by means of complementary base-pairing of the antisense sequence with the target sequence for mediating sequence-specific RNA interference. It is known in the art that in some cell culture systems, certain types of unmodified siRNAs can exhibit "off target" effects. It is hypothesized that this off-target effect involves the participation of the sense sequence instead of the antisense sequence of the siRNA in the RISC complex (see for example Schwarz et al., 2003, Cell, 115, 199-208). In this instance the sense sequence is believed to direct the RISC complex to a sequence (off-target sequence) that is distinct from the intended target sequence, resulting in the inhibition of the off-target sequence. In these double stranded nucleic acid molecules, each strand is complementary to a distinct target nucleic acid sequence. However, the off-targets that are affected by these dsRNAs are not entirely predictable and are non-specific.

[0495] Distinct from the double stranded nucleic acid molecules known in the art, the applicants have developed a novel, potentially cost effective and simplified method of down regulating or inhibiting the expression of more than one target nucleic acid sequence using a single multifunctional siNA construct. The multifunctional siNA molecules of the invention are designed to be double-stranded or partially double stranded, such that a portion of each strand or region

of the multifunctional siNA is complementary to a target nucleic acid sequence of choice. As such, the multifunctional siNA molecules of the invention are not limited to targeting sequences that are complementary to each other, but rather to any two differing target nucleic acid sequences. Multifunctional siNA molecules of the invention are designed such that each strand or region of the multifunctional siNA molecule, that is complementary to a given target nucleic acid sequence, is of suitable length (e.g., from about 16 to about 28 nucleotides in length, preferably from about 18 to about 28 nucleotides in length) for mediating RNA interference against the target nucleic acid sequence. The complementarity between the target nucleic acid sequence and a strand or region of the multifunctional siNA must be sufficient (at least about 8 base pairs) for cleavage of the target nucleic acid sequence by RNA interference. Multifunctional siNA of the invention is expected to minimize off-target effects seen with certain siRNA sequences, such as those described in Schwarz et al., supra.

[0496] It has been reported that dsRNAs of length between 29 base pairs and 36 base pairs (Tuschl et al., International PCT Publication No. WO 02/44321) do not mediate RNAi. One reason these dsRNAs are inactive may be the lack of turnover or dissociation of the strand that interacts with the target RNA sequence, such that the RISC complex is not able to efficiently interact with multiple copies of the target RNA resulting in a significant decrease in the potency and efficiency of the RNAi process. Applicant has surprisingly found that the multifunctional siNAs of the invention can overcome this hurdle and are capable of enhancing the efficiency and potency of RNAi process. As such, in certain embodiments of the invention, multifunctional siNAs of length of about 29 to about 36 base pairs can be designed such that, a portion of each strand of the multifunctional siNA molecule comprises a nucleotide sequence region that is complementary to a target nucleic acid of length sufficient to mediate RNAi efficiently (e.g., about 15 to about 23 base pairs) and a nucleotide sequence region that is not complementary to the target nucleic acid. By having both complementary and non-complementary portions in each strand of the multifunctional siNA, the multifunctional siNA can mediate RNA interference against a target nucleic acid sequence without being prohibitive to turnover or dissociation (e.g., where the length of each strand is too long to mediate RNAi against the respective target nucleic acid sequence). Furthermore, design of multifunctional siNA molecules of the invention with internal overlapping regions allows the multifunctional siNA molecules to be of favorable (decreased) size for mediating RNA interference and of size that is well suited for use as a therapeutic agent (e.g., wherein each strand is independently from about 18 to about 28 nucleotides in length). Non-limiting examples are illustrated in FIGS. 16-28 and Table III.

[0497] In one embodiment, a multifunctional siNA molecule of the invention comprises a first region and a second region, where the first region of the multifunctional siNA comprises a nucleotide sequence complementary to a nucleic acid sequence of a first target nucleic acid molecule, and the second region of the multifunctional siNA comprises nucleic acid sequence complementary to a nucleic acid sequence of a second target nucleic acid molecule. In one embodiment, a multifunctional siNA molecule of the invention comprises a first region and a second region, where the first region of the multifunctional siNA comprises nucleotide sequence complementary to a nucleic acid sequence of the first region

of a target nucleic acid molecule, and the second region of the multifunctional siNA comprises nucleotide sequence complementary to a nucleic acid sequence of a second region of a target nucleic acid molecule. In another embodiment, the first region and second region of the multifunctional siNA can comprise separate nucleic acid sequences that share some degree of complementarity (e.g., from about 1 to about 10 complementary nucleotides). In certain embodiments, multifunctional siNA constructs comprising separate nucleic acid sequences can be readily linked post-synthetically by methods and reagents known in the art and such linked constructs are within the scope of the invention. Alternately, the first region and second region of the multifunctional siNA can comprise a single nucleic acid sequence having some degree of self complementarity, such as in a hairpin or stem-loop structure. Non-limiting examples of such double stranded and hairpin multifunctional short interfering nucleic acids are illustrated in FIGS. 16 and 17 respectively. These multifunctional short interfering nucleic acids (multifunctional siNAs) can optionally include certain overlapping nucleotide sequence where such overlapping nucleotide sequence is present in between the first region and the second region of the multifunctional siNA (see for example FIGS. 18 and 19).

[0498] In one embodiment, the invention features a multifunctional short interfering nucleic acid (multifunctional siNA) molecule, wherein each strand of the multifunctional siNA independently comprises a first region of nucleic acid sequence that is complementary to a distinct target nucleic acid sequence and the second region of nucleotide sequence that is not complementary to the target sequence. The target nucleic acid sequence of each strand is in the same target nucleic acid molecule or different target nucleic acid molecules.

[0499] In another embodiment, the multifunctional siNA comprises two strands, where: (a) the first strand comprises a region having sequence complementarity to a target nucleic acid sequence (complementary region 1) and a region having no sequence complementarity to the target nucleotide sequence (non-complementary region 1); (b) the second strand of the multifunctional siNA comprises a region having sequence complementarity to a target nucleic acid sequence that is distinct from the target nucleotide sequence complementary to the first strand nucleotide sequence (complementary region 2), and a region having no sequence complementarity to the target nucleotide sequence of complementary region 2 (non-complementary region 2); (c) the complementary region 1 of the first strand comprises a nucleotide sequence that is complementary to a nucleotide sequence in the non-complementary region 2 of the second strand and the complementary region 2 of the second strand comprises a nucleotide sequence that is complementary to a nucleotide sequence in the non-complementary region 1 of the first strand. The target nucleic acid sequence of complementary region 1 and complementary region 2 is in the same target nucleic acid molecule or different target nucleic acid molecules.

[0500] In another embodiment, the multifunctional siNA comprises two strands, where: (a) the first strand comprises a region having sequence complementarity to a target nucleic acid sequence derived from a gene (e.g., a first PCSK9 gene) (complementary region 1) and a region having no sequence complementarity to the target nucleotide sequence of complementary region 1 (non-complementary region 1); (b) the second strand of the multifunctional siNA comprises a

region having sequence complementarity to a target nucleic acid sequence derived from a gene (e.g., a second PCSK9 gene) that is distinct from the gene of complementary region 1 (complementary region 2), and a region having no sequence complementarity to the target nucleotide sequence of complementary region 2 (non-complementary region 2); (c) the complementary region 1 of the first strand comprises a nucleotide sequence that is complementary to a nucleotide sequence in the non-complementary region 2 of the second strand and the complementary region 2 of the second strand comprises a nucleotide sequence that is complementary to a nucleotide sequence in the non-complementary region 1 of the first strand.

[0501] In another embodiment, the multifunctional siNA comprises two strands, where: (a) the first strand comprises a region having sequence complementarity to a target nucleic acid sequence derived from a gene (e.g., PCSK9 gene) (complementary region 1) and a region having no sequence complementarity to the target nucleotide sequence of complementary region 1 (non-complementary region 1); (b) the second strand of the multifunctional siNA comprises a region having sequence complementarity to a target nucleic acid sequence distinct from the target nucleic acid sequence of complementary region 1 (complementary region 2), provided, however, that the target nucleic acid sequence for complementary region 1 and target nucleic acid sequence for complementary region 2 are both derived from the same gene, and a region having no sequence complementarity to the target nucleotide sequence of complementary region 2 (non-complementary region 2); (c) the complementary region 1 of the first strand comprises a nucleotide sequence that is complementary to a nucleotide sequence in the non-complementary region 2 of the second strand and the complementary region 2 of the second strand comprises a nucleotide sequence that is complementary to nucleotide sequence in the non-complementary region 1 of the first strand.

[0502] In one embodiment, the invention features a multifunctional short interfering nucleic acid (multifunctional siNA) molecule, wherein the multifunctional siNA comprises two complementary nucleic acid sequences in which the first sequence comprises a first region having nucleotide sequence complementary to nucleotide sequence within a first target nucleic acid molecule, and in which the second sequence comprises a first region having nucleotide sequence complementary to a distinct nucleotide sequence within the same target nucleic acid molecule. Preferably, the first region of the first sequence is also complementary to the nucleotide sequence of the second region of the second sequence, and where the first region of the second sequence is complementary to the nucleotide sequence of the second region of the first sequence.

[0503] In one embodiment, the invention features a multifunctional short interfering nucleic acid (multifunctional siNA) molecule, wherein the multifunctional siNA comprises two complementary nucleic acid sequences in which the first sequence comprises a first region having a nucleotide sequence complementary to a nucleotide sequence within a first target nucleic acid molecule, and in which the second sequence comprises a first region having a nucleotide sequence complementary to a distinct nucleotide sequence within a second target nucleic acid molecule. Preferably, the first region of the first sequence is also complementary to the nucleotide sequence of the second region of the second

sequence, and where the first region of the second sequence is complementary to the nucleotide sequence of the second region of the first sequence.

[0504] In one embodiment, the invention features a multifunctional siNA molecule comprising a first region and a second region, where the first region comprises a nucleic acid sequence having about 18 to about 28 nucleotides complementary to a nucleic acid sequence within a first target nucleic acid molecule, and the second region comprises nucleotide sequence having about 18 to about 28 nucleotides complementary to a distinct nucleic acid sequence within a second target nucleic acid molecule.

[0505] In one embodiment, the invention features a multifunctional siNA molecule comprising a first region and a second region, where the first region comprises nucleic acid sequence having about 18 to about 28 nucleotides complementary to a nucleic acid sequence within a target nucleic acid molecule, and the second region comprises nucleotide sequence having about 18 to about 28 nucleotides complementary to a distinct nucleic acid sequence within the same target nucleic acid molecule.

[0506] In one embodiment, the invention features a double stranded multifunctional short interfering nucleic acid (multifunctional siNA) molecule, wherein one strand of the multifunctional siNA comprises a first region having nucleotide sequence complementary to a first target nucleic acid sequence, and the second strand comprises a first region having a nucleotide sequence complementary to a second target nucleic acid sequence. The first and second target nucleic acid sequences can be present in separate target nucleic acid molecules or can be different regions within the same target nucleic acid molecule. As such, multifunctional siNA molecules of the invention can be used to target the expression of different genes, splice variants of the same gene, both mutant and conserved regions of one or more gene transcripts, or both coding and non-coding sequences of the same or differing genes or gene transcripts.

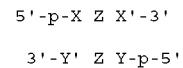
[0507] In one embodiment, a target nucleic acid molecule of the invention encodes a single protein. In another embodiment, a target nucleic acid molecule encodes more than one protein (e.g., 1, 2, 3, 4, 5 or more proteins). As such, a multifunctional siNA construct of the invention can be used to down regulate or inhibit the expression of several proteins. For example, a multifunctional siNA molecule comprising a region in one strand having nucleotide sequence complementary to a first target nucleic acid sequence derived from a PCSK9 target, and the second strand comprising a region with nucleotide sequence complementary to a second target nucleic acid sequence present in target nucleic acid molecules from genes encoding two proteins (e.g., two differing proteins) selected from the group consisting of PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, F-box-only protein 3 or any combination thereof, which can be used to down regulate, inhibit, or shut down a particular biologic pathway by targeting multiple PCSK9 or PCSK9 pathway genes.

[0508] In one embodiment the invention takes advantage of conserved nucleotide sequences present in different PCSK9 variants. By designing multifunctional siNAs in a manner where one strand includes a sequence that is complementary to one or more target nucleic acid sequences that are con-

served among various PCSK9 family members and the other strand optionally includes sequence that is complementary to PCSK9 pathway target nucleic acid sequence, such as any of PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, F-box-only protein 3, it is possible to selectively and effectively inhibit a PCSK9 disease related biological pathway (e.g., hyperlipidemia and/or insulin resistance) using a single multifunctional siNA.

[0509] In one embodiment, a multifunctional short interfering nucleic acid (multifunctional siNA) of the invention comprises a first region and a second region, wherein the first region comprises nucleotide sequence complementary to a first PCSK9 RNA of a first PCSK9 target and the second region comprises nucleotide sequence complementary to a second PCSK9 RNA of a second PCSK9 target. In one embodiment, the first and second regions can comprise nucleotide sequence complementary to shared or conserved RNA sequences of differing PCSK9 target sites within the same PCSK9 target sequence or shared amongst different PCSK9 target sequences.

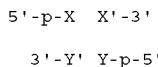
[0510] In one embodiment, a double stranded multifunctional siNA molecule of the invention comprises a structure having Formula MF-I:



wherein each $5'$ -p-XZ X' - $3'$ and $3'$ -Y Z Y-p- $5'$ are independently an oligonucleotide of length about 20 nucleotides to about 300 nucleotides, preferably about 20 to about 200 nucleotides, about 20 to about 100 nucleotides, about 20 to about 40 nucleotides, about 20 to about 40 nucleotides, about 24 to about 38 nucleotides, or about 26 to about 38 nucleotides; XZ comprises a nucleic acid sequence that is complementary to a first PCSK9 target nucleic acid sequence; YZ is an oligonucleotide comprising nucleic acid sequence that is complementary to a second PCSK9 target nucleic acid sequence; Z comprises nucleotide sequence of length about 1 to about 24 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 nucleotides) that is self complementary; X comprises nucleotide sequence of length about 1 to about 100 nucleotides, preferably about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotides) that is complementary to nucleotide sequence present in region Y'; Y comprises nucleotide sequence of length about 1 to about 100 nucleotides, preferably about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 nucleotides) that is complementary to nucleotide sequence present in region X'; each p comprises a terminal phosphate group that is independently present or absent; each XZ and YZ is independently of length sufficient to stably interact (i.e., base pair) with the first and second target nucleic acid sequence, respectively, or a portion thereof. For example, each sequence X and Y can independently comprise sequence from about 12 to about 21 or more nucleotides in length (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more) that is complementary to a target nucleotide sequence in different target nucleic acid molecules, such as target RNAs or a portion thereof. In another

non-limiting example, the length of the nucleotide sequence of X and Z together that is complementary to the first PCSK9 target nucleic acid sequence or a portion thereof is from about 12 to about 21 or more nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more). In another non-limiting example, the length of the nucleotide sequence of Y and Z together, that is complementary to the second PCSK9 target nucleic acid sequence or a portion thereof is from about 12 to about 21 or more nucleotides (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more). In one embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in the same target nucleic acid molecule (e.g., PCSK9 target RNA or PCSK9 pathway target RNA such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In another embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in different target nucleic acid molecules (e.g., PCSK9 target RNA and PCSK9 pathway target RNA). In one embodiment, Z comprises a palindrome or a repeat sequence. In one embodiment, the lengths of oligonucleotides X and X' are identical. In another embodiment, the lengths of oligonucleotides X and X' are not identical. In one embodiment, the lengths of oligonucleotides Y and Y' are identical. In another embodiment, the lengths of oligonucleotides Y and Y' are not identical. In one embodiment, the double stranded oligonucleotide construct of Formula I(a) includes one or more, specifically 1, 2, 3 or 4, mismatches, to the extent such mismatches do not significantly diminish the ability of the double stranded oligonucleotide to inhibit target gene expression.

[0511] In one embodiment, a multifunctional siNA molecule of the invention comprises a structure having Formula MF-II:



wherein each 5'-p-XX'-3' and 5'-p-YY'-3' are independently an oligonucleotide of length about 20 nucleotides to about 300 nucleotides, preferably about 20 to about 200 nucleotides, about 20 to about 100 nucleotides, about 20 to about 40 nucleotides, about 20 to about 40 nucleotides, about 24 to about 38 nucleotides, or about 26 to about 38 nucleotides; X comprises a nucleic acid sequence that is complementary to a first target nucleic acid sequence; Y is an oligonucleotide comprising nucleic acid sequence that is complementary to a second target nucleic acid sequence; X comprises a nucleotide sequence of length about 1 to about 100 nucleotides, preferably about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotides) that is complementary to nucleotide sequence present in region Y'; Y comprises nucleotide sequence of length about 1 to about 100 nucleotides, preferably about 1 to about 21 nucleotides (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 nucleotides) that is complementary to nucleotide sequence present in region X'; each p comprises a terminal phosphate group that is independently present or absent; each X and Y independently is of length sufficient to stably interact (i.e., base pair) with the first

and second target nucleic acid sequence, respectively, or a portion thereof. For example, each sequence X and Y can independently comprise sequence from about 12 to about 21 or more nucleotides in length (e.g., about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more) that is complementary to a target nucleotide sequence in different target nucleic acid molecules, such as PCSK9 target RNAs or a portion thereof. In one embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in the same target nucleic acid molecule (e.g., PCSK9 target RNA or PCSK9 pathway target RNA such as H6PD, PTP-1B, apoAI/CIII/AIV, and/or CETP RNA). In another embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in different target nucleic acid molecules (e.g., PCSK9 target RNA and PCSK9 pathway target RNA, such as H6PD, PTP-1B, apoAI/CIII/AIV, and/or CETP RNA). In one embodiment, Z comprises a palindrome or a repeat sequence. In one embodiment, the lengths of oligonucleotides X and X' are identical. In another embodiment, the lengths of oligonucleotides X and X' are not identical. In one embodiment, the lengths of oligonucleotides Y and Y' are identical. In another embodiment, the lengths of oligonucleotides Y and Y' are not identical. In one embodiment, the double stranded oligonucleotide construct of Formula I(a) includes one or more, specifically 1, 2, 3 or 4, mismatches, to the extent such mismatches do not significantly diminish the ability of the double stranded oligonucleotide to inhibit target gene expression.

[0512] In one embodiment, a multifunctional siNA molecule of the invention comprises a structure having Formula MF-III:



wherein each X, X', Y, and Y' is independently an oligonucleotide of length about 15 nucleotides to about 50 nucleotides, preferably about 18 to about 40 nucleotides, or about 19 to about 23 nucleotides; X comprises nucleotide sequence that is complementary to nucleotide sequence present in region Y'; X' comprises nucleotide sequence that is complementary to nucleotide sequence present in region Y; each X and X' is independently of length sufficient to stably interact (i.e., base pair) with a first and a second PCSK9 target nucleic acid sequence, respectively, or a portion thereof; W represents a nucleotide or non-nucleotide linker that connects sequences Y' and Y; and the multifunctional siRNA directs cleavage of the first and second PCSK9 target sequence via RNA interference. In one embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in the same target nucleic acid molecule (e.g., PCSK9 target RNA or PCSK9 pathway target RNA such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In another embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in different target nucleic acid molecules (e.g., PCSK9 target RNA and PCSK9 pathway target RNA such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA).

AIY, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In one embodiment, region W connects the 3'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, region W connects the 3'-end of sequence Y' with the 5'-end of sequence Y. In one embodiment, region W connects the 5'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence X. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence X'. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence Y. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence Y'. In one embodiment, W connects sequences Y and Y' via a biodegradable linker. In one embodiment, W further comprises a conjugate, table, aptamer, ligand, lipid, or polymer.

[0513] In one embodiment, a multifunctional siNA molecule of the invention comprises a structure having Formula MF-IV:



wherein each X, X', Y, and Y' is independently an oligonucleotide of length about 15 nucleotides to about 50 nucleotides, preferably about 18 to about 40 nucleotides, or about 19 to about 23 nucleotides; X comprises nucleotide sequence that is complementary to nucleotide sequence present in region Y'; X' comprises nucleotide sequence that is complementary to nucleotide sequence present in region Y; each Y and Y' is independently of length sufficient to stably interact (i.e., base pair) with a first and a second PCSK9 target nucleic acid sequence, respectively, or a portion thereof; W represents a nucleotide or non-nucleotide linker that connects sequences Y' and Y; and the multifunctional siNA directs cleavage of the first and second PCSK9 target sequence via RNA interference. In one embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in the same target nucleic acid molecule (e.g., PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In another embodiment, the first PCSK9 target nucleic acid sequence and the second PCSK9 target nucleic acid sequence are present in different target nucleic acid molecules (e.g., PCSK9 target RNA and PCSK9 pathway target RNA such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In one embodiment, region W connects the 3'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, region W connects the 3'-end of sequence Y' with the 5'-end of sequence Y. In one embodiment, region W connects the 5'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, region W connects the 5'-end of sequence Y' with the 5'-end of sequence Y'. In one embodiment, W connects

the 5'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence X. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence X'. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence Y. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence Y'. In one embodiment, W connects sequences Y and Y' via a biodegradable linker. In one embodiment, W further comprises a conjugate, table, aptamer, ligand, lipid, or polymer.

[0514] In one embodiment, a multifunctional siNA molecule of the invention comprises a structure having Formula MF-V:



wherein each X, X', Y, and Y' is independently an oligonucleotide of length about 15 nucleotides to about 50 nucleotides, preferably about 18 to about 40 nucleotides, or about 19 to about 23 nucleotides; X comprises nucleotide sequence that is complementary to nucleotide sequence present in region Y'; X' comprises nucleotide sequence that is complementary to nucleotide sequence present in region Y; each X, X', Y, or Y' is independently of length sufficient to stably interact (i.e., base pair) with a first, second, third, or fourth PCSK9 target nucleic acid sequence, respectively, or a portion thereof; W represents a nucleotide or non-nucleotide linker that connects sequences Y' and Y; and the multifunctional siNA directs cleavage of the first, second, third, and/or fourth target sequence via RNA interference. In one embodiment, the first, second, third and fourth PCSK9 target nucleic acid sequence are all present in the same target nucleic acid molecule (e.g., PCSK9 target RNA or PCSK9 pathway target RNA such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In another embodiment, the first, second, third and fourth PCSK9 target nucleic acid sequence are independently present in different target nucleic acid molecules (e.g., PCSK9 target RNA and PCSK9 pathway target RNA such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA). In one embodiment, region W connects the 3'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, region W connects the 3'-end of sequence Y' with the 5'-end of sequence Y. In one embodiment, region W connects the 5'-end of sequence Y' with the 3'-end of sequence Y. In one embodiment, region W connects the 5'-end of sequence Y' with the 5'-end of sequence Y'. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence X. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence X'. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence Y. In one embodiment, a terminal phosphate group is present at the 5'-end of sequence Y'. In one embodiment, W connects

sequences Y and Y' via a biodegradable linker. In one embodiment, W further comprises a conjugate, label, aptamer, ligand, lipid, or polymer.

[0515] In one embodiment, regions X and Y of multifunctional siNA molecule of the invention (e.g., having any of Formula MF-I-MF-V), are complementary to different target nucleic acid sequences that are portions of the same target nucleic acid molecule. In one embodiment, such target nucleic acid sequences are at different locations within the coding region of a RNA transcript. In one embodiment, such target nucleic acid sequences comprise coding and non-coding regions of the same RNA transcript. In one embodiment, such target nucleic acid sequences comprise regions of alternately spliced transcripts or precursors of such alternately spliced transcripts.

[0516] In one embodiment, a multifunctional siNA molecule having any of Formula MF-I-MF-V can comprise chemical modifications as described herein without limitation, such as, for example, nucleotides having any of Formulae I-VII described herein, stabilization chemistries as described in Table IV, or any other combination of modified nucleotides and non-nucleotides as described in the various embodiments herein.

[0517] In one embodiment, the palindrome or repeat sequence or modified nucleotide (e.g., nucleotide with a modified base, such as 2-amino purine or a universal base) in Z of multifunctional siNA constructs having Formula MF-I or MF-II comprises chemically modified nucleotides that are able to interact with a portion of the target nucleic acid sequence (e.g., modified base analogs that can form Watson Crick base pairs or non-Watson Crick base pairs).

[0518] In one embodiment, a multifunctional siNA molecule of the invention, for example each strand of a multifunctional siNA having MF-I-MF-V, independently comprises about 15 to about 40 nucleotides (e.g., about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 nucleotides). In one embodiment, a multifunctional siNA molecule of the invention comprises one or more chemical modifications. In a non-limiting example, the introduction of chemically modified nucleotides and/or non-nucleotides into nucleic acid molecules of the invention provides a powerful tool in overcoming potential limitations of in vivo stability and bioavailability inherent to unmodified RNA molecules that are delivered exogenously. For example, the use of chemically modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically modified nucleic acid molecules tend to have a longer half-life in serum or in cells or tissues. Furthermore, certain chemical modifications can improve the bioavailability and/or potency of nucleic acid molecules by not only enhancing half-life but also facilitating the targeting of nucleic acid molecules to particular organs, cells or tissues and/or improving cellular uptake of the nucleic acid molecules. Therefore, even if the activity of a chemically modified nucleic acid molecule is reduced in vitro as compared to a native/unmodified nucleic acid molecule, for example when compared to an unmodified RNA molecule, the overall activity of the modified nucleic acid molecule can be greater than the native or unmodified nucleic acid molecule due to improved stability, potency, duration of effect, bioavailability and/or delivery of the molecule.

[0519] In another embodiment, the invention features multifunctional siNAs, wherein the multifunctional siNAs are

assembled from two separate double-stranded siNAs, with one of the ends of each sense strand is tethered to the end of the sense strand of the other siNA molecule, such that the two antisense siNA strands are annealed to their corresponding sense strand that are tethered to each other at one end (see FIG. 22). The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0520] In one embodiment, the invention features a multifunctional siNA, wherein the multifunctional siNA is assembled from two separate double-stranded siNAs, with the 5'-end of one sense strand of the siNA is tethered to the 5'-end of the sense strand of the other siNA molecule, such that the 5'-ends of the two antisense siNA strands, annealed to their corresponding sense strand that are tethered to each other at one end, point away (in the opposite direction) from each other (see FIG. 22 (A)). The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0521] In one embodiment, the invention features a multifunctional siNA, wherein the multifunctional siNA is assembled from two separate double-stranded siNAs, with the 3'-end of one sense strand of the siNA is tethered to the 3'-end of the sense strand of the other siNA molecule, such that the 5'-ends of the two antisense siNA strands, annealed to their corresponding sense strand that are tethered to each other at one end, face each other (see FIG. 22 (B)). The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0522] In one embodiment, the invention features a multifunctional siNA, wherein the multifunctional siNA is assembled from two separate double-stranded siNAs, with the 5'-end of one sense strand of the siNA is tethered to the 3'-end of the sense strand of the other siNA molecule, such that the 5'-end of the one of the antisense siNA strands annealed to their corresponding sense strand that are tethered to each other at one end, faces the 3'-end of the other antisense strand (see FIG. 22 (C-D)). The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0523] In one embodiment, the invention features a multifunctional siNA, wherein the multifunctional siNA is assembled from two separate double-stranded siNAs, with the 5'-end of one antisense strand of the siNA is tethered to the 3'-end of the antisense strand of the other siNA molecule, such that the 5'-end of the one of the sense siNA strands annealed to their corresponding antisense sense strand that are tethered to each other at one end, faces the 3'-end of the other sense strand (see FIG. 22 (G-H)). In one embodiment, the linkage between the 5'-end of the first antisense strand and the 3'-end of the second antisense strand is designed in such a way as to be readily cleavable (e.g., biodegradable linker) such that the 5' end of each antisense strand of the multifunctional siNA has a free 5'-end suitable to mediate RNA interference-based cleavage of the target RNA. The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0524] In one embodiment, the invention features a multifunctional siNA, wherein the multifunctional siNA is assembled from two separate double-stranded siNAs, with the 5'-end of one antisense strand of the siNA is tethered to the 5'-end of the antisense strand of the other siNA molecule,

such that the 3'-end of the one of the sense siNA strands annealed to their corresponding antisense sense strand that are tethered to each other at one end, faces the 3'-end of the other sense strand (see FIG. 22 (E)). In one embodiment, the linkage between the 5'-end of the first antisense strand and the 5'-end of the second antisense strand is designed in such a way as to be readily cleavable (e.g., biodegradable linker) such that the 5' end of each antisense strand of the multifunctional siNA has a free 5'-end suitable to mediate RNA interference-based cleavage of the target RNA. The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0525] In one embodiment, the invention features a multifunctional siNA, wherein the multifunctional siNA is assembled from two separate double-stranded siNAs, with the 3'-end of one antisense strand of the siNA is tethered to the 3'-end of the antisense strand of the other siNA molecule, such that the 5'-end of the one of the sense siNA strands annealed to their corresponding antisense sense strand that are tethered to each other at one end, faces the 3'-end of the other sense strand (see FIG. 22 (F)). In one embodiment, the linkage between the 5'-end of the first antisense strand and the 5'-end of the second antisense strand is designed in such a way as to be readily cleavable (e.g., biodegradable linker) such that the 5' end of each antisense strand of the multifunctional siNA has a free 5'-end suitable to mediate RNA interference-based cleavage of the target RNA. The tethers or linkers can be nucleotide-based linkers or non-nucleotide based linkers as generally known in the art and as described herein.

[0526] In any of the above embodiments, a first target nucleic acid sequence or second target nucleic acid sequence can independently comprise PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA. In one embodiment, the first PCSK9 target nucleic acid sequence is a PCSK9 target RNA or a portion thereof and the second PCSK9 target nucleic acid sequence is a PCSK9 pathway target RNA, such as PCSK9, H6PD, PTP-1B, apoAI/CIII/AIV, CETP, ApoB, SREBP-1a, SREBP-2, calcium/calmodulin-dependent protein kinase 1D, fatty acid binding protein 5, proprotein convertase subtilisin/kexin 9, LXR target genes, metalloprotease domain 11, apoptosis-inhibitory 6, and/or F-box-only protein 3 RNA of a portion thereof.

Synthesis of Nucleic Acid Molecules

[0527] Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; e.g., individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

[0528] Oligonucleotides (e.g., certain modified oligonucleotides or portions of oligonucleotides lacking ribonucle-

otides) are synthesized using protocols known in the art, for example as described in Caruthers et al., 1992, *Methods in Enzymology* 211, 3-19, Thompson et al., International PCT Publication No. WO 99/54459, Wincott et al., 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott et al., 1997, *Methods Mol. Bio.*, 74, 59, Brennan et al., 1998, *Biotechnol Bioeng.*, 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μ mol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 second coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. Table V outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μ mol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, Calif.) with minimal modification to the cycle. A 33-fold excess (60 μ L of 0.11 M=6.6 μ mol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μ L of 0.25 M=15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μ L of 0.11 M=4.4 μ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μ L of 0.25 M=10 μ mol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% N-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I₂, 49 mM pyridine, 9% water in THF (PerSeptive Biosystems, Inc.). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

[0529] Deprotection of the DNA-based oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aqueous methylamine (1 mL) at 65° C. for 10 minutes. After cooling to -20° C., the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. In one embodiment, the nucleic acid molecules of the invention are synthesized, deprotected, and analyzed according to methods described in U.S. Pat. No. 6,995,259, U.S. Pat. No. 6,686,463, U.S. Pat. No. 6,673,918, U.S. Pat. No. 6,649,751, U.S. Pat. No. 6,989,442, and U.S. Ser. No. 10/190,359, all incorporated by reference herein in their entirety.

[0530] The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman et al., 1987, *J. Am. Chem. Soc.*,

109, 7845; Scaringe et al., 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott et al., 1995, *Nucleic Acids Res.* 23, 2677-2684. Wincott et al., 1997, *Methods Mol. Bio.*, 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μ mol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. Table V outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μ mol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, Calif.) with minimal modification to the cycle. A 33-fold excess (60 μ L of 0.11 M=6.6 μ mol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 μ L of 0.25 M=15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 μ L of 0.11 M=13.2 μ mol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 μ L of 0.25 M=30 μ mol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% N-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I₂, 49 mM pyridine, 9% water in THF (PerSeptive Biosystems, Inc.). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide 0.05 M in acetonitrile) is used.

[0531] Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65° C. for 10 min. After cooling to -20° C., the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 μ L of a solution of 1.5 mL N-methylpyrrolidinone, 750 μ L TEA and 1 mL TEA.3HF to provide a 1.4 M HF concentration) and heated to 65° C. After 1.5 h, the oligomer is quenched with 1.5 M NH₄HCO₃. In one embodiment, the nucleic acid molecules of the invention are synthesized, deprotected, and analyzed according to methods described in U.S. Pat. No. 6,995,259, U.S. Pat. No. 6,686,463, U.S. Pat. No. 6,673,918, U.S. Pat. No. 6,649,751, U.S. Pat. No. 6,989,442, and U.S. Ser. No. 10/190,359, all incorporated by reference herein in their entirety.

[0532] Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33%

ethanolic methylamine/DMSO:1/1 (0.8 mL) at 65° C. for 15 minutes. The vial is brought to room temperature TEA.3HF (0.1 mL) is added and the vial is heated at 65° C. for 15 minutes. The sample is cooled at -20° C. and then quenched with 1.5 M NH₄HCO₃.

[0533] For purification of the trityl-on oligomers, the quenched NH₄HCO₃ solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 minutes. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

[0534] The average stepwise coupling yields are typically >98% (Wincott et al., 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

[0535] Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore et al., 1992, *Science* 256, 9923; Draper et al., International PCT publication No. WO 93/23569; Shabarov et al., 1991, *Nucleic Acids Research* 19, 4247; Bellon et al., 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon et al., 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

[0536] The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siNA fragments or strands that hybridize and permit purification of the siNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as described herein can also be readily adapted to large scale synthesis platforms employing batch reactors, synthesis columns and the like.

[0537] A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the RNA molecule.

[0538] The nucleic acid molecules of the present invention can be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TBSI* 17, 34; Usman et al., 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high pressure liquid chromatography (HPLC; see Wincott et al., supra, the totality of which is hereby incorporated herein by reference) and re-suspended in water.

[0539] In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adenovirus-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in

target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

Optimizing Activity of the Nucleic Acid Molecule of the Invention.

[0540] Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) can prevent their degradation by serum ribonucleases, which can increase their potency (see e.g., Eckstein et al., International Publication No. WO 92/07065; Perrault et al., 1990 *Nature* 344, 565; Pieken et al., 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman et al., International Publication No. WO 93/15187; and Rossi et al., International Publication No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold et al., U.S. Pat. No. 6,300,074; and Burgin et al., *supra*; all of which are incorporated by reference herein). All of the above references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein. Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

[0541] There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TBBS* 17, 34; Usman et al., 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin et al., 1996, *Biochemistry*, 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein et al., International Publication PCT No. WO 92/07065; Perrault et al., *Nature*, 1990, 344, 565-568; Pieken et al. *Science*, 1991, 253, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman et al. International Publication PCT No. WO 93/15187; Sproat, U.S. Pat. No. 5,334,711 and Beigelman et al., 1995, *J. Biol. Chem.*, 270, 25702; Beigelman et al., International PCT publication No. WO 97/26270; Beigelman et al., U.S. Pat. No. 5,716,824; Usman et al., U.S. Pat. No. 5,627,053; Woolf et al., International PCT Publication No. WO 98/13526; Thompson et al., U.S. Ser. No. 60/082,404 which was filed on Apr. 20, 1998; Karpeisky et al., 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.*, 67, 99-134; and Burlina et al., 1997, *Bioorg. Med. Chem.*, 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to promote RNAi in cells is not significantly inhibited.

[0542] In one embodiment, a nucleic acid molecule of the invention is chemically modified as described in US 20050020521, incorporated by reference herein in its entirety.

[0543] While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity. Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

[0544] Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott et al., 1995, *Nucleic Acids Res.* 23, 2677; Caruthers et al., 1992, *Methods in Enzymology* 211, 3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

[0545] In one embodiment, nucleic acid molecules of the invention include one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.*, 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2',4'-C methylene bicyclo nucleotide (see for example Wengel et al., International PCT Publication No. WO 00/66604 and WO 99/14226).

[0546] In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, cholesterol, phospholipids, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used

either individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues, in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

[0547] The term “biodegradable linker” as used herein, refers to a nucleic acid or non-nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

[0548] The term “biodegradable” as used herein, refers to degradation in a biological system, for example, enzymatic degradation or chemical degradation.

[0549] The term “biologically active molecule” as used herein refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include therapeutically active molecules such as antibodies, cholesterol, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

[0550] The term “phospholipid” as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

[0551] Therapeutic nucleic acid molecules (e.g., siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript.

The nucleic acid molecules are resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

[0552] In yet another embodiment, siNA molecules having chemical modifications that maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

[0553] Use of the nucleic acid-based molecules of the invention will lead to better treatments by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes; nucleic acid molecules coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and aptamers.

[0554] In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'-cap structure, for example, on only the sense siNA strand, the antisense siNA strand, or both siNA strands.

[0555] By “cap structure” is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Adamic et al., U.S. Pat. No. 5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or may be present on both termini. In non-limiting examples, the 5'-cap includes, but is not limited to, glyceryl, inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl)nucleotide; 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide; 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; amino-hexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphate moiety. Non-limiting examples of cap moieties are shown in FIG. 10.

[0556] Non-limiting examples of the 3'-cap include, but are not limited to, glyceryl, inverted deoxy abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl)nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propylphosphate; 3-aminopropyl phosphate; 6-aminoxyethyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide,

5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butane-diol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

[0557] By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

[0558] An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, $=O$, $=S$, NO_2 or $N(CH_3)_2$, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, $=O$, $=S$, NO_2 or $N(CH_3)_2$, amino or SH.

[0559] Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thieryl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an $-C(O)-NH-R$, where R is either

alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an $-C(O)-OR'$, where R is either alkyl, aryl, alkylaryl or hydrogen.

[0560] By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, *supra*; Eckstein et al., International PCT Publication No. WO 92/07065; Usman et al., International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach et al., 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2,4,6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (e.g., 5-methylcytidine), 5-alkyluridines (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6-methyluridine), propyne, and others (Burgin et al., 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

[0561] In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amide carbamate, carboxymethyl, acetimidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties, in Modern Synthetic Methods*, VCH, 331-417, and Mesmaeker et al., 1994, *Novel Backbone Replacements for Oligonucleotides, in Carbohydrate Modifications in Antisense Research*, ACS, 24-39.

[0562] By "abasic" is meant sugar moieties lacking a nucleobase or having a hydrogen atom (H) or other other non-nucleobase chemical groups in place of a nucleobase at the 1' position of the sugar moiety, see for example Adamic et al., U.S. Pat. No. 5,998,203. In one embodiment, an abasic moiety of the invention is a ribose, deoxyribose, or dideoxyribose sugar.

[0563] By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of β -D-ribo-furanose.

[0564] By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

[0565] In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'- NH_2 or 2'- $O-NH_2$, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein

et al., U.S. Pat. No. 5,672,695 and Matulic-Adamic et al., U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

[0566] Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life in vitro, stability, and ease of introduction of such oligonucleotides to the target site, e.g., to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Administration of Nucleic Acid Molecules

[0567] A siNA molecule of the invention can be adapted for use to prevent or treat diseases, traits, disorders, and/or conditions described herein or otherwise known in the art to be related to PCSK9 gene or PCSK9 pathway gene expression, and/or any other trait, disease, disorder or condition that is related to or will respond to the levels of PCSK9 polynucleotides or proteins expressed therefrom in a cell or tissue, alone or in combination with other therapies. In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to a cell, subject, or organism as is described herein and as is generally known in the art.

[0568] In one embodiment, a siNA composition of the invention can comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar et al., 1992, *Trends Cell Bio.*, 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer et al., 1999, *Mol. Membr. Biol.*, 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.*, 137, 165-192; and Lee et al., 2000, *ACS Symp. Ser.*, 752, 184-192, all of which are incorporated herein by reference. Beigelman et al., U.S. Pat. No. 6,395,713 and Sullivan et al., PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as biodegradable polymers, hydrogels, cyclodextrins (see for example Gonzalez et al., 1999, *Bioconjugate Chem.*, 10, 1068-1074; Wang et al., International PCT publication Nos. WO 03/47518 and WO 03/46185), poly(lactic-co-glycolic)acid (PLGA) and PLCA microspheres (see for example U.S. Pat. No. 6,447,796 and US Patent Application Publication No. US 2002130430), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). In another embodiment, the nucleic acid molecules of the invention can also be formulated or complexed with polyethyleneimine and derivatives thereof, such as polyethyleneimine-polyethyleneglycol-N-acetylgalactosamine (PEI-PEG-GAL) or polyethyleneimine-polyethyleneglycol-tri-N-acetylgalactosamine (PEI-PEG-triGAL) derivatives. In one embodiment, the nucleic acid molecules of the invention are formulated as described in United States Patent Application Publication No. 20030077829, incorporated by reference herein in its entirety.

[0569] In one embodiment, a siNA molecule of the invention is formulated as a composition described in U.S. Provisional patent application No. 60/678,531 and in related U.S. Provisional patent application No. 60/703,946, filed Jul. 29, 2005, U.S. Provisional patent application No. 60/737,024, filed Nov. 15, 2005, and U.S. Ser. No. 11/353,630, filed Feb. 14, 2006 (Vargeese et al.), all of which are incorporated by reference herein in their entirety. Such siNA formulations are generally referred to as "lipid nucleic acid particles" (LNP). In one embodiment, a siNA molecule of the invention is formulated with one or more LNP compositions described herein in Table IV (see U.S. Ser. No. 11/353,630 *supra*).

[0570] In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to lung tissues and cells as is described in US 2006/0062758; US 2006/0014289; and US 2004/0077540.

[0571] In one embodiment, a siNA molecule of the invention is complexed with membrane disruptive agents such as those described in U.S. Patent Application Publication No. 20010007666, incorporated by reference herein in its entirety including the drawings. In another embodiment, the membrane disruptive agent or agents and the siNA molecule are also complexed with a cationic lipid or helper lipid molecule, such as those lipids described in U.S. Pat. No. 6,235,310, incorporated by reference herein in its entirety including the drawings.

[0572] In one embodiment, a siNA molecule of the invention is complexed with delivery systems as described in U.S. Patent Application Publication No. 2003077829 and International PCT Publication Nos. WO 00/03683 and WO 02/087541, all incorporated by reference herein in their entirety including the drawings.

[0573] In one embodiment, a siNA molecule of the invention is complexed with delivery systems as is generally described in U.S. Patent Application Publication Nos. 20050287551; 20050164220; 20050191627; 20050118594; 20050153919; 20050085486; and 20030158133; all incorporated by reference herein in their entirety including the drawings.

[0574] In one embodiment, the nucleic acid molecules of the invention and formulations thereof (e.g., LNP formulations of double stranded nucleic acid molecules of the invention) are administered via pulmonary delivery, such as by inhalation of an aerosol or spray dried formulation administered by an inhalation device or nebulizer, providing rapid local uptake of the nucleic acid molecules into relevant pulmonary tissues. Solid particulate compositions containing respirable dry particles of micronized nucleic acid compositions can be prepared by grinding dried or lyophilized nucleic acid compositions, and then passing the micronized composition through, for example, a 400 mesh screen to break up or separate out large agglomerates. A solid particulate composition comprising the nucleic acid compositions of the invention can optionally contain a dispersant which serves to facilitate the formation of an aerosol as well as other therapeutic compounds. A suitable dispersant is lactose, which can be blended with the nucleic acid compound in any suitable ratio, such as a 1 to 1 ratio by weight.

[0575] Aerosols of liquid particles comprising a nucleic acid composition of the invention can be produced by any suitable means, such as with a nebulizer (see for example U.S. Pat. No. 4,501,729). Nebulizers are commercially available devices which transform solutions or suspensions of an active ingredient into a therapeutic aerosol mist either by means of

acceleration of a compressed gas, typically air or oxygen, through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in nebulizers comprise the active ingredient in a liquid carrier in an amount of up to 40% w/w preferably less than 20% w/w of the formulation. The carrier is typically water or a dilute aqueous alcoholic solution, preferably made isotonic with body fluids by the addition of, for example, sodium chloride or other suitable salts. Optional additives include preservatives if the formulation is not prepared sterile, for example, methyl hydroxybenzoate, anti-oxidants, flavorings, volatile oils, buffering agents and emulsifiers and other formulation surfactants. The aerosols of solid particles comprising the active composition and surfactant can likewise be produced with any solid particulate aerosol generator. Aerosol generators for administering solid particulate therapeutics to a subject produce particles which are respirable, as explained above, and generate a volume of aerosol containing a predetermined metered dose of a therapeutic composition at a rate suitable for human administration.

[0576] In one embodiment, a solid particulate aerosol generator of the invention is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which can be delivered by means of an insufflator. In the insufflator, the powder, e.g., a metered dose thereof effective to carry out the treatments described herein, is contained in capsules or cartridges, typically made of gelatin or plastic, which are either pierced or opened in situ and the powder delivered by air drawn through the device upon inhalation or by means of a manually-operated pump. The powder employed in the insufflator consists either solely of the active ingredient or of a powder blend comprising the active ingredient, a suitable powder diluent, such as lactose, and an optional surfactant. The active ingredient typically comprises from 0.1 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically containing a suspension or solution formulation of the active ingredient in a liquified propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume to produce a fine particle spray containing the active ingredient. Suitable propellants include certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane and mixtures thereof. The formulation can additionally contain one or more co-solvents, for example, ethanol, emulsifiers and other formulation surfactants, such as oleic acid or sorbitan trioleate, anti-oxidants and suitable flavoring agents. Other methods for pulmonary delivery are described in, for example US Patent Application No. 20040037780, and U.S. Pat. Nos. 6,592,904; 6,582,728; 6,565,885, all incorporated by reference herein.

[0577] In one embodiment, the siNA and LNP compositions and formulations provided herein for use in pulmonary delivery further comprise one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the compositions of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dip almitoylphosphatidylchol-Me, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones, lysophos-

phatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycero-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly(vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be used either as single or part of a multiple component surfactant in a formulation, or as covalently bound additions to the 5' and/or 3' ends of the nucleic acid component of a pharmaceutical composition herein.

[0578] The composition of the present invention may be administered into the respiratory system as a formulation including particles of respirable size, e.g. particles of a size sufficiently small to pass through the nose, mouth and larynx upon inhalation and through the bronchi and alveoli of the lungs. In general, respirable particles range from about 0.5 to 10 microns in size. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is thus minimized. For nasal administration, a particle size in the range of 10-500 um is preferred to ensure retention in the nasal cavity.

[0579] In one embodiment, the siNA molecules of the invention and formulations or compositions thereof are administered to the liver as is generally known in the art (see for example Wen et al., 2004, *World J. Gastroenterol.*, 10, 244-9; Murao et al., 2002, *Pharm Res.*, 19, 1808-14; Liu et al., 2003, *Gene Ther.*, 10, 180-7; Hong et al., 2003, *J Pharm Pharmacol.*, 54, 51-8; Herrmann et al., 2004, *Arch Virol.*, 149, 1611-7; and Matsuno et al., 2003, *Gene Ther.*, 10, 1559-66).

[0580] In one embodiment, a siNA molecule of the invention is administered iontophoretically, for example to a particular organ or compartment (e.g., the eye, back of the eye, heart, liver, kidney, bladder, prostate, tumor, CNS etc.). Non-limiting examples of iontophoretic delivery are described in, for example, WO 03/043689 and WO 03/030989, which are incorporated by reference in their entireties herein.

[0581] In one embodiment, siNA compounds and compositions of the invention are administered either systemically or locally about every 1-50 weeks (e.g., about every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 weeks), alone or in combination with other compounds and/or therapies herein. In one embodiment, siNA compounds and compositions of the invention are administered systemically (e.g., via intravenous, subcutaneous, intramuscular, infusion, pump, implant etc.) about every 1-50 weeks (e.g., about every 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 weeks), alone or in combination with other compounds and/or therapies described herein and/or otherwise known in the art.

[0582] In one embodiment, delivery systems of the invention include, for example, aqueous and nonaqueous gels,

creams, multiple emulsions, microemulsions, liposomes, ointments, aqueous and nonaqueous solutions, lotions, aerosols, hydrocarbon bases and powders, and can contain excipients such as solubilizers, permeation enhancers (e.g., fatty acids, fatty acid esters, fatty alcohols and amino acids), and hydrophilic polymers (e.g., polycarbophil and polyvinylpyrrolidone). In one embodiment, the pharmaceutically acceptable carrier is a liposome or a transdermal enhancer. Examples of liposomes which can be used in this invention include the following: (1) CellFectin, 1:1.5 (M/M) liposome formulation of the cationic lipid N,NI,NII,NIII-tetramethyl-N,NI,NII,NIII-tetrapalmit-y-spermine and dioleoyl phosphatidylethanolamine (DOPE) (GIBCO BRL); (2) Cytofectin GSV, 2:1 (M/M) liposome formulation of a cationic lipid and DOPE (Glen Research); (3) DOTAP (N-[1-(2,3-dioleoyloxy)-N,N,N-tri-methyl-ammoniummethylsulfate] (Boehringer Manheim); and (4) Lipofectamine, 3:1 (M/M) liposome formulation of the polycationic lipid DOSPA and the neutral lipid DOPE (GIBCO BRL).

[0583] In one embodiment, delivery systems of the invention include patches, tablets, suppositories, pessaries, gels and creams, and can contain excipients such as solubilizers and enhancers (e.g., propylene glycol, bile salts and amino acids), and other vehicles (e.g., polyethylene glycol, fatty acid esters and derivatives, and hydrophilic polymers such as hydroxypropylmethylcellulose and hyaluronic acid).

[0584] In one embodiment, siNA molecules of the invention are formulated or complexed with polyethylenimine (e.g., linear or branched PEI) and/or polyethylenimine derivatives, including for example grafted PEIs such as galactose PEI, cholesterol PEI, antibody derivatized PEI, and polyethylene glycol PEI (PEG-PEI) derivatives thereof (see for example Ogris et al., 2001, *AAPA PharmSci*, 3, 1-11; Furge-son et al., 2003, *Bioconjugate Chem.*, 14, 840-847; Kunath et al., 2002, *Pharmaceutical Research*, 19, 810-817; Choi et al., 2001, *Bull. Korean Chem. Soc.*, 22, 46-52; Bettinger et al., 1999, *Bioconjugate Chem.*, 10, 558-561; Peterson et al., 2002, *Bioconjugate Chem.*, 13, 845-854; Erbacher et al., 1999, *Journal of Gene Medicine Preprint*, 1, 1-18; Godbey et al., 1999., *PNAS USA*, 96, 5177-5181; Godbey et al., 1999, *Journal of Controlled Release*, 60, 149-160; Diebold et al., 1999, *Journal of Biological Chemistry*, 274, 19087-19094; Thomas and Klibanov, 2002, *PNAS USA*, 99, 14640-14645; and Sagara, U.S. Pat. No. 6,586,524, incorporated by reference herein.

[0585] In one embodiment, a siNA molecule of the invention comprises a bioconjugate, for example a nucleic acid conjugate as described in Vargeese et al., U.S. Ser. No. 10/427,160, filed Apr. 30, 2003; U.S. Pat. No. 6,528,631; U.S. Pat. No. 6,335,434; U.S. Pat. No. 6,235,886; U.S. Pat. No. 6,153,737; U.S. Pat. No. 5,214,136; U.S. Pat. No. 5,138,045, all incorporated by reference herein.

[0586] Thus, the invention features a pharmaceutical composition comprising one or more nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and the like. The polynucleotides of the invention can be administered (e.g., RNA, DNA or protein) and introduced to a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as creams, gels, sprays, oils and other

suitable compositions for topical, dermal, or transdermal administration as is known in the art.

[0587] The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, e.g., acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

[0588] A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, e.g., systemic or local administration, into a cell or subject, including for example a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (i.e., a cell to which the negatively charged nucleic acid is desirable for delivery). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that prevent the composition or formulation from exerting its effect.

[0589] In one embodiment, siNA molecules of the invention are administered to a subject by systemic administration in a pharmaceutically acceptable composition or formulation. By "systemic administration" is meant *in vivo* systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, portal vein, intra-peritoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue (e.g., lung). The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells.

[0590] By "pharmaceutically acceptable formulation" or "pharmaceutically acceptable composition" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85); biodegradable polymers, such as poly(DL-lactide-co-glycolide) microspheres for sustained release delivery (Emerich, D F et al, 1999, *Cell Transplant*, 8, 47-58); and loaded nanoparticles, such as those made of polybutylcyanoacrylate. Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado et al., 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler et al., 1999, *FEBS Lett.*, 421, 280-284; Pardridge et al., 1995, *PNAS USA*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada et al., 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler et al., 1999, *PNAS USA*, 96, 7053-7058.

[0591] The invention also features the use of a composition comprising surface-modified liposomes containing poly(ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes) and nucleic acid molecules of the invention. These formulations offer a method for increasing the accumulation of drugs (e.g., siNA) in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic et al. *Chem. Rev.* 1995, 95, 2601-2627; Ishiwata et al., *Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic et al., *Science* 1995, 267, 1275-1276; Oku et al., 1995, *Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu et al., *J. Biol. Chem.* 1995, 42, 24864-24870; Choi et al., International PCT Publication No. WO 96/10391; Ansell et al., International PCT Publication No. WO 96/10390; Holland et al., International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

[0592] In one embodiment, a liposomal formulation of the invention comprises a double stranded nucleic acid molecule of the invention (e.g., siNA) formulated or complexed with compounds and compositions described in U.S. Pat. Nos. 6,858,224; 6,534,484; 6,287,591; 6,835,395; 6,586,410; 6,858,225; 6,815,432; U.S. Pat. Nos. 6,586,001; 6,120,798; U.S. Pat. No. 6,977,223; U.S. Pat. Nos. 6,998,115; 5,981,501; 5,976,567; 5,705,385; US 2006/0019912; US 2006/0019258; US 2006/0008909; US 2005/0255153; US 2005/0079212; US 2005/0008689; US 2003/0077829; US 2005/0064595; US 2005/0175682; US 2005/0118253; US 2004/0071654; US 2005/0244504; US 2005/0265961 and US 2003/0077829, all of which are incorporated by reference herein in their entirety.

[0593] The present invention also includes compositions prepared for storage or administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A. R. Gennaro edit. 1985), hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of p-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

[0594] A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day

of active ingredients is administered dependent upon potency of the negatively charged polymer.

[0595] The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (e.g., intravenous), intramuscular, or intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

[0596] Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate can be employed.

[0597] Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

[0598] Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropyl-methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and

hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

[0599] Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid.

[0600] Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

[0601] Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

[0602] Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

[0603] The nucleic acid molecules of the invention can also be administered in the form of suppositories, e.g., for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

[0604] Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either

be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

[0605] Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

[0606] It is understood that the specific dose level for any particular subject depends upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

[0607] For administration to non-human animals, the composition can also be added to the animal feed or drinking water. It can be convenient to formulate the animal feed and drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

[0608] The nucleic acid molecules of the present invention can also be administered to a subject in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

[0609] In one embodiment, the invention comprises compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432) is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as asialoorosomucoid (ASOR). In another example, the folate receptor is overexpressed in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly depends on the degree of branching of the oligosaccharide chain, for example, triantennary structures are bound with greater affinity than biantennary or monoantennary chains (Baenziger and Fiete, 1980, *Cell*, 22, 611-620; Connolly et al., 1982, *J. Biol. Chem.*, 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety, which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom et al., 1981, *J. Med. Chem.*, 24, 1388-1395). The use of galactose, galactosamine, or folate based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavailability, pharmacodynamics, and pharmacokinetic parameters can be modulated through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such bioconjugates are described in Vargeese et al., U.S. Ser.

No. 10/201,394, filed Aug. 13, 2001; and Matulic-Adamic et al., U.S. Ser. No. 60/362,016, filed Mar. 6, 2002.

[0610] Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, *Science*, 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci., USA* 83, 399; Scanlon et al., 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet et al., 1992, *Antisense Res. Dev.*, 2, 3-15; propulic et al., 1992, *J. Virol.*, 66, 1432-41; Weerasinghe et al., 1991, *J. Virol.*, 65, 5531-4; Ojwang et al., 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen et al., 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver et al., 1990 *Science*, 247, 1222-1225; Thompson et al., 1995, *Nucleic Acids Res.*, 23, 2259; Good et al., 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper et al., PCT WO 93/23569, and Sullivan et al., PCT WO 94/02595; Ohkawa et al., 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira et al., 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura et al., 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira et al., 1994, *J. Biol. Chem.*, 269, 25856.

[0611] In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture et al., 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture et al., 1996, *TIG.*, 12, 510).

[0612] In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression vector can encode one or both strands of a siNA duplex, or a single self-complementary strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul et al., 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee et al., 2002, *Nature Biotechnology*, 19, 500; and Novina et al., 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725).

[0613] In another aspect, the invention features an expression vector comprising: a) a transcription initiation region (e.g., eukaryotic pol I, II or III initiation region); b) a transcription termination region (e.g., eukaryotic pol I, II or III termination region); and c) a nucleic acid sequence encoding

at least one of the siNA molecules of the instant invention, wherein said sequence is operably linked to said initiation region and said termination region in a manner that allows expression and/or delivery of the siNA molecule. The vector can optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the invention; and/or an intron (intervening sequences).

[0614] Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, *Proc. Natl. Acad. Sci. USA*, 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21, 2867-72; Lieber et al., 1993, *Methods Enzymol.*, 217, 47-66; Zhou et al., 1990, *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992, *Antisense Res. Dev.*, 2, 3-15; Ojwang et al., 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen et al., 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu et al., 1993, *Proc. Natl. Acad. Sci. USA*, 90, 6340-4; L'Huillier et al., 1992, *EMBO J.*, 11, 4411-8; Lisziewicz et al., 1993, *Proc. Natl. Acad. Sci. U.S.A.*, 90, 8000-4; Thompson et al., 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thompson et al., supra; Couture and Stinchcomb, 1996, supra; Noonberg et al., 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg et al., U.S. Pat. No. 5,624,803; Good et al., 1997, *Gene Ther.*, 4, 45; Beigelman et al., International PCT Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, supra).

[0615] In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

[0616] In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the termination region in a manner that allows expression and/or

delivery of the siNA molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

[0617] In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

PCSK9 Biology and Biochemistry

[0618] Proprotein Convertase Subtilisin Kexin 9 (PCSK9), also known as Neural apoptosis-regulated convertase (NARC-1), is a serine proteinase belonging to the proteinase K subfamily of subtilases. Its NARC-1 acronym reflects the fact that its mRNA was upregulated when apoptosis was induced in neuronal primary cultures and that it is similar to 8 other subtilase-like proteinases, called proprotein convertases (see for example International PCT Publication No. WO 01/57081). PCs are involved in the processing (and activation) of precursors of hormones, receptors, surface glycoproteins, etc, which transit through the secretory pathway. Seven of them, PC1/3, PC2, furin, PC4, PACE4, PC5/6, and PC7/LPC, recognize basic sites and belong to the kexin subfamily. The eighth member, SKI-1/S1P, is classified in the pyrolysin subfamily of subtilases. It has been involved in the processing of endoplasmic reticulum (ER)-anchored transcription factors such as sterol regulatory element (SRE)-binding proteins (SREBPs) and thus plays a key role in cholesterol homeostasis. When cellular cholesterol is low, SREBPs are relocated from the ER to the Golgi apparatus, where SKI-1/S1P cleaves in their luminal loop. A second cleavage by the metalloprotease S2P in their first transmembrane domain liberates the cytosolic N-terminal region that goes to the nucleus and activates target genes. SREBP-1c, the isoform that is dominant in liver, regulates the lipogenic pathway, whereas SREBP-2 preferentially activates genes of cholesterol metabolism.

[0619] PCSK9 is highly expressed in embryonic liver. It then decreases in the adult liver but significantly increases after hepatectomy. The transcript is also detected transiently in specific areas such as the telencephalon, skin, kidney, intestine, and cerebellum. It has been hypothesized that PCSK9 may be expressed preferentially in progenitor cells and play a role in hepatic and neuronal differentiation. In human, the PCSK9 gene is approximately 22 kilobases long and comprises 12 exons encoding a 692 amino acid protein. Located on chromosome 1p32, PCSK9 was identified recently as the third locus involved in autosomal dominant hypercholesterolemia (ADH), characterized by high levels of low-density lipoprotein (LDL) cholesterol, xanthomas, and a high frequency of coronary artery diseases. The majority of familial hypercholesterolemia cases are attributable to mutations in the genes encoding the LDL receptor (LDLR) and apolipoprotein B (apoB), the main component of LDL particles. By genetic analyses of several French families, 2 exonic PCSK9

mutations, S127R and F216L, were associated with haplotypes segregating with the disease. This work was confirmed recently by the identification of a new PCSK9 mutation, D374Y, in a large Utah kindred and 2 Japanese polymorphisms, intron 1/C(-161)T and I474V, all associated with abnormally high levels of LDL-cholesterol. (see Dubuc et al., 2004, *Arteriosclerosis, Thrombosis, and Vascular Biology*, 24:1454).

[0620] Based upon the current understanding of PCSK9 function, the modulation of PCSK9 and other related genes is instrumental in the development of new therapeutics for metabolic disease. As such, modulation of PCSK9 using small interfering nucleic acid (siNA) mediated RNAi represents a novel approach to the treatment and study of diseases and conditions related to PCSK9 activity and/or gene expression including hyperlipidemia, hypercholesterolemia, cardiovascular disease, atherosclerosis, hypertension, diabetes (e.g., type I and/or type II diabetes), insulin resistance, obesity and/or other disease states, conditions, or traits associated with PCSK9 gene expression or activity in a subject or organism.

EXAMPLES

[0621] The following are non-limiting examples showing the selection, isolation, synthesis and activity of nucleic acids of the instant invention.

Example 1

Tandem Synthesis of siNA Constructs

[0622] Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example, a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well synthesis platforms.

[0623] After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the oligonucleotides are deprotected as described above. Following deprotection, the siNA sequence strands are allowed to spontaneously hybridize. This hybridization yields a duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example, by using a C18 cartridge.

[0624] Standard phosphoramidite synthesis chemistry is used up to the point of introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceral succinate linker (see FIG. 1) or an equivalent cleavable linker. A non-limiting example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexafluorophosphate (PyBrOP). After the linker is coupled, standard synthesis chemistry is utilized to complete

synthesis of the second sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50 mM NaOAc or 1.5M NH₄H₂CO₃.

[0625] Purification of the siNA duplex can be readily accomplished using solid phase extraction, for example, using a Waters C18 SepPak 1 g cartridge conditioned with 1 column volume (CV) of acetonitrile, 2 CV H₂O, and 2 CV 50 mM NaOAc. The sample is loaded and then washed with 1 CV H₂O 2CV or 50 mM NaOAc. Failure sequences are eluted with 1 CV 14% ACN (Aqueous with 50 mM NaOAc and 50 mM NaCl). The column is then washed, for example with 1 CV H₂O followed by on-column detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA) over the column, then adding a second CV of 1% aqueous TFA to the column and allowing to stand for approximately 10 minutes. The remaining TFA solution is removed and the column washed with H₂O followed by 1 CV 1M NaCl and additional H₂O. The siNA duplex product is then eluted, for example, using 1 CV 20% aqueous CAN.

[0626] FIG. 2 provides an example of MALDI-TOF mass spectrometry analysis of a purified siNA construct in which each peak corresponds to the calculated mass of an individual siNA strand of the siNA duplex. The same purified siNA provides three peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably corresponding to the duplex siNA, and two peaks presumably corresponding to the separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA construct only shows a single peak. Testing of the purified siNA construct using a luciferase reporter assay described below demonstrated the same RNAi activity compared to siNA constructs generated from separately synthesized oligonucleotide sequence strands.

Example 2

Identification of Potential siNA Target Sites in any RNA Sequence

[0627] The sequence of an RNA target of interest, such as a human PCSK9 mRNA transcript, is screened for target sites, for example by using a computer folding algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript derived from a database, such as Genbank, is used to generate siNA targets having complementarity to the target. Such sequences can be obtained from a database, or can be determined experimentally as known in the art. Target sites that are known, for example, those target sites determined to be effective target sites based on studies with other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease, trait, or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using in vitro RNA cleavage assays, cell culture, or animal models. In a non-limiting example, any-

where from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays to determine efficient reduction in target gene expression.

Example 3

Selection of siNA Molecule Target Sites in a RNA

[0628] The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

[0629] 1. The target sequence is parsed in silico into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.

[0630] 2. In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences that are present in most or all of the target sequences. Alternately, the ranking can identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.

[0631] 3. In some instances the siNA subsequences are absent in one or more sequences while present in the desired target sequence; such would be the case if the siNA targets a gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene but are absent in the untargeted paralog.

[0632] 4. The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.

[0633] 5. The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin structures are to be avoided.

[0634] 6. The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever better sequences are available. CCC is searched in the target strand because that will place GGG in the antisense strand.

[0635] 7. The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3'

UU on the antisense sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.

[0636] 8. Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper (sense) strand of the siNA duplex, while the reverse complement of the left 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see Table II). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.

[0637] 9. The siNA molecules are screened in an in vitro, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

[0638] 10. Other design considerations can be used when selecting target nucleic acid sequences, see, for example, Reynolds et al., 2004, *Nature Biotechnology Advanced Online Publication*, 1 Feb. 2004, doi:10.1038/nbt936 and Ui-Tei et al., 2004, *Nucleic Acids Research*, 32, doi:10.1093/nar/gkh247.

[0639] In an alternate approach, a pool of siNA constructs specific to a target sequence is used to screen for target sites in cells expressing target RNA, such as cultured Jurkat, HeLa, A549 or 293T cells. The general strategy used in this approach is shown in FIG. 9. Cells expressing the target RNA are transfected with the pool of siNA constructs and cells that demonstrate a phenotype associated with target inhibition are sorted. The pool of siNA constructs can be expressed from transcription cassettes inserted into appropriate vectors (see for example FIG. 7 and FIG. 8). The siNA from cells demonstrating a positive phenotypic change (e.g., decreased proliferation, decreased target mRNA levels or decreased target protein expression), are sequenced to determine the most suitable target site(s) within the target target RNA sequence.

[0640] In one embodiment, siNA molecules of the invention are selected using the following methodology. The following guidelines were compiled to predict hyper-active siNAs that contain chemical modifications described herein. These rules emerged from a comparative analysis of hyper-active (>75% knockdown of target mRNA levels) and inactive (<75% knockdown of target mRNA levels) siNAs against several different targets. A total of 242 siNA sequences were analyzed. Thirty-five siNAs out of 242 siRNAs were grouped into hyper-active and the remaining siNAs were grouped into inactive groups. The hyper-active siNAs clearly showed a preference for certain bases at particular nucleotide positions within the siNA sequence. For example, A or U nucleobase was overwhelmingly present at position 19 of the sense strand in hyper-active siNAs and opposite was true for inactive siNAs. There was also a pattern of a A/U rich (3 out of 5 bases as A or U) region between positions 15-19 and G/C rich region between positions 1-5 (3 out of 5 bases as G or C) of the sense strand in hyperactive siNAs. As shown in Table VII, 12 such patterns were identified that were characteristics of hyper-active siNAs. It is to be noted that not every pattern was present in each hyper-active siNA. Thus, to design an algorithm for predicting hyper-active siNAs, a different score was assigned for each pattern. Depending on how frequently such patterns occur in hyper-active siRNAs versus inactive siRNAs,

NAs, the design parameters were assigned a score with the highest being 10. If a certain nucleobase is not preferred at a position, then a negative score was assigned. For example, at positions 9 and 13 of the sense strand, a G nucleotide was not preferred in hyper-active siNAs and therefore they were given score of -3(minus 3). The differential score for each pattern is given in Table VII. The pattern # 4 was given a maximum score of -100. This is mainly to weed out any sequence that contains string of 4Gs or 4Cs as they can be highly incompatible for synthesis and can allow sequences to self-aggregate, thus rendering the siNA inactive. Using this algorithm, the highest score possible for any siNA is 66. As there are numerous siNA sequences possible against any given target of reasonable size (approximately 1000 nucleotides), this algorithm is useful to generate hyper-active siNAs.

[0641] In one embodiment, rules 1-11 shown in Table VII are used to generate active siNA molecules of the invention. In another embodiment, rules 1-12 shown in Table VII are used to generate active siNA molecules of the invention.

Example 4

PCSK9 siNA Design

[0642] siNA target sites were chosen by analyzing sequences of the PCSK9 target and optionally prioritizing the target sites on the basis of the rules presented in Example 3 above, and alternately on the basis of folding (structure of any given sequence analyzed to determine siNA accessibility to the target), or by using a library of siNA molecules as described in Example 3, or alternately by using an in vitro siNA system as described in Example 6 herein. siNA molecules were designed that could bind each target and are selected using the algorithm above and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of the siNA molecules can be chosen to optimize activity. Generally, a sufficient number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA duplexes or varying length or base composition. By using such methodologies, siNA molecules can be designed to target sites within any known RNA sequence, for example those RNA sequences corresponding to the any gene transcript.

[0643] PCSK9 sequences (Table I) were analysed to generate PCSK9 targets from which double stranded siNA were designed (Table II). To generate synthetic siNA constructs (Table III), the algorithm described in Example 3 was utilized to pick active double stranded constructs and chemically modified versions thereof. In each of Tables II and III, the target sequence is shown, along with the upper (sense strand) and lower (antisense strand) of the siNA duplex. Multifunctional siNAs are designed by searching for homologous sites between different target sequences (e.g., 11 nucleotide regions of shared homology) and allowing for up to 3 wobble by (G:U) or up to 2 mismatches.

[0644] Chemically modified siNA constructs were designed as described herein (see for example Table V) to provide nuclease stability for systemic administration in vivo and/or improved pharmacokinetic, localization, and delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA

constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantify RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example FIG. 11).

Example 5

Chemical Synthesis and Purification of siNA

[0645] siNA molecules can be designed to interact with various sites in the RNA message, for example, target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can be synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman et al., U.S. Pat. Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 6,362,323; 6,437,117; 6,469,158; Scaringe et al., U.S. Pat. Nos. 6,111,086; 6,008,400; 6,111,086 all incorporated by reference herein in their entirety).

[0646] In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-dimethoxytrityl, 2'-O-tert-butylidimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoramide groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine, N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2'-O—Silyl Ethers can be used in conjunction with acid-labile 2'-O-orthoester protecting groups in the synthesis of RNA as described by Scaringe supra. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman et al., U.S. Pat. No. 5,631,360, incorporated by reference herein in its entirety).

[0647] During solid phase synthesis, each nucleotide is added sequentially (3'- to 5'-direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5'-end of the first nucleoside. The support is then washed and any unreacted 5'-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5'-acetyl moieties. The trivalent phosphorus linkage is then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition cycle, the 5'-O-protecting group is cleaved under suitable

conditions (e.g., acidic conditions for trityl-based groups and fluoride for silyl-based groups). The cycle is repeated for each subsequent nucleotide.

[0648] Modification of synthesis conditions can be used to optimize coupling efficiency, for example by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be synthesized. Deprotection and purification of the siNA can be performed as is generally described in Usman et al., U.S. Pat. No. 5,831,071, U.S. Pat. No. 6,353,098, U.S. Pat. No. 6,437,117, and Bellon et al., U.S. Pat. No. 6,054,576, U.S. Pat. No. 6,162,909, U.S. Pat. No. 6,303,773, or Scaringe supra, incorporated by reference herein in their entireties. Additionally, deprotection conditions can be modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides can degrade under inappropriate deprotection conditions. Such oligonucleotides are deprotected using aqueous methylamine at about 35° C. for 30 minutes. If the 2'-deoxy-2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous methylamine at about 35° C. for 30 minutes, TEA-HF is added and the reaction maintained at about 65° C. for an additional 15 minutes.

Example 6

RNAi In Vitro Assay to Assess siNA Activity

[0649] An in vitro assay that recapitulates RNAi in a cell-free system is used to evaluate siNA constructs targeting target RNA targets. The assay comprises the system described by Tuschl et al., 1999, *Genes and Development*, 13, 3191-3197 and Zamore et al., 2000, *Cell*, 101, 25-33 adapted for use with a target RNA. A *Drosophila* extract derived from syncytial blastoderm is used to reconstitute RNAi activity in vitro. Target RNA is generated via in vitro transcription from an appropriate target expressing plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 minute at 90° C. followed by 1 hour at 37° C., then diluted in lysis buffer (for example 100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2 mM magnesium acetate). Annealing can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The *Drosophila* lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant isolated. The assay comprises a reaction mixture containing 50% lysate [vol/vol], RNA (10-50 pM final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug/ml creatine phosphokinase, 100 um GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final concentration of potassium acetate is adjusted to 100 mM. The reactions are pre-assembled on ice and preincubated at 25° C. for 10 minutes before adding RNA, then incubated at 25° C. for an additional 60 minutes. Reactions are quenched with 4 volumes of 1.25×Passive Lysis Buffer (Promega). Target

RNA cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in which siNA is omitted from the reaction.

[0650] Alternately, internally-labeled target RNA for the assay is prepared by in vitro transcription in the presence of [α - 32 P] CTP, passed over a G50 Sephadex column by spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'- 32 P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed as described above and target RNA and the specific RNA cleavage products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by PHOSPHOR IMAGER® (autoradiography) quantitation of bands representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

[0651] In one embodiment, this assay is used to determine target sites in the target RNA target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the target RNA target, for example, by analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

Example 7

Nucleic Acid Inhibition of PCSK9 Target RNA

[0652] siNA molecules targeted to PCSK9 RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for cleavage activity in vivo, for example, using the following procedure. The target sequences and the nucleotide location within the PCSK9 RNA are given in Table II and III.

[0653] Two formats are used to test the efficacy of siNAs targeting PCSK9. First, the reagents are tested in cell culture using HepG2, Jurkat, HeLa, A549 or 293T cells, to determine the extent of RNA and protein inhibition. siNA reagents (e.g.; see Tables II and III) are selected against the PCSK9 target as described herein. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to, for example, HepG2, Jurkat, HeLa, A549 or 293T cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of amplification (e.g., ABI 7700 TAQMAN®). A comparison is made to a mixture of oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition.

Delivery of siNA to Cells

[0654] Cells (e.g., HepG2, Jurkat, HeLa, A549 or 293T cells) are seeded, for example, at 1×10^5 cells per well of a six-well dish in EGM-2 (BioWhittaker) the day before transfection. siNA (final concentration, for example 20 nM) and cationic lipid (e.g., LNP formulations herein, or another suitable lipid such as Lipofectamine, final concentration 2 μ g/ml) are complexed in EGM basal media (Biowhittaker) at 37° C. for 30 minutes in polystyrene tubes. Following vortexing, the complexed siNA is added to each well and incubated for the times indicated. For initial optimization experiments, cells are seeded, for example, at 1×10^3 in 96 well plates and siNA

complex added as described. Efficiency of delivery of siNA to cells is determined using a fluorescent siNA complexed with lipid. Cells in 6-well dishes are incubated with siNA for 24 hours, rinsed with PBS and fixed in 2% paraformaldehyde for 15 minutes at room temperature. Uptake of siNA is visualized using a fluorescent microscope.

TAQMAN® (Real-Time PCR Monitoring of Amplification) and Lightcycler Quantification of mRNA

[0655] Total RNA is prepared from cells following siNA delivery, for example, using Qiagen RNA purification kits for 6-well or Rneasy extraction kits for 96-well assays. For TAQMAN® analysis (real-time PCR monitoring of amplification), dual-labeled probes are synthesized with the reporter dye, FAM or JOE, covalently linked at the 5'-end and the quencher dye TAMRA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM 7700 Sequence Detector using 50 μ l reactions consisting of 10 μ l total RNA, 100 nM forward primer, 900 nM reverse primer, 100 nM probe, 1 \times TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5 mM MgCl₂, 300 μ M each dATP, dCTP, dGTP, and dTTP, 10U RNase Inhibitor (Promega), 1.25U AMPLITAQ GOLD® (DNA polymerase) (PE-Applied Biosystems) and 10U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can consist of 30 minutes at 48° C., 10 minutes at 95° C., followed by 40 cycles of 15 seconds at 95° C. and 1 minute at 60° C. Quantitation of mRNA levels is determined relative to standards generated from serially diluted total cellular RNA (300, 100, 33, 11 ng/reaction) and normalizing to β -actin or GAPDH mRNA in parallel TAQMAN® reactions (real-time PCR monitoring of amplification). For each gene of interest an upper and lower primer and a fluorescently labeled probe are designed. Real time incorporation of SYBR Green I dye into a specific PCR product can be measured in glass capillary tubes using a lightcycler. A standard curve is generated for each primer pair using control cRNA. Values are represented as relative expression to GAPDH in each sample.

Western Blotting

[0656] Nuclear extracts can be prepared using a standard micro preparation technique (see for example Andrews and Faller, 1991, *Nucleic Acids Research*, 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody for 16 hour at 4° C. Following washes, the secondary antibody is applied, for example (1:10,000 dilution) for 1 hour at room temperature and the signal detected with SuperSignal reagent (Pierce).

Example 8

Models Useful to Evaluate the Down-Regulation of PCSK9 Gene Expression

[0657] Evaluating the efficacy of siNA molecules of the invention in animal models is an important prerequisite to human clinical trials. Various animal models of metabolic and

cardiovascular diseases, conditions, or disorders as are known in the art can be adapted for use for pre-clinical evaluation of the efficacy of nucleic acid compositions of the invention in modulating target (e.g., PCSK9) gene expression toward therapeutic or research use. Goldberg, 2004, *J Clin Invest.* 114(5): 613-615, provides a review of animal models useful for evaluating therapeutic agents for metabolic disease, including hyperlipidemia and diabetes. These models and others can be utilized to evaluate the efficacy of siNA molecules and compositions of the invention in treating metabolic and related diseases and conditions.

Example 9

RNAi Mediated Inhibition of PCSK9 Gene Expression

[0658] In Vitro siNA Mediated Inhibition of PCSK9 RNA
[0659] siNA constructs are tested for efficacy in reducing PCSK9 RNA expression in cells, (e.g., HepG2 cells). Cells are plated approximately 24 hours before transfection in 96-well plates at 5,000-7,500 cells/well, 100 μ l/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 μ l/well and incubated for 20 minutes at room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 μ l. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24 hours in the continued presence of the siNA transfection mixture. At 24 hours, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the PCSK9 gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs is determined.

Example 10

Indications

[0660] Particular conditions and disease states that can be associated with gene expression modulation include, but are not limited to metabolic and cardiovascular diseases, conditions, or disorders as described herein or otherwise known in the art, and any other diseases, conditions or disorders that are related to or will respond to the levels of a target (e.g., target PCSK9 protein or target PCSK9 polynucleotide) in a cell or tissue, alone or in combination with other therapies. Non-limiting examples of such diseases and conditions include hyperlipidemia, hypercholesterolemia, dyslipidemia, cardiovascular disease, atherosclerosis, hypertension, diabetes (e.g., type I and/or type II diabetes), insulin resistance, obesity, and/or metabolic syndrome.

Example 11

Multifunctional siNA Inhibition of Target RNA Expression

[0661] Multifunctional siNA Design

[0662] Once target sites have been identified for multifunctional siNA constructs, each strand of the siNA is designed with a complementary region of length, for example, of about 18 to about 28 nucleotides, that is complementary to a different target nucleic acid sequence. Each complementary region is designed with an adjacent flanking region of about 4 to about 22 nucleotides that is not complementary to the target sequence, but which comprises complementarity to the complementary region of the other sequence (see for example FIG. 16). Hairpin constructs can likewise be designed (see for example FIG. 17). Identification of complementary, palindrome or repeat sequences that are shared between the different target nucleic acid sequences can be used to shorten the overall length of the multifunctional siNA constructs (see for example FIGS. 18 and 19).

[0663] In a non-limiting example, three additional categories of additional multifunctional siNA designs are presented that allow a single siNA molecule to silence multiple targets. The first method utilizes linkers to join siNAs (or multifunctional siNAs) in a direct manner. This can allow the most potent siNAs to be joined without creating a long, continuous stretch of RNA that has potential to trigger an interferon response. The second method is a dendrimeric extension of the overlapping or the linked multifunctional design; or alternatively the organization of siNA in a supramolecular format. The third method uses helix lengths greater than 30 base pairs. Processing of these siNAs by Dicer will reveal new, active 5' antisense ends. Therefore, the long siNAs can target the sites defined by the original 5' ends and those defined by the new ends that are created by Dicer processing. When used in combination with traditional multifunctional siNAs (where the sense and antisense strands each define a target) the approach can be used for example to target 4 or more sites.
I. Tethered Bifunctional siNAs

[0664] The basic idea is a novel approach to the design of multifunctional siNAs in which two antisense siNA strands are annealed to a single sense strand. The sense strand oligonucleotide contains a linker (e.g., non-nucleotide linker as described herein) and two segments that anneal to the anti-sense siNA strands (see FIG. 22). The linkers can also optionally comprise nucleotide-based linkers. Several potential advantages and variations to this approach include, but are not limited to:

[0665] 1. The two antisense siNAs are independent. Therefore, the choice of target sites is not constrained by a requirement for sequence conservation between two sites. Any two highly active siNAs can be combined to form a multifunctional siNA.

[0666] 2. When used in combination with target sites having homology, siNAs that target a sequence present in two genes (e.g., different isoforms), the design can be used to target more than two sites. A single multifunctional siNA can be for example, used to target RNA of two different target RNAs.

[0667] 3. Multifunctional siNAs that use both the sense and antisense strands to target a gene can also be incorporated into a tethered multifunctional design. This leaves open the possibility of targeting 6 or more sites with a single complex.

[0668] 4. It can be possible to anneal more than two anti-sense strand siRNAs to a single tethered sense strand.

[0669] 5. The design avoids long continuous stretches of dsRNA. Therefore, it is less likely to initiate an interferon response.

[0670] 6. The linker (or modifications attached to it, such as conjugates described herein) can improve the pharmacokinetic properties of the complex or improve its incorporation into liposomes. Modifications introduced to the linker should not impact siRNA activity to the same extent that they would if directly attached to the siRNA (see for example FIGS. 27 and 28).

[0671] 7. The sense strand can extend beyond the annealed antisense strands to provide additional sites for the attachment of conjugates.

[0672] 8. The polarity of the complex can be switched such that both of the antisense 3' ends are adjacent to the linker and the 5' ends are distal to the linker or combination thereof.

Dendrimer and Supramolecular siRNAs

[0673] In the dendrimer siRNA approach, the synthesis of siRNA is initiated by first synthesizing the dendrimer template followed by attaching various functional siRNAs. Various constructs are depicted in FIG. 23. The number of functional siRNAs that can be attached is only limited by the dimensions of the dendrimer used.

Supramolecular Approach to Multifunctional siRNA

[0674] The supramolecular format simplifies the challenges of dendrimer synthesis. In this format, the siRNA strands are synthesized by standard RNA chemistry, followed by annealing of various complementary strands. The individual strand synthesis contains an antisense sense sequence of one siRNA at the 5'-end followed by a nucleic acid or synthetic linker, such as hexaethyleneglycol, which in turn is followed by sense strand of another siRNA in 5' to 3' direction. Thus, the synthesis of siRNA strands can be carried out in a standard 3' to 5' direction. Representative examples of trifunctional and tetrafunctional siRNAs are depicted in FIG. 24. Based on a similar principle, higher functionality siRNA constructs can be designed as long as efficient annealing of various strands is achieved.

Dicer Enabled Multifunctional siRNA

[0675] Using bioinformatic analysis of multiple targets, stretches of identical sequences shared between differing target sequences can be identified ranging from about two to about fourteen nucleotides in length. These identical regions can be designed into extended siRNA helices (e.g., >30 base pairs) such that the processing by Dicer reveals a secondary functional 5'-antisense site (see for example FIG. 25). For example, when the first 17 nucleotides of a siRNA antisense strand (e.g., 21 nucleotide strands in a duplex with 3'-TT overhangs) are complementary to a target RNA, robust silencing was observed at 25 nM. 80% silencing was observed with only 16 nucleotide complementarity in the same format.

[0676] Incorporation of this property into the designs of siRNAs of about 30 to 40 or more base pairs results in additional multifunctional siRNA constructs. The example in FIG. 25 illustrates how a 30 base-pair duplex can target three distinct sequences after processing by Dicer-RNaseIII; these sequences can be on the same mRNA or separate RNAs, such as viral and host factor messages, or multiple points along a given pathway (e.g., inflammatory cascades). Furthermore, a 40 base-pair duplex can combine a bifunctional design in

tandem, to provide a single duplex targeting four target sequences. An even more extensive approach can include use of homologous sequences to enable five or six targets silenced for one multifunctional duplex. The example in FIG. 25 demonstrates how this can be achieved. A 30 base pair duplex is cleaved by Dicer into 22 and 8 base pair products from either end (8 b.p. fragments not shown). For ease of presentation the overhangs generated by dicer are not shown—but can be compensated for. Three targeting sequences are shown. The required sequence identity overlapped is indicated by grey boxes. The N's of the parent 30 b.p. siRNA are suggested sites of 2'-OH positions to enable Dicer cleavage if this is tested in stabilized chemistries. Note that processing of a 30 mer duplex by Dicer RNase III does not give a precise 22+8 cleavage, but rather produces a series of closely related products (with 22+8 being the primary site). Therefore, processing by Dicer will yield a series of active siRNAs. Another non-limiting example is shown in FIG. 26. A 40 base pair duplex is cleaved by Dicer into 20 base pair products from either end. For ease of presentation the overhangs generated by dicer are not shown, but can be compensated for. Four targeting sequences are shown. The required sequence identity overlapped is indicated by shaded boxes. This design format can be extended to larger RNAs. If chemically stabilized siRNAs are bound by Dicer, then strategically located ribonucleotide linkages can enable designer cleavage products that permit our more extensive repertoire of multifunctional designs. For example, cleavage products not limited to the Dicer standard of approximately 22-nucleotides can allow multifunctional siRNA constructs with a target sequence identity overlap ranging from, for example, about 3 to about 15 nucleotides.

Example 12

Diagnostic Uses

[0677] The siRNA molecules of the invention can be used in a variety of diagnostic applications, such as in the identification of molecular targets (e.g., RNA) in a variety of applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siRNA molecules involves utilizing reconstituted RNAi systems, for example, using cellular lysates or partially purified cellular lysates. siRNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or exogenous, for example viral, RNA in a cell. The close relationship between siRNA activity and the structure of the target RNA allows the detection of mutations in any region of the molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siRNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function in vitro, as well as in cells and tissues. Cleavage of target RNAs with siRNA molecules can be used to inhibit gene expression and define the role of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siRNA molecules targeted to different genes, siRNA molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations siRNA molecules and/or other chemical or biological molecules). Other in vitro uses of siRNA molecules of this invention

tion are well known in the art, and include detection of the presence of mRNAs associated with a disease, infection, or related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a siNA using standard methodologies, for example, fluorescence resonance emission transfer (FRET).

[0678] In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (i.e., those that cleave only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (i.e., those that cleave only mutant forms of target RNA) are used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus, each analysis requires two siNA molecules, two substrates and one unknown sample, which is combined into six reactions. The presence of cleavage products is determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (i.e., disease related or infection related) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

[0679] All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

[0680] One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred

embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

[0681] It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches one skilled in the art to test various combinations and/or substitutions of chemical modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting and one skilled in the art can readily appreciate that specific combinations of the modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

[0682] The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

[0683] In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

TABLE I

PCSK9 Accession Numbers

| NM_174936
Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA
gi 31317306 ref NM_174936.2 [31317306] | (SEQ ID NO: 597) |
|--|------------------|
| cagcgacguc gaggcgcuca uggugcagg cgggcgcgc cguucaguuc agggucugag
ccuggaggag ugagccaggc agugagacug ucugccggc ggcggggacgc gugcuugcag
cagcgccucc cagccucccg ccaggauuc gcgcgcgcgc uacgcgcgc ugcuccugaa
cuucacgcucc ugcacagcuc ucccccccg aaggcucaag gcgcgcgcgc cguggaccgc
gcacggccuc uaggucuccu cgecaggaca gcaaccucuc cccuggcuccu cauggggacc
gucagcucca ggcggccug guggccgcug ccacugcugc ugcugcugcu gcugcuccug
ggucccccgg ggcggccggc gcaggaggac gaggacggcg acuacgagga gcuggugcua
gcccuiugcguu ccgaggagga cggccggcc gaagcaccgg agcacggaaac cacagccacc
uuccaccgcu gcgccaaggga uccguggagg uugccuggca ccaucguggu ggugcugaag | |

TABLE I-continued

PCSK9 Accession Numbers

gaggagaccc accucucgca gucagagcgc acugcccgcc gcuugcaggc ccaggcugcc
 cgccggggau accucaccaa gauccugcau gucuuccaung gcuuuccuucc ugguuccug
 gugaagauga guggcgaccu gcuggagcug gcuuugaagu ugcccuaugu cgacuacauc
 gaggaggacu cuccugucuu ugcccagac aucccgugga accuggagcgc gauuacccu
 ccaacgguaacc gggcggauga auaccagccc cccgacggag gcagccuggu ggaggugau
 cuccuagaca caagcauaca gagugaccac cgggaaaucg agggcagggu cauggucacc
 gacagucagga augugcccgaa ggaggacggg acccgcuuacc acagacaggc cagaagugu
 gacagucaug gcaccacccu ggcaggggug gucagccgc gggauggccgg cguggccaag
 ggugccgca ugcgcagccu gcgcgugcuc aacugccaa ggaaggccac gguuagccgc
 acccucauag gccuggaguu uacccggaaa agccagcugg ucagccugu gggccacug
 guggugcugc ucggccuggc ggugggguac agccgcgc cuaacgcgc cugccagcgc
 cuggcgaggg cuggggcugc gcuggucacc gcugccggea acuuccggga cgaugccugc
 cuccuacucc cagccuacg ucccgagguc aucacaguug gggccaccaa ugcccac
 cagccgguga cccuggggac uuuggggacc aacuuiuggc gcuugugugga ccuuiugcc
 ccaggggagg acauauugg ugcccacgac gacugcagca cugccuuugu gucacagagu
 gggcaucac ggcugcugc ccacugggc ggcauuugc ccaugauge gucugccag
 cccgagouca cccugccga guuaggcag agacuacca acuucucugc caaagauguc
 aucaaugagg ccugguuccc ugaggaccag cggguacuga cccccaaaccu gguggccgc
 cugcccccga gcacccaaugg ggcaggwuug cugcuguuuu gcaaggacwg auggugcagca
 cacucggggc cuacacggau ggcacacgac ggcggccgcu gegecccaaga ugaggagcug
 cugagecugc caaguuuucu cugaguggg aagggggcggc gcaugccau ggaggccaa
 gggggcaage ugugcugccg ggcacacaac guuuuugggg gugaggugu cuacgccaau
 gcaaggugcugc gccugcuacc ccaggccaaac ugcaegcucc acacagcucc accagcugag
 gcaugccagg ggcacccug gcaugccac caacaggcgc acguccuac agcugcagc
 ucccacuggg aggugggagga cuuuggcacc cacaaggccg cugugcugag gccacagg
 cagcccaacc agugccuggg ccacagggg gccagcaucc acguccuucug cugccaugcc
 ccaggucugg aaugcaauu caaggagcau ggaaucccg cccucagga gcaggugacc
 guggcugcugc aggaggccug gaccugugc ggcugcugc cccuuccugg gaccuccac
 guccuggggg cuacacggc agacaacactg uguguaguca ggagccggga cguacagcacu
 acaggcagca ccaacggagg ggcggugaca ggcguuugca ucugcugcc gaggccgcac
 cuggcgcagg cuucccaggc gcuuaggcua cagccccau ccaaggagg ugugcugggg
 gggucaaggg cuggggcuga gcuuuuuaau gguuucgacu uguccucuc ucagccucc
 auggcugcugc acgaggggau ggggaugcua cccuuccugg gaccuccac
 ugagugggc acuccuuug cuuggaacuc acuacacuc ggcugcucu cccaggugg
 aggugccagg aagccuccuc cuucacugug ggcguuua ccauuuac acggucagac
 gugcucggg gugccagc gcuuccaaug ugcccguuuc cagggcagg ugugcuggg
 uugagcucuu guuccugue aggcauuua uccuagguc uccaccaagg aggagg
 cuuuccaugg auagggagg ggcgcguagg ggcugcaggg acaaacauig uuggggggug
 agugugaaag gugcugauug cccuacuucu cagcuuacuug ugagaaaggc cuugggggc
 cccugauua uggaggcua gcuuucugga uggucauug ccauuuac acggucagac
 cgcggggu ggcacaggc ugugccuugg uuuucugc caccuuuacu cugcucuau
 ccaggcugug cuagcaacac ccaaggugg cugcgggg gcaucacccu aggacugacu
 cggcagugug caguggugca ugcacugcu cagccaaacc guuccacuac cccgcagg
 acacauucgc accccuacu cacaaggaa guaaggcagg accaggagg ggcugccugc
 caagcucaca cagcaggaaac ugagccagaa acgcagauug ggcuggcucu gaagccaa
 cuciucuucuac uucacccggc ugugccuucc auuuuuac acggcaggaa ggcuggg
 gggAACACAG accaggaaac ucggugagug auggcagaac gaugccugca ggcuggg
 uuuuuuccguu auacaccagg ccugauucac ugcccuggc gagaugcuc uaggc
 ugccccggaga gggcaacaa cugccuccuc uugagcacc gcccacca agcaagcaga
 cauuuauuc uggggcugu cuccucugu gcuuuuuuac agccaacuuu ucuagac
 uuuugcuiii guaacuugaa gauuuuuau cuggguuuw uagcauuuuu uuuauauugg
 ugacuuuuua aaauaaaaac aaacaaacgu ugucc

AK075365

Homo sapiens cDNA PSEC0052 fis, clone NT2RP2000279, weakly similar to
 AQUALYSIN I PRECURSOR (EC 3.4.21.-)
 gi|22761404|dbj|AK075365.1|[22761404]

AK122717

Homo sapiens cDNA FLJ16214 fis, clone CTONG2024614, weakly similar to
 AQUALYSIN I PRECURSOR (EC 3.4.21.-)
 gi|34527909|dbj|AK122717.1|[34527909]

BC042095

Homo sapiens proprotein convertase subtilisin/kexin type 9, mRNA (cDNA
 clone IMAGE: 5767792), partial cds
 gi|27694359|gb|BC042095.1|[27694359]

AK124635

Homo sapiens cDNA FLJ42644 fis, clone BRACE3025630
 gi|34530476|dbj|AK124635.1|[34530476]

TABLE I-continued

PCSK9 Accession Numbers

| |
|--|
| AC091609 |
| <i>Homo sapiens</i> chromosome 1 clone RP11-109I2, complete sequence
gi 15042908 gb AC091609.2 [15042908] |
| AY829011 |
| <i>Homo sapiens</i> proprotein convertase subtilisin/kexin type 9 (PCSK9) gene, complete cds
gi 55925153 gb AY829011.1 [55925153] |
| AL589790 |
| Human DNA sequence from clone GS1-118I5 on chromosome 1 Contains the 3' end of the gene for barttin (BSND) and the 5' end of the PCSK9 gene for proprotein convertase subtilisin/kexin type 9, complete sequence
gi 17973948 emb AL589790.22 [17973948] |
| AY415992 |
| <i>Homo sapiens</i> HCM5742 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence
gi 39771952 gb AY415992.1 [39771952] |
| NM_000389 |
| <i>Homo sapiens</i> cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 1, mRNA
gi 17978496 ref NM_000389.2 [17978496] |
| NM_078467 |
| <i>Homo sapiens</i> cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 2, mRNA
gi 17978494 ref NM_078467.1 [17978494] |
| NM_000384 |
| <i>Homo sapiens</i> apolipoprotein B (including Ag(x) antigen) (APOB), mRNA
gi 105990531 ref NM_000384.2 [105990531] |
| NM_002746 |
| <i>Homo sapiens</i> mitogen-activated protein kinase 3 (MAPK3), transcript variant 1, mRNA
gi 91718898 ref NM_002746.2 [91718898] |
| NM_001040056 |
| <i>Homo sapiens</i> mitogen-activated protein kinase 3 (MAPK3), transcript variant 2, mRNA
gi 91718896 ref NM_001040056.1 [91718896] |
| NM_138957 |
| <i>Homo sapiens</i> mitogen-activated protein kinase 1 (MAPK1), transcript variant 2, mRNA
gi 75709179 ref NM_138957.2 [75709179] |
| NM_002745 |
| <i>Homo sapiens</i> mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, mRNA
gi 75709178 ref NM_002745.41 [75709178] |
| NM_001005291 |
| <i>Homo sapiens</i> sterol regulatory element binding transcription factor 1 (SREBF1), transcript variant 1, mRNA
gi 52630418 ref NM_001005291.1 [52630418] |
| NM_004176 |
| <i>Homo sapiens</i> sterol regulatory element binding transcription factor 1 (SREBF1), transcript variant 2, mRNA
gi 52630417 ref NM_004176.31 [52630417] |
| NM_005896 |
| <i>Homo sapiens</i> isocitrate dehydrogenase 1 (NADP+), soluble (IDH1), mRNA
gi 28178824 ref NM_005896.21 [28178824] |
| NM_004599 |
| <i>Homo sapiens</i> sterol regulatory element binding transcription factor 2 (SREBF2), mRNA
gi 27477112 ref NM_004599.2 [27477112] |

TABLE I-continued

| PCSK9 Accession Numbers | |
|--|--|
| 1AM9H | |
| Chain H, Human Srebp-1a Bound To Ldl Receptor Promoter | |
| gi 3318717 pdb 1AM9 H [3318717] | |
| 1AM9G | |
| Chain G, Human Srebp-1a Bound To Ldl Receptor Promoter | |
| gi 3318716 pdb 1AM9 G [3318716] | |
| 1AM9F | |
| Chain F, Human Srebp-1a Bound To Ldl Receptor Promoter | |
| gi 3318715 pdb 1AM9 F [3318715] | |
| 1AM9E | |
| Chain E, Human Srebp-1a Bound To Ldl Receptor Promoter | |
| gi 3318714 pdb 1AM9 E [3318714] | |

TABLE II

| PCSK9 siNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | |
|---|-----------------------|------|-----------|-----------------------|------|-----------|-----------------------|
| Pos | Seq | Seq | Seq | Seq | Seq | Seq | Seq |
| | ID | UPos | Upper seq | ID | LPos | Lower seq | ID |
| 3 | GCGACGU CGAGGCGCUAU | 1 | 3 | GCGACGU CGAGGCGCUAU | 1 | 21 | AUGAGGCCUCGACGUCGC |
| 21 | UGGUUGCAGGCGGGCGCG | 2 | 21 | UGGUUGCAGGCGGGCGCG | 2 | 39 | CGCGCCCGCCUGCAACCCA |
| 39 | GCCGUUCAGUU CAGGGUCU | 3 | 39 | GCCGUUCAGUU CAGGGUCU | 3 | 57 | AGACCCUGAACUGAACGGC |
| 57 | UGAGCCUGGAGGAGUGAGC | 4 | 57 | UGAGCCUGGAGGAGUGAGC | 4 | 75 | GCUCACUCCUCCAGGCUCU |
| 75 | CCAGGCAGUGAGACUGGU | 5 | 75 | CCAGGCAGUGAGACUGGU | 5 | 93 | AGCCAGUCUCACUGCCUGG |
| 93 | UCGGGC GGGCCGGGACGCG | 6 | 93 | UCGGGC GGGCCGGGACGCG | 6 | 111 | CGCGUCCC GGGCCGCCCCGA |
| 111 | GUCCGUU UGCAGCAGCGGCU | 7 | 111 | GUCCGUU UGCAGCAGCGGCU | 7 | 129 | GAGCCG CUGCUUGCAACGAC |
| 129 | CCCAGCU CCCAGCCAGGAU | 8 | 129 | CCCAGCU CCCAGCCAGGAU | 8 | 147 | AUCCUGGCUGGGAGCUGGG |
| 147 | UUCCGCGCGCCCCUUCACG | 9 | 147 | UUCCGCGCGCCCCUUCACG | 9 | 165 | CGUGAAGGGCGCGCGAA |
| 165 | GCGCCCUGCUCCUGAACUU | 10 | 165 | GCGCCCUGCUCCUGAACUU | 10 | 183 | AAGUUUCAGGAGCAGGGCGC |
| 183 | UCAGCUCCUGCACAGUCCU | 11 | 183 | UCAGCUCCUGCACAGUCCU | 11 | 201 | AGGACUGUGCAGGAGCUGA |
| 201 | UCCCCACCGCAAGGCUAA | 12 | 201 | UCCCCACCGCAAGGCUAA | 12 | 219 | UUGAGCCUUGCGGUGGGGA |
| 219 | AGGCGCCGCCGGCGUGGAC | 13 | 219 | AGGCGCCGCCGGCGUGGAC | 13 | 237 | GUCCACGCCGGCGGCCU |
| 237 | CCGCGCACGGCCUCUAGGU | 14 | 237 | CCGCGCACGGCCUCUAGGU | 14 | 255 | ACCUAGAGGCCUGCGCGCG |
| 255 | UCUCCUCGCCAGGACAGCA | 15 | 255 | UCUCCUCGCCAGGACAGCA | 15 | 273 | UGCUGUCCUGCGAGGAGA |
| 273 | AACCUCUCCCCUUGGCCUC | 16 | 273 | AACCUCUCCCCUUGGCCUC | 16 | 291 | GAGGGCCAGGGAGAGGUU |
| 291 | CAUGGGCACCGUCAGCUCC | 17 | 291 | CAUGGGCACCGUCAGCUCC | 17 | 309 | GGAGCUGACGGUGGCCAUG |
| 309 | CAGGCGGUCCUGGUGGCCG | 18 | 309 | CAGGCGGUCCUGGUGGCCG | 18 | 327 | CGGCCACCAGGACCGCCUG |
| 327 | GCUGCCACUGCUGCUGCUG | 19 | 327 | GCUGCCACUGCUGCUGCUG | 19 | 345 | CAGCAGCAGCAGUGGCAGC |
| 345 | GCUGCUGCUGCUCCUGGU | 20 | 345 | GCUGCUGCUGCUCCUGGU | 20 | 363 | ACCCAGGAGCAGCAGCAGC |
| 363 | UCCCGCGGGCGCCCGUGCG | 21 | 363 | UCCCGCGGGCGCCCGUGCG | 21 | 381 | CGCACGGCGCCCGCGGGA |
| 381 | GCAGGAGGAGCAGGGACGGC | 22 | 381 | GCAGGAGGAGCAGGGACGGC | 22 | 399 | GCCGUCCUCGUCCUCCUGC |
| 399 | CGACUACGAGGAGCUGGUG | 23 | 399 | CGACUACGAGGAGCUGGUG | 23 | 417 | CACCAGCUCCUCGUAGUCG |
| 417 | GCUAGCCUUGCGUUCGAG | 24 | 417 | GCUAGCCUUGCGUUCGAG | 24 | 435 | CUCGGAACGCAAGGCUAGC |

TABLE II-continued

| PCSK9 siRNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | |
|--|----------------------|------|--------------------------|-----|---------------------------|-----------|-----|
| Pos | Seq | Seq | Seq | Seq | Seq | Seq | Seq |
| | ID | UPos | Upper seq | ID | LPos | Lower seq | ID |
| 435 | GGAGGACGGCCUGGCCGAA | 25 | 435 GGAGGACGGCCUGGCCGAA | 25 | 453 UUCGGCCAGGCCGUCCUCC | 257 | |
| 453 | AGCACCCGAGCACGGAAC | 26 | 453 AGCACCCGAGCACGGAAC | 26 | 471 GGUUCCGUGCUCGGGUGCU | 258 | |
| 471 | CACAGCCACCUUCCACCAC | 27 | 471 CACAGCCACCUUCCACCAC | 27 | 489 GC GGUGGAAGGUGGGCUGUG | 259 | |
| 489 | CUGCGCCAAGGAUCCGUGG | 28 | 489 CUGCGCCAAGGAUCCGUGG | 28 | 507 CCACGGAUCCUUGGCGCAG | 260 | |
| 507 | GAGGUUGCCUGGCACCUAC | 29 | 507 GAGGUUGCCUGGCACCUAC | 29 | 525 GUAGGUGCCAGGCAACCUC | 261 | |
| 525 | CGUGGUGGUGCUGAAGGAG | 30 | 525 CGUGGUGGUGCUGAAGGAG | 30 | 543 CUCCUUCAGCACCACACG | 262 | |
| 543 | GGAGACCCACCUCUCGAG | 31 | 543 GGAGACCCACCUCUCGAG | 31 | 561 CUGCGAGAGGUGGGUCUCC | 263 | |
| 561 | GUCAGAGCGCACUGCCCG | 32 | 561 GUCAGAGCGCACUGCCCG | 32 | 579 GCGGGCAGUGCGCUCUGAC | 264 | |
| 579 | CCGCCUGCCAGGCCAGGU | 33 | 579 CCGCCUGCCAGGCCAGGU | 33 | 597 AGCCUGGGCCUGCAGCGG | 265 | |
| 597 | UGCCCCCGGGGAUACCUC | 34 | 597 UGCCCCGGGGGAUACCUC | 34 | 615 GAGGUAIUCCCCGGGGCA | 266 | |
| 615 | CACCAAGAUCCUGCAUGUC | 35 | 615 CACCAAGAUCCUGCAUGUC | 35 | 633 GACAUGCAGGAUUCUGUG | 267 | |
| 633 | CUUCCAUGGCCUUUCUCCU | 36 | 633 CUUCCAUGGCCUUUCUCCU | 36 | 651 AGGAAGAAGGCCAUGGAAG | 268 | |
| 651 | UGGCUUUCCUGGUGAAGAUG | 37 | 651 UGGCUUCCUGGUGAAGAUG | 37 | 669 CAUCUUCACCAGGAAGCCA | 269 | |
| 669 | GAGUGGCGACCUGCUGGAG | 38 | 669 GAGUGGCGACCUGCUGGAG | 38 | 687 CUCCAGCAGGUCGCCACUC | 270 | |
| 687 | GCUGGCCUUUGAAGUUGCC | 39 | 687 GCUGGCCUUUGAAGUUGCC | 39 | 705 GGGCAACUUCAAGGCCAGC | 271 | |
| 705 | CCAUGUCGACUACUCGAG | 40 | 705 CCAUGUCGACUACUCGAG | 40 | 723 CUCGAUGUAGUCGACAUGG | 272 | |
| 723 | GGAGGACUCCUCUGCUUU | 41 | 723 GGAGGACUCCUCUGCUUU | 41 | 741 AAAGACAGAGGAGUCCUCC | 273 | |
| 741 | UGCCCCAGAGCAUCCCGUGG | 42 | 741 UGCCCCAGAGCAUCCCGUGG | 42 | 759 CCACGGGAUGCUCUGGGCA | 274 | |
| 759 | GAACCUGGAGCGGAUUAACC | 43 | 759 GAACCUGGAGCGGAUUAACC | 43 | 777 GGUAAUCCGCUCCAGGUUC | 275 | |
| 777 | CCCUCCACGGUACCGGGCG | 44 | 777 CCCUCCACGGUACCGGGCG | 44 | 795 CGCCCGGUACCGUGGGAGGG | 276 | |
| 795 | GGAUGAAUACCAGCCCCCCC | 45 | 795 GGAUGAAUACCAGCCCCCCC | 45 | 813 GGGGGCGUGGUAAUCAUCC | 277 | |
| 813 | CGACGGAGGCAGCCUGGUG | 46 | 813 CGACGGAGGCAGCCUGGUG | 46 | 831 CACCAGGCUGCCUCCGUCG | 278 | |
| 831 | GGAGGUGUAUCUCCUAGAC | 47 | 831 GGAGGUGUAUCUCCUAGAC | 47 | 849 GUCUAGGAGAUACACCUCC | 279 | |
| 849 | CACCAGCAUACAGAGUGAC | 48 | 849 CACCAGCAUACAGAGUGAC | 48 | 867 GUCACUCUGUAUGCUGGUG | 280 | |
| 867 | CCACCGGGAAAUCGAGGGC | 49 | 867 CCACCGGGAAAUCGAGGGC | 49 | 885 GCCCUCGAUUUCCCGGUGG | 281 | |
| 885 | CAGGGUCAUGGUACCGAC | 50 | 885 CAGGGUCAUGGUACCGAC | 50 | 903 GUCGGUGACCAUGACCCUG | 282 | |
| 903 | CUUCGAGAAUGUGCCCGAG | 51 | 903 CUUCGAGAAUGUGCCCGAG | 51 | 921 CUCGGGCACAUUCUCGAG | 283 | |
| 921 | GGAGGACGGGACCCGCUUC | 52 | 921 GGAGGACGGGACCCGCUUC | 52 | 939 GAAGCGGGUCCCGUCCUCC | 284 | |
| 939 | CCACAGACAGGCCAGCAAG | 53 | 939 CCACAGACAGGCCAGCAAG | 53 | 957 CUUGCUGGCCUGUCUGGG | 285 | |
| 957 | GUGUGACAGUCAUGGCACC | 54 | 957 GUGUGACAGUCAUGGCACC | 54 | 975 GGUGCCAUGACUGUCACAC | 286 | |
| 975 | CCACCUGGCAGGGUGGUCC | 55 | 975 CCACCUGGCAGGGUGGUCC | 55 | 993 GACCACCCUGCCAGGUGG | 287 | |
| 993 | CAGCGGCCGGGAUGCCGGC | 56 | 993 CAGCGGCCGGGAUGCCGGC | 56 | 1011 GCCGGCAUCCCGGCCUG | 288 | |
| 1011 | CGUGGCCAAGGGUGCCAGC | 57 | 1011 CGUGGCCAAGGGUGCCAGC | 57 | 1029 GCUGGCACCCUUGGCCACG | 289 | |
| 1029 | CAUGCGCAGCCUGCGCGUG | 58 | 1029 CAUGCGCAGCCUGCGCGUG | 58 | 1047 CACGCGCAGGCUGCGCAUG | 290 | |
| 1047 | GCUAACUGCCAAGGGAAG | 59 | 1047 GCUAACUGCCAAGGGAAG | 59 | 1065 CUUCCUUGGCAGUUGAGC | 291 | |

TABLE II-continued

| PCSK9 siRNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | | | | | |
|--|----------------------|------|---------------------------|-----|---------------------------|-----------|----|--|--|--|--|
| Pos | Seq | Seq | Seq | Seq | | | | | | | |
| | ID | UPos | Upper seq | ID | LPos | Lower seq | ID | | | | |
| 1065 | GGGCACGUUAGCGGCACC | 60 | 1065 GGGCACGUUAGCGGCACC | 60 | 1083 GGUGCCGCUAACCGUGCCC | 292 | | | | | |
| 1083 | CCUCAUAGGCCUGGAGUUU | 61 | 1083 CCUCAUAGGCCUGGAGUUU | 61 | 1101 AAACUCCAGGCCUAUGAGG | 293 | | | | | |
| 1101 | UAUUCGGAAAAGCCAGCUG | 62 | 1101 UAUUCGGAAAAGCCAGCUG | 62 | 1119 CAGCUGGCCUUUUCGAAUA | 294 | | | | | |
| 1119 | GGUCCAGCCUGGGGGCCA | 63 | 1119 GGUCCAGCCUGGGGGCCA | 63 | 1137 UGGCCCCACAGGCUGGACC | 295 | | | | | |
| 1137 | ACUGGUGGUGCUGCUGCCC | 64 | 1137 ACUGGUGGUGCUGCUGCCC | 64 | 1155 GGGCAGCAGCACCACAGU | 296 | | | | | |
| 1155 | CCUGGCGGGUGGGUACAGC | 65 | 1155 CCUGGCGGGUGGGUACAGC | 65 | 1173 GCUGUACCCACCCGCCAGG | 297 | | | | | |
| 1173 | CCCGCUCUCAACGCCGCC | 66 | 1173 CCCGUCCUCAACGCCGCC | 66 | 1191 GGCGGCGUUGAGGACGCCGG | 298 | | | | | |
| 1191 | CUGCCAGCGCCUGGCGAGG | 67 | 1191 CUGCCAGCGCCUGGCGAGG | 67 | 1209 CCUCGCCAGGCGCUGGCAG | 299 | | | | | |
| 1209 | GGCUGGGGUCGUGCUGGUC | 68 | 1209 GGCUGGGGUCGUGCUGGUC | 68 | 1227 GACCAGCACGACCCAGCC | 300 | | | | | |
| 1227 | CACCGCUCCCGGCAACUUC | 69 | 1227 CACCGCUCCCGGCAACUUC | 69 | 1245 GAAGUUGCCGGCAGCGGUG | 301 | | | | | |
| 1245 | CCGGGACGAUGCCUGCCUC | 70 | 1245 CCGGGACGAUGCCUGCCUC | 70 | 1263 GAGGCAGGCAUCGUCCCCG | 302 | | | | | |
| 1263 | CUACUCCCCAGCCUCAGCU | 71 | 1263 CUACUCCCCAGCCUCAGCU | 71 | 1281 AGCUGAGGCUGGGGAGUAG | 303 | | | | | |
| 1281 | UCCCGAGGUCAUCACAGUU | 72 | 1281 UCCCGAGGUCAUCACAGUU | 72 | 1299 AACUGUGAUGACCUCGGGA | 304 | | | | | |
| 1299 | UGGGGCCACCAAUGCCAA | 73 | 1299 UGGGGCCACCAAUGCCAA | 73 | 1317 UGGGGCAUUGGUGGGCCCA | 305 | | | | | |
| 1317 | AGACCAGCCGGUGACCCUG | 74 | 1317 AGACCAGCCGGUGACCCUG | 74 | 1335 CAGGGUCACCCGGCUGGU | 306 | | | | | |
| 1335 | GGGGACUUUUGGGGACCAAC | 75 | 1335 GGGGACUUUUGGGGACCAAC | 75 | 1353 GUUGGUCCCCAAAGUCCCC | 307 | | | | | |
| 1353 | CUUUGGCCGUCUGUGGGAC | 76 | 1353 CUUUGGCCGUCUGUGGGAC | 76 | 1371 GUCCACACAGCGGCCAAAG | 308 | | | | | |
| 1371 | CCUCUUUUGCCCCAGGGAG | 77 | 1371 CCUCUUUUGCCCCAGGGAG | 77 | 1389 CUCCCCUUGGGCAAAGAGG | 309 | | | | | |
| 1389 | GGACAUCAUUGGUGCCUC | 78 | 1389 GGACAUCAUUGGUGCCUC | 78 | 1407 GGAGGCACCAAUGAUUCC | 310 | | | | | |
| 1407 | CAGCGACUGCAGCACCUUC | 79 | 1407 CAGCGACUGCAGCACCUUC | 79 | 1425 GCAGGUGCUGCAGUCGCUG | 311 | | | | | |
| 1425 | CUUUGUGUCACAGAGUGGG | 80 | 1425 CUUUGUGUCACAGAGUGGG | 80 | 1443 CCCACUCUGUGACACAAAG | 312 | | | | | |
| 1443 | GACAUCACAGGCUGCUGGCC | 81 | 1443 GACAUCACAGGCUGCUGGCC | 81 | 1461 GGCAGCAGCCUGUGAUGUC | 313 | | | | | |
| 1461 | CCACGUGGCUGGCAUUGCA | 82 | 1461 CCACGUGGCUGGCAUUGCA | 82 | 1479 UGCAAUGCCAGCCACGU | 314 | | | | | |
| 1479 | AGCCAUGAUGCUGUCUGCC | 83 | 1479 AGCCAUGAUGCUGUCUGCC | 83 | 1497 GGCAGACAGCAUCAUGGU | 315 | | | | | |
| 1497 | CGAGCCGGAGCUCACCCUG | 84 | 1497 CGAGCCGGAGCUCACCCUG | 84 | 1515 CAGGGUGAGCUCCGGCUCG | 316 | | | | | |
| 1515 | GGCCGAGUUGAGGCAGAGA | 85 | 1515 GGCCGAGUUGAGGCAGAGA | 85 | 1533 UCUCUGCCUCAACUCGGCC | 317 | | | | | |
| 1533 | ACUGAUCCACUUUCUCUGCC | 86 | 1533 ACUGAUCCACUUUCUCUGCC | 86 | 1551 GGCAGAGAAGUGGAUCAGU | 318 | | | | | |
| 1551 | CAAAGAUGUCAUCAAUGAG | 87 | 1551 CAAAGAUGUCAUCAAUGAG | 87 | 1569 CUCAUUGAUGACAUCUUUG | 319 | | | | | |
| 1569 | GGCCUGGUUCCCCUGAGGAC | 88 | 1569 GGCCUGGUUCCCCUGAGGAC | 88 | 1587 GUCCUCAGGGAACCCAGGCC | 320 | | | | | |
| 1587 | CCAGCGGGUACUGACCCCC | 89 | 1587 CCAGCGGGUACUGACCCCC | 89 | 1605 GGGGGUCAGUACCCCGCUGG | 321 | | | | | |
| 1605 | CAACCUGGUGGCCGCCUG | 90 | 1605 CAACCUGGUGGCCGCCUG | 90 | 1623 CAGGGCGGCCACCCAGGUUG | 322 | | | | | |
| 1623 | GCCCCCCCAGCACCAUGGG | 91 | 1623 GCCCCCCCAGCACCAUGGG | 91 | 1641 CCCAUGGGUGCUGGGGGC | 323 | | | | | |
| 1641 | GGCAGGUUGGCAGCUGUUU | 92 | 1641 GGCAGGUUGGCAGCUGUUU | 92 | 1659 AACAGCUGCCAACCUUGCC | 324 | | | | | |
| 1659 | UUGCAGGACUGUAUGGUCA | 93 | 1659 UUGCAGGACUGUAUGGUCA | 93 | 1677 UGACCAUACAGUCCUGCAA | 325 | | | | | |
| 1677 | AGCACACUCGGGGCUACA | 94 | 1677 AGCACACUCGGGGCUACA | 94 | 1695 UGUAGGCCCCAGUGUGCU | 326 | | | | | |

TABLE II-continued

| PCSK9 siRNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | |
|--|-----------------------|------|-----------|-----------------------|------|-----------|--------------------------|
| Pos | Seq | Seq | Seq | Seq | Seq | Seq | ID |
| | ID | UPos | Upper seq | ID | LPos | Lower seq | ID |
| 1695 | ACGGAUGGCCACAGCCGUC | 95 | 1695 | ACGGAUGGCCACAGCCGUC | 95 | 1713 | GACGGCUGUGGCCAUCCGU 327 |
| 1713 | CGCCCCGUGCGCCCCAGAU | 96 | 1713 | CGCCCCGUGCGCCCCAGAU | 96 | 1731 | AUCUGGGGCGCAGCGGGCG 328 |
| 1731 | UGAGGGAGCUGCUGAGCUGC | 97 | 1731 | UGAGGGAGCUGCUGAGCUGC | 97 | 1749 | GCAGCUCAGCAGCUCCUCA 329 |
| 1749 | CUCCAGUUUCUCCAGGAGU | 98 | 1749 | CUCCAGUUUCUCCAGGAGU | 98 | 1767 | ACUCCUGGAGAACUGGAG 330 |
| 1767 | UGGGAAGCGGGCGGGCGAG | 99 | 1767 | UGGGAAGCGGGCGGGCGAG | 99 | 1785 | CUCGCCCGCCGUUCCCA 331 |
| 1785 | GCGCAUGGAGGCCAAGGG | 100 | 1785 | GCGCAUGGAGGCCAAGGG | 100 | 1803 | CCCUUUGGCCUCCAUGCGC 332 |
| 1803 | GGGCAAGCUGGUUCUGCCGG | 101 | 1803 | GGGCAAGCUGGUUCUGCCGG | 101 | 1821 | CCGGCAGACCAGCUUGGCC 333 |
| 1821 | GGCCCACAAACGCUUUUUGGG | 102 | 1821 | GGCCCACAAACGCUUUUUGGG | 102 | 1839 | CCCAAAAGCGUUGUGGGCC 334 |
| 1839 | GGGUGAGGGUGUCUACGCC | 103 | 1839 | GGGUGAGGGUGUCUACGCC | 103 | 1857 | GGCGUAGACACCCUCACCC 335 |
| 1857 | CAUUGCCAGGUGCUGCCUG | 104 | 1857 | CAUUGCCAGGUGCUGCCUG | 104 | 1875 | CAGGCAGCACCUCCGAAUG 336 |
| 1875 | GCUACCCCAGGCCAACUGC | 105 | 1875 | GCUACCCCAGGCCAACUGC | 105 | 1893 | GCAGUUGGCCUUGGGUAGC 337 |
| 1893 | CAGCGUCCACACAGCUCCA | 106 | 1893 | CAGCGUCCACACAGCUCCA | 106 | 1911 | UGGAGCUGUGUGGACGCUG 338 |
| 1911 | ACCAGCUGAGGCCAGCAUG | 107 | 1911 | ACCAGCUGAGGCCAGCAUG | 107 | 1929 | CAUGCUGGCCUAGCUGGU 339 |
| 1929 | GGGGACCCGUGUCCACUGC | 108 | 1929 | GGGGACCCGUGUCCACUGC | 108 | 1947 | GCAGUGGACACGGGUCCCC 340 |
| 1947 | CCACCAAACAGGCCACGUC | 109 | 1947 | CCACCAAACAGGCCACGUC | 109 | 1965 | GACGUGGCCUUGGGUGG 341 |
| 1965 | CCUCACAGGCUGCAGCUCC | 110 | 1965 | CCUCACAGGCUGCAGCUCC | 110 | 1983 | GGAGCUGCAGCCUGUGAGG 342 |
| 1983 | CCACUGGGAGGUGGAGGAC | 111 | 1983 | CCACUGGGAGGUGGAGGAC | 111 | 2001 | GUCCUCCACCUCCAGUGG 343 |
| 2001 | CCUUGGCACCCACAAGCCG | 112 | 2001 | CCUUGGCACCCACAAGCCG | 112 | 2019 | CGGCUUGUGGGUGCCAAGG 344 |
| 2019 | GCCUGUGCUGAGGCCACGA | 113 | 2019 | GCCUGUGCUGAGGCCACGA | 113 | 2037 | UCGUGGCCUAGCACAGGC 345 |
| 2037 | AGGUCAGCCAACAGUGC | 114 | 2037 | AGGUCAGCCAACAGUGC | 114 | 2055 | GCACUGGUUGGGCUGACCU 346 |
| 2055 | CGUGGGCCACAGGGAGGCC | 115 | 2055 | CGUGGGCCACAGGGAGGCC | 115 | 2073 | GGCCUCCUGUGGCCACG 347 |
| 2073 | CAGCAUCCACGCUUCCUGC | 116 | 2073 | CAGCAUCCACGCUUCCUGC | 116 | 2091 | GCAGGAAGCGUGGAUGCUG 348 |
| 2091 | CUGCCAUGCCCCAGGUCUG | 117 | 2091 | CUGCCAUGCCCCAGGUCUG | 117 | 2109 | CAGACCUGGGCAUGGCAG 349 |
| 2109 | GGAAUGCAAAGUCAAGGAG | 118 | 2109 | GGAAUGCAAAGUCAAGGAG | 118 | 2127 | CUCCUUGACUUUGCAUCC 350 |
| 2127 | GCAUGGAAUCCCGGCCCCU | 119 | 2127 | GCAUGGAAUCCCGGCCCCU | 119 | 2145 | AGGGGCCGGGAUCCAUGC 351 |
| 2145 | UCAGGAGCAGGUGACCGUG | 120 | 2145 | UCAGGAGCAGGUGACCGUG | 120 | 2163 | CACGGUCACCUUCUCCUGA 352 |
| 2163 | GGCCUGCGAGGAGGGCUGG | 121 | 2163 | GGCCUGCGAGGAGGGCUGG | 121 | 2181 | CCAGCCCUCCUCGCAGGCC 353 |
| 2181 | GACCCUGACUGGCUGCAGU | 122 | 2181 | GACCCUGACUGGCUGCAGU | 122 | 2199 | ACUGCAGCCAGUCAGGGUC 354 |
| 2199 | UGCCCUCCUGGGACCUCC | 123 | 2199 | UGCCCUCCUGGGACCUCC | 123 | 2217 | GGAGGUCCCAAGGGAGGGCA 355 |
| 2217 | CCACGUCCUGGGGCCUAC | 124 | 2217 | CCACGUCCUGGGGCCUAC | 124 | 2235 | GUAGGCCCCCAGGACGUGG 356 |
| 2235 | CGCCGUAGACAACACGUGU | 125 | 2235 | CGCCGUAGACAACACGUGU | 125 | 2253 | ACACGUGUUGCUACGGCG 357 |
| 2253 | UGUAGUCAGGAGCCGGGAC | 126 | 2253 | UGUAGUCAGGAGCCGGGAC | 126 | 2271 | GUCCCGGUCCUGACUACA 358 |
| 2271 | CGUCAGCACUACAGGCAGC | 127 | 2271 | CGUCAGCACUACAGGCAGC | 127 | 2289 | GCUGCCUGUAGUGCUGACG 359 |
| 2289 | CACCAGCGAAGGGCCGUG | 128 | 2289 | CACCAGCGAAGGGCCGUG | 128 | 2307 | CACGGCCCCUUCGCUGGUG 360 |
| 2307 | GACAGCCGUUGCCAUCUGC | 129 | 2307 | GACAGCCGUUGCCAUCUGC | 129 | 2325 | GCAGAUGGCAACGGCUGUC 361 |

TABLE II-continued

| PCSK9 siRNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | | |
|--|----------------------|--------|-----------|----------------------|--------|-----------|----------------------|-----|
| Pos | Seq | Seq | Seq | Seq | Seq | Seq | ID | |
| | ID | UPos | Upper seq | ID | LPos | Lower seq | ID | |
| 2325 | CUGCCGGAGCCGGCACCUUG | 130 | 2325 | CUGCCGGAGCCGGCACCUUG | 130 | 2343 | CAGGUGCCGGCUCCGGCAG | 362 |
| 2343 | GCGCAGGCCUCCCAGGAG | 131 | 2343 | GGCGCAGGCCUCCCAGGAG | 131 | 2361 | CUCCUGGGAGGCCUGCGCC | 363 |
| 2361 | GCUCCAGUGACAGCCCCAU | 132 | 2361 | GCUCCAGUGACAGCCCCAU | 132 | 2379 | AUGGGGCUGUCACUGGAGC | 364 |
| 2379 | UCCCAGGAUGGGUGUCUGG | 133 | 2379 | UCCCAGGAUGGGUGUCUGG | 133 | 2397 | CCAGACACCCAUCUCUGGGA | 365 |
| 2397 | GGGAGGGUCAAGGGCUGGG | 134 | 2397 | GGGAGGGUCAAGGGCUGGG | 134 | 2415 | CCCAGCCUUGACCCUCCC | 366 |
| 2415 | GGCUGAGCUUUAAAUGGU | 135 | 2415 | GGCUGAGCUUUAAAUGGU | 135 | 2433 | ACCAUUUUAAAGCUCAGCC | 367 |
| 2433 | UUCCGACUUGGUCCUCU | 136 | 2433 | UUCCGACUUGGUCCUCU | 136 | 2451 | AGAGAGGGACAAGUCGGAA | 368 |
| 2451 | UCAGCCCUCCAUGGCCUGG | 137 | 2451 | UCAGCCCUCCAUGGCCUGG | 137 | 2469 | CCAGGCCAUGGAGGGCUGA | 369 |
| 2469 | GCACGAGGGGAUGGGGAUG | 138 | 2469 | GCACGAGGGGAUGGGGAUG | 138 | 2487 | CAUCCCCAUCCCCUCGUGC | 370 |
| 2487 | GCUUCCCCUUUCCGGGGC | 139 | 2487 | GCUUCCCCUUUCCGGGGC | 139 | 2505 | GCCCCGAAAGGCCGAAGC | 371 |
| 2505 | CUGCUGGCCUGGCCUUGA | 140 | 2505 | CUGCUGGCCUGGCCUUGA | 140 | 2523 | UCAAGGGCCAGGCCAGCAG | 372 |
| 2523 | AGUGGGGCAGCCUCCU | UGC141 | 2523 | AGUGGGGCAGCCUCCU | UGC141 | 2541 | GCAAGGAGGCUGCCCCACU | 373 |
| 2541 | CCUGGAACUCACUCACU | 142 | 2541 | CCUGGAACUCACUCACU | 142 | 2559 | AGAGUGAGUGAGUUCCAGG | 374 |
| 2559 | UGGGUGCCUCCUCCCCAGG | 143 | 2559 | UGGGUGCCUCCUCCCCAGG | 143 | 2577 | CCUGGGAGGAGGACCCCA | 375 |
| 2577 | GUGGAGGUGCCAGGAAGCU | 144 | 2577 | GUGGAGGUGCCAGGAAGCU | 144 | 2595 | AGCUUCCUGGCACCUCAC | 376 |
| 2595 | UCCCUCCCUCACUGUGGGG | 145 | 2595 | UCCCUCCCUCACUGUGGGG | 145 | 2613 | CCCCACAGUGAGGGAGGGA | 377 |
| 2613 | GCAUUUCACCAUCAAACA | 146 | 2613 | GCAUUUCACCAUCAAACA | 146 | 2631 | UGUUUGAAUGGUGAAUGC | 378 |
| 2631 | AGGUCGAGCUGUGCUCGGG | 147 | 2631 | AGGUCGAGCUGUGCUCGGG | 147 | 2649 | CCCGAGCACAGCUCGACCU | 379 |
| 2649 | GUGCUGCCAGCUGCUCCCA | 148 | 2649 | GUGCUGCCAGCUGCUCCCA | 148 | 2667 | UGGGAGCAGCUGGCAGCAC | 380 |
| 2667 | AAUGUGCCGAUGUCCGUGG | 149 | 2667 | AAUGUGCCGAUGUCCGUGG | 149 | 2685 | CCACGGACAUCCGACAUU | 381 |
| 2685 | GGCAGAAUGACUUUUUAUG | 150 | 2685 | GGCAGAAUGACUUUUUAUG | 150 | 2703 | CAAUAAAAGUCAUUCUGCC | 382 |
| 2703 | GAGCUCUUGUUCCGUGCCA | 151 | 2703 | GAGCUCUUGUUCCGUGCCA | 151 | 2721 | UGGCACGGAACAAGAGCUC | 383 |
| 2721 | AGGCAUUCAUCCUCAGGU | 152 | 2721 | AGGCAUUCAUCCUCAGGU | 152 | 2739 | ACCUGAGGAUUGAAUGGCC | 384 |
| 2739 | UCUCCACCAAGGAGGCAGG | 153 | 2739 | UCUCCACCAAGGAGGCAGG | 153 | 2757 | CCUGCCUCCUUGGUGGAGA | 385 |
| 2757 | GAUUCUCCCCAUGGAUAGG | 154 | 2757 | GAUUCUCCCCAUGGAUAGG | 154 | 2775 | CCUUAUCCAUGGGAAGAAC | 386 |
| 2775 | GGGAGGGGGCGGUAGGGC | 155 | 2775 | GGGAGGGGGCGGUAGGGC | 155 | 2793 | GCCCCUACCGCCCCCUCCC | 387 |
| 2793 | CUGCAGGGACAAACAUCGU | 156 | 2793 | CUGCAGGGACAAACAUCGU | 156 | 2811 | ACGAUGUUUGUCCUCAGC | 388 |
| 2811 | UUGGGGGGUGAGUGUGAAA | 157 | 2811 | UUGGGGGGUGAGUGUGAAA | 157 | 2829 | UUUCACACUACCCCCCAA | 389 |
| 2829 | AGGUGCUGAUGGCCCUAU | 158 | 2829 | AGGUGCUGAUGGCCCUAU | 158 | 2847 | AUGAGGGCCAUAGCACC | 390 |
| 2847 | UCUCCAGCUAACUGUGGAG | 159 | 2847 | UCUCCAGCUAACUGUGGAG | 159 | 2865 | CUCCACAGUUAGCUGGAGA | 391 |
| 2865 | GAAGCCCCUGGGGGCUCCC | 160 | 2865 | GAAGCCCCUGGGGGCUCCC | 160 | 2883 | GGGAGCCCCAGGGGCUUC | 392 |
| 2883 | CUGAUAAAUGGAGGCUUAG | 161 | 2883 | CUGAUAAAUGGAGGCUUAG | 161 | 2901 | CUAAGCCUCCAUAAAUCAG | 393 |
| 2901 | GCUUUCUGGAUGGCAUCUA | 162 | 2901 | GCUUUCUGGAUGGCAUCUA | 162 | 2919 | UAGAUGCCAUCAGAAAGC | 394 |
| 2919 | AGCCAGAGGCUGGAGACAG | 163 | 2919 | AGCCAGAGGCUGGAGACAG | 163 | 2937 | CUGUCUCCAGCCUCUGGU | 395 |
| 2937 | GGUGCGCCCCUGGGGUCA | 164 | 2937 | GGUGCGCCCCUGGGGUCA | 164 | 2955 | UGACCACCAGGGCGCACC | 396 |

TABLE II-continued

| PCSK9 siRNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | |
|--|----------------------|------|---------------------------|-----|---------------------------|-----------|----|
| Pos | Seq | Seq | Seq | Seq | Seq | Seq | ID |
| | ID | UPos | Upper seq | ID | LPos | Lower seq | ID |
| 2955 | ACAGGCUGUGCCUUGGUUU | 165 | 2955 ACAGGCUGUGCCUUGGUUU | 165 | 2973 AAACCAAGGCACAGCCUGU | 397 | |
| 2973 | UCCUGAGCCACCUUUACUC | 166 | 2973 UCCUGAGCCACCUUUACUC | 166 | 2991 GAGUAAAGGUUGGCUAGGA | 398 | |
| 2991 | CUGCUCUAUGCAGGCUGU | 167 | 2991 CUGCUCUAUGCAGGCUGU | 167 | 3009 ACAGCCUGGCAUAGAGCAG | 399 | |
| 3009 | UGCUAGCAACACCCAAAGG | 168 | 3009 UGCUAGCAACACCCAAAGG | 168 | 3027 CCUUUGGGUGUUGCUAGCA | 400 | |
| 3027 | GUGGCCUGCGGGGAGCCAU | 169 | 3027 GUGGCCUGCGGGGAGCCAU | 169 | 3045 AUGGCUCCCCGCAGGCCAC | 401 | |
| 3045 | UCACCUAGGACUGACUCGG | 170 | 3045 UCACCUAGGACUGACUCGG | 170 | 3063 CCGAGUCAGGUCCUAGGUGA | 402 | |
| 3063 | GCAGUGUGCAGUGGUGCAU | 171 | 3063 GCAGUGUGCAGUGGUGCAU | 171 | 3081 AUGCACACUGCACACUGC | 403 | |
| 3081 | UGCACUGUCUCAGCCAACC | 172 | 3081 UGCACUGUCUCAGCCAACC | 172 | 3099 GGUUGGCUGAGACAGUGCA | 404 | |
| 3099 | CCGCUCACAUCCGGCAG | 173 | 3099 CCGCUCACAUCCGGCAG | 173 | 3117 CUGCCGGUAGUGGAGCGG | 405 | |
| 3117 | GGGUACACAUUCGCACCCC | 174 | 3117 GGGUACACAUUCGCACCCC | 174 | 3135 GGGGUGCGAAUGUGUACCC | 406 | |
| 3135 | CUACUUACACAGAGGAAGAA | 175 | 3135 CUACUUACACAGAGGAAGAA | 175 | 3153 UUCUUCCUCUGUGAAGUAG | 407 | |
| 3153 | AACCUGGAACCAGAGGGGG | 176 | 3153 ACCUGGAACCAGAGGGGG | 176 | 3171 CCCCCUCUGGUUCCAGGUU | 408 | |
| 3171 | GCGUGCCUGCCAAGCUCAC | 177 | 3171 GCGUGCCUGCCAAGCUCAC | 177 | 3189 GUGAGCUUJGGCAGGCACGC | 409 | |
| 3189 | CACAGCAGGAACUGAGCCA | 178 | 3189 CACAGCAGGAACUGAGCCA | 178 | 3207 UGGCUCAGUUCUGCUGUG | 410 | |
| 3207 | AGAAACGCAGAUUGGGCUG | 179 | 3207 AGAAACGCAGAUUGGGCUG | 179 | 3225 CAGCCCAAUCUGCGUUUCU | 411 | |
| 3225 | GGCUCUGAAGCCAAGCCUC | 180 | 3225 GGCUCUGAAGCCAAGCCUC | 180 | 3243 GAGGCUCUGGUUCAGAGCC | 412 | |
| 3243 | CUUCUUACUUACCCGGCU | 181 | 3243 CUUCUUACUUACCCGGCU | 181 | 3261 AGCCGGGUGAAGUAAGAAG | 413 | |
| 3261 | UGGGCUCCUCAUUUUUACG | 182 | 3261 UGGGCUCCUCAUUUUUACG | 182 | 3279 CGUAAAAAUGAGGGAGCCCA | 414 | |
| 3279 | GGGUAAACAGUGAGGCUGGG | 183 | 3279 GGGUAAACAGUGAGGCUGGG | 183 | 3297 CCCAGCCUCACUGUUACCC | 415 | |
| 3297 | GAAGGGGAACACAGACCAG | 184 | 3297 GAAGGGGAACACAGACCAG | 184 | 3315 CUGGUCUGGUUCCCCUUC | 416 | |
| 3315 | GGAAGCUCGGUGAGUGAUG | 185 | 3315 GGAAGCUCGGUGAGUGAUG | 185 | 3333 CAUCACUCACCAGCUUCC | 417 | |
| 3333 | GGCAGAACGAUGCCUGCAG | 186 | 3333 GGCAGAACGAUGCCUGCAG | 186 | 3351 CUGCAGGCAUCGUUCUGCC | 418 | |
| 3351 | GGCAUGGAACUUUUUCCGU | 187 | 3351 GGCAUGGAACUUUUUCCGU | 187 | 3369 ACGGAAAAGUUCCAUGCC | 419 | |
| 3369 | UUAUCACCCAGGCCUGAUU | 188 | 3369 UUAUCACCCAGGCCUGAUU | 188 | 3387 AAUCAGGCCUGGGUGAUAA | 420 | |
| 3387 | UCACUGGCCUGGCGGAGAU | 189 | 3387 UCACUGGCCUGGCGGAGAU | 189 | 3405 AUCUCGCCAGGCCAGUGA | 421 | |
| 3405 | UGCUUCUAAGGCAUGGUCG | 190 | 3405 UGCUUCUAAGGCAUGGUCG | 190 | 3423 CGACCAUGCCUAGAAGCA | 422 | |
| 3423 | GGGGGAGAGGGCAACAAAC | 191 | 3423 GGGGGAGAGGGCAACAAAC | 191 | 3441 GUUGUUGGCCUCUCCCCC | 423 | |
| 3441 | CUGUCCCUCUUGAGCACC | 192 | 3441 CUGUCCCUCUUGAGCACC | 192 | 3459 GGUGCUAAGGAGGGACAG | 424 | |
| 3459 | CAGCCCCACCCAAGCAAGC | 193 | 3459 CAGCCCCACCCAAGCAAGC | 193 | 3477 GCUUGCUUJGGGUGGGCUG | 425 | |
| 3477 | CAGACAUUAUCUUUUGGG | 194 | 3477 CAGACAUUAUCUUUUGGG | 194 | 3495 CCCAAAAGAUAAAUGUCUG | 425 | |
| 3495 | GUCUGUCCUCUCUGUUGCC | 195 | 3495 GUCUGUCCUCUCUGUUGCC | 195 | 3513 GGCAACAGAGAGGACAGAC | 427 | |
| 3513 | CUUUUUACAGCCAACUUUU | 196 | 3513 CUUUUUACAGCCAACUUUU | 196 | 3531 AAAAGUUGGCUGUAAAAG | 428 | |
| 3531 | UCUAGACCUGUUUUGCUUU | 197 | 3531 UCUAGACCUGUUUUGCUUU | 197 | 3549 AAAGCAAAACAGGCUAGA | 429 | |
| 3549 | UUGUAACUUGAAGAUUU | 198 | 3549 UUGUAACUUGAAGAUUU | 198 | 3567 AAAUAUCUUCAAGUUACAA | 430 | |
| 3567 | UAUUCUGGGUUUUGUAGCA | 199 | 3567 UAUUCUGGGUUUUGUAGCA | 199 | 3585 UGCUACAAAACCCAGAAUA | 431 | |

TABLE II-continued

| PCSK9 siRNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | |
|--|----------------------|-------------------------------|--------------------------------|-----|
| Pos | Seq | Seq | Seq | |
| | ID UPos Upper seq | ID LPos Lower seq | ID | |
| 3585 | AUUUUUUAUAAAUAUGGUGA | 200 3585 AUUUUUAUAAAUAUGGUGA | 200 3603 UCACCAUAAAUAUAAAAAU | 432 |
| 3603 | ACUUUUUAAAUAACACA | 201 3603 ACUUUUUAAAUAACACA | 201 3621 UGUUUUUAUUUAAAAGU | 433 |
| 988 | GUGGUCAGCGGCCGGGAUG | 202 988 GUGGUCAGCGGCCGGGAUG | 202 1006 CAUCCCGGCCUGACCAC | 434 |
| 989 | UGGUUCAGCGGCCGGGAUGC | 203 989 UGGUUCAGCGGCCGGGAUGC | 203 1007 GCAUCCCGGCCUGACCA | 435 |
| 1075 | AGCGGCACCCCUAUAGGCC | 204 1075 AGCGGCACCCCUAUAGGCC | 204 1093 GGCCUAUGAGGGUGCCGCU | 436 |
| 1076 | GCGGCACCCCUAUAGGCCU | 205 1076 GCGGCACCCCUAUAGGCCU | 205 1094 AGGCCUAUGAGGGUGCCG | 437 |
| 1077 | CGGCACCCCUAUAGGCCUG | 206 1077 CGGCACCCCUAUAGGCCUG | 206 1095 CAGGCCUAUGAGGGUGCCG | 438 |
| 1078 | GGCACCCCUAUAGGCCUGG | 207 1078 GGCACCCCUAUAGGCCUGG | 207 1096 CCAGGCCUAUGAGGGUGCC | 439 |
| 1079 | GCACCCCUAUAGGCCUGGA | 208 1079 GCACCCCUAUAGGCCUGGA | 208 1097 UCCAGGCCUAUGAGGGUGC | 440 |
| 1080 | CACCCCUAUAGGCCUGGAG | 209 1080 CACCCCUAUAGGCCUGGAG | 209 1098 CUCCAGGCCUAUGAGGGUG | 441 |
| 1081 | ACCCCUAUAGGCCUGGAGU | 210 1081 ACCCCCUAUAGGCCUGGAGU | 210 1099 ACUCCAGGCCUAUGAGGGU | 441 |
| 1082 | CCCUAUAGGCCUGGAGUU | 211 1082 CCCCUAUAGGCCUGGAGUU | 211 1100 AACUCCAGGCCUAUGAGGG | 443 |
| 1084 | CUCAUAGGCCUGGAGUUUA | 212 1084 CUCAUAGGCCUGGAGUUUA | 212 1102 UAAACUCCAGGCCUAUGAG | 444 |
| 1085 | UCAUAGGCCUGGAGUUUAU | 213 1085 UCAUAGGCCUGGAGUUUAU | 213 1103 AAUAAACUCCAGGCCUAUGA | 445 |
| 1086 | CAUAGGCCUGGAGUUUAUU | 214 1086 CAUAGGCCUGGAGUUUAUU | 214 1104 AAUAAACUCCAGGCCUAUG | 446 |
| 1087 | AUAGGCCUGGAGUUUAUUC | 215 1087 AUAGGCCUGGAGUUUAUUC | 215 1105 GAAUAAACUCCAGGCCUAU | 447 |
| 1088 | UAGGCCUGGAGUUUAUUCG | 216 1088 UAGGCCUGGAGUUUAUUCG | 216 1106 CGAAUAAACUCCAGGCCUA | 448 |
| 1089 | AGGCCUGGAGUUUAUUCGG | 217 1089 AGGCCUGGAGUUUAUUCGG | 217 1107 CCGAAUAAACUCCAGGCCUA | 449 |
| 1090 | GGCCUGGAGUUUAUUCGGA | 218 1090 GGCCUGGAGUUUAUUCGGA | 218 1108 UCCGAAUAAACUCCAGGCC | 450 |
| 1091 | GCCUGGAGUUUAUUCGGA | 219 1091 GCCUGGAGUUUAUUCGGA | 219 1109 UUCCGAAUAAACUCCAGGC | 451 |
| 1255 | GCCUGGCCUACUCCCCAG | 220 1255 GCCUGGCCUACUCCCCAG | 220 1273 CUGGGGAGUAGAGGCAGGC | 452 |
| 1256 | CCUGGCCUACUCCCCAGC | 221 1256 CCUGGCCUACUCCCCAGC | 221 1274 CGUGGGGAGUAGAGGCAGG | 453 |
| 1570 | GCCUGGUUCCCCUGAGGACC | 222 1570 GCCUGGUUCCCCUGAGGACC | 222 1588 GGUCCUCAGGGAACCGAGC | 454 |
| 1571 | CCUGGUUCCCCUGAGGACCA | 223 1571 CCUGGUUCCCCUGAGGACCA | 223 1589 UGGUCCUCAGGGAACCGAG | 455 |
| 1572 | CUGGUUCCCCUGAGGACAG | 224 1572 CUGGUUCCCCUGAGGACAG | 224 1590 CUGGUUCCCCUGAGGACAG | 456 |
| 1573 | UGGUUCCCCUGAGGACAGC | 225 1573 UGGUUCCCCUGAGGACAGC | 225 1591 GCUGGUUCCCCUGAGGACAG | 457 |
| 1834 | UUUGGGGGUGAGGGUGUCU | 226 1834 UUUGGGGGUGAGGGUGUCU | 226 1852 AGACACCCUCACCCCCAAA | 458 |
| 1835 | UUGGGGGUGAGGGUGUCUA | 227 1835 UUGGGGGUGAGGGUGUCUA | 227 1853 UAGACACCCUCACCCCCAA | 459 |
| 2316 | UGCCAUCUGCUGCCGGAGC | 228 2316 UGCCAUCUGCUGCCGGAGC | 228 2334 GCUCCGGCAGCAGAUGGCA | 460 |
| 2317 | GCCAUCUGCUGCCGGAGCC | 229 2317 GCCAUCUGCUGCCGGAGCC | 229 2335 GGCUCUCCGGCAGCAGAUGGC | 461 |
| 2318 | CCAUCUGCUGCCGGAGCCG | 230 2318 CCAUCUGCUGCCGGAGCCG | 230 2336 CGGCUCUCCGGCAGCAGAUGG | 462 |

TABLE II-continued

| PCSK9 siNA and Target Sequences PCSK9 NM_174936.21
<i>Homo sapiens proprotein convertase subtilisin/kexin type 9 (PCSK9), mRNA</i> | | | | | | | |
|---|---------------------|------|--------------------------|-----|--------------------------|------|-----------|
| Pos | Seq | Seq | Seq | Pos | Seq | Seq | ID |
| | ID | UPos | Upper seq | | ID | LPos | Lower seq |
| 2319 | CAUCUGCUGCCGGAGCCGG | 231 | 2319 CAUCUGCUGCCGGAGCCGG | 231 | 2337 CCGGCUCCGGCAGCAGAUG | 463 | |
| 2320 | AUCUGCUGCCGGAGCCGGC | 232 | 2320 AUCUGCUGCCGGAGCCGGC | 232 | 2338 GCCGGCUCCGGCAGCAGAU | 464 | |

The 3'-ends of the Upper sequence and the Lower sequence of the siNA construct can include an overhang sequence, for example about 1, 2, 3, or 4 nucleotides in length, preferably 2 nucleotides in length, wherein the overhanging sequence of the lower sequence is optionally complementary to a portion of the target sequence. The upper sequence is also referred to as the sense strand, whereas the lower sequence is also referred to as the antisense strand. The upper and lower sequences in the Table can further comprise a chemical modification having Formulae I-VII, such as exemplary siNA constructs shown in FIGS. 4 and 5, or having modifications described in Table IV or any combination thereof.

TABLE III

| PCSK9 Synthetic Modified siNA constructs | | | | | |
|--|--------------------------|-------------|---|--|----------------------------|
| Target Pos | Target | Seq Cmpd ID | # | Aliases | Seq ID |
| 1093 | AGGCCUGGAGUUUAUCGGAAAA | 465 | | PCSK9: 1093U21 siRNA | GCCUGGAGUUUAUCGGATT 473 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC | 466 | | PCSK9: 1087U21 siRNA | UCAUAGGCCUGGAGUUUAUTT 474 |
| 1084 | CACCCUCAUAGGCCUGGAGUUU | 467 | | PCSK9: 1084U21 siRNA | CCCUCAUAGGCCUGGAGUUTT 475 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG | 468 | | PCSK9: 1078U21 siRNA | GCGGCACCCUCAUAGGCCUTT 476 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU | 469 | | PCSK9: 1081U21 siRNA | GCACCCUCAUAGGCCUGGATT 477 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA | 470 | | PCSK9: 1092U21 siRNA | GGCCUGGAGUUUAUCGGATT 478 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU | 471 | | PCSK9: 1082U21 siRNA | CACCCUCAUAGGCCUGGAGTT 479 |
| 1573 | GGCCUGGUUCCCCUGAGGACCAGC | 472 | | PCSK9: 1573U21 siRNA | CCUGGUUCCCCUGAGGACCATT 480 |
| 1093 | AGGCCUGGAGUUUAUCGGAAAA | 465 | | PCSK9: 1111L21 siRNA (1093C) UUCCGAUAAAUCUCCAGGCTT | 481 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC | 466 | | PCSK9: 1105L21 siRNA (1087C) AUAAAUCUCCAGGCCUAUGATT | 482 |
| 1084 | CACCCUCAUAGGCCUGGAGUUU | 467 | | PCSK9: 1102L21 siRNA (1084C) AACUCCAGGCCUAUGAGGGTT | 483 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG | 468 | | PCSK9: 1096L21 siRNA (1078C) AGGCCUAUGAGGGUGCCGCTT | 484 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU | 469 | | PCSK9: 1099L21 siRNA (1081C) UCCAGGCCUAUGAGGGUGCTT | 485 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA | 470 | | PCSK9: 1110L21 siRNA (1092C) UCCGAUAAAUCUCCAGGCTT | 486 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU | 471 | | PCSK9: 1100L21 siRNA (1082C) CUCCAGGCCUAUGAGGGUGTT | 487 |
| 1573 | GGCCUGGUUCCCCUGAGGACCAGC | 472 | | PCSK9: 1591L21 siRNA (1573C) UGGUCCUCAGGGAACAGGTT | 488 |
| 1093 | AGGCCUGGAGUUUAUCGGAAAA | 465 | | PCSK9: 1093U21 siRNA stab04 B GccuGGAGuuuAuucGGATT B | 489 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC | 466 | | PCSK9: 1087U21 siRNA stab04 B ucAuAGGccuGGAGuuuAuTT B | 490 |
| 1084 | CACCCUCAUAGGCCUGGAGUUU | 467 | | PCSK9: 1084U21 siRNA stab04 B cccucAuAGGccuGGAGuu TT B | 491 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG | 468 | | PCSK9: 1078U21 siRNA stab04 B GoGGcAcccucAuAGGccuTT B | 492 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU | 469 | | PCSK9: 1081U21 siRNA stab04 B GcAcccucAuAGGccuGGATT B | 493 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA | 470 | | PCSK9: 1092U21 siRNA stab04 B GGccuGGAGuuuAuucGGATT B | 494 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU | 471 | | PCSK9: 1082U21 siRNA stab04 B cAcccucAuAGGccuGGAGTT B | 495 |
| 1573 | GGCCUGGUUCCCCUGAGGACCAGC | 472 | | PCSK9: 1573U21 siRNA stab04 B ccuGuuccuGAGGAccATT B | 496 |

TABLE III-continued

| PCSK9 Synthetic Modified siNA constructs | | | | | |
|--|------------------------------|-------------|----------------|--|--------|
| Target Pos | Target | Seq Cmpd ID | Cmpd # Aliases | Sequence | Seq ID |
| 1093 | AGGCCUGGAGUUUAUCGGAAA 465 | PCSK9: | 1111L21 | siRNA (1093C) uuccGAAuAAAcuccAGGcTsT
stab05 | 497 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC 466 | PCSK9: | 1105L21 | siRNA (1087C) AuAAAcuccAGGccuAuGATsT
stab05 | 498 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA 467 | PCSK9: | 1102L21 | siRNA (1084C) AAuccAGGccuAuGAGGGTsT
stab05 | 499 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG 468 | PCSK9: | 1096L21 | siRNA (1078C) AGGccuAuGAGGGuGccGcTsT
stab05 | 500 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU 469 | PCSK9: | 1099L21 | siRNA (1081C) uccAGGccuAuGAGGGuGcTsT
stab05 | 501 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA 470 | PCSK9: | 1110L21 | siRNA (1092C) uccGAAuAAAcuccAGGcTsT
stab05 | 502 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU 471 | PCSK9: | 1100L21 | siRNA (1082C) cuccAGGccuAuGAGGGuGTsT
stab05 | 503 |
| 1573 | GGCCUGGUUCCCCUGAGGACCAGC 472 | PCSK9: | 1591L21 | siRNA (1573C) uGGuccucAGGGAccAGGTsT
stab05 | 504 |
| 1093 | AGGCCUGGAGUUUAUCGGAAA 465 | PCSK9: | 1093U21 | siRNA stab07 B GccuGGAGuuuAuucGGATT B | 505 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC 466 | PCSK9: | 1087U21 | siRNA stab07 B ucAuAGGccuGGAGuuuAuTT B | 506 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA 467 | PCSK9: | 1084U21 | siRNA stab07 B cccucAuAGGccuGGAGuuTT B | 507 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG 468 | PCSK9: | 1078U21 | siRNA stab07 B GcGGcAcccucAuAGGccuTT B | 508 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU 469 | PCSK9: | 1081U21 | siRNA stab07 B GcAcccucAuAGGccuGGATT B | 509 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA 470 | PCSK9: | 1092U21 | siRNA stab07 B GGccuGGAGuuuAuucGGATT B | 510 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU 471 | PCSK9: | 1082U21 | siRNA stab07 B cAcccucAuAGGccuGGAGTT B | 511 |
| 1573 | GGCCUGGUUCCCCUGAGGACCAGC 472 | PCSK9: | 1573U21 | siRNA stab07 B ccuGGGuuccuGAGGAccATT B | 512 |
| 1093 | AGGCCUGGAGUUUAUCGGAAA 465 | PCSK9: | 1111L21 | siRNA (1093C) uuccGAAuAAAcuccAGGcTsT
stab11 | 513 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC 466 | PCSK9: | 1105L21 | siRNA (1087C) AuAAAcuccAGGccuAuGATsT
stab11 | 514 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA 467 | PCSK9: | 1102L21 | siRNA (1084C) AAuccAGGccuAuGAGGGTsT
stab11 | 515 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG 468 | PCSK9: | 1096L21 | siRNA (1078C) AGGccuAuGAGGGuGccGcTsT
stab11 | 516 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU 469 | PCSK9: | 1099L21 | siRNA (1081C) uccAGGccuAuGAGGGuGcTsT
stab11 | 517 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA 470 | PCSK9: | 1110L21 | siRNA (1092C) uccGAAuAAAcuccAGGcTsT
stab11 | 518 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU 471 | PCSK9: | 1100L21 | siRNA (1082C) cuccAGGccuAuGAGGGuGTsT
stab11 | 519 |
| 1573 | GGCCUGGUUCCCCUGAGGACCAGC 472 | PCSK9: | 1591L21 | siRNA (1573C) uGGuccucAGGGAccAGGTsT
stab11 | 520 |
| 1093 | AGGCCUGGAGUUUAUCGGAAA 465 | PCSK9: | 1093U21 | siRNA stab18 B GccuGGAGuuuAuucGGATT B | 521 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC 466 | PCSK9: | 1087U21 | siRNA stab18 B ucAuAGGccuGGAGuuuAuTT B | 522 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA 467 | PCSK9: | 1084U21 | siRNA stab18 B cccucAuAGGccuGGAGuuTT B | 523 |

TABLE III-continued

| PCSK9 Synthetic Modified siNA constructs | | | | | |
|--|------------------------------|----------------|----------------------|---|--------|
| Target Pos | Target | Seq ID | Cmpd # | Aliases | Seq ID |
| 1078 | UAGCGGCACCCCUAUAGGCCUGG 468 | PCSK9: 1078U21 | siRNA stab18 | B <u>GcGGcA</u> ccuc <u>AuAGG</u> ccuTT | B 524 |
| 1081 | CGGCACCCCUAUAGGCCUGGAGU 469 | PCSK9: 1081U21 | siRNA stab18 | B <u>GcA</u> ccuc <u>AuAGG</u> ccu <u>GGATT</u> | B 525 |
| 1092 | UAGGCCUGGAGUUUUAUUCGGAAA 470 | PCSK9: 1092U21 | siRNA stab18 | B <u>GG</u> ccu <u>GGAG</u> uuuu <u>Auuc</u> <u>GGATT</u> | B 526 |
| 1082 | GGCACCCCUAUAGGCCUGGAGUU 471 | PCSK9: 1082U21 | siRNA stab18 | B <u>cA</u> ccuc <u>AuAGG</u> ccu <u>GGAGTT</u> | B 527 |
| 1573 | GGCCUGGUUCCCUGAGGACCAGC 472 | PCSK9: 1573U21 | siRNA stab18 | B <u>ccuGG</u> uucc <u>ccuGAGG</u> accATT | B 528 |
| 1093 | AGGCCUGGAGUUUAUCGGAAAA 465 | PCSK9: 1111L21 | siRNA (1093C) stab08 | uucc <u>GA</u> au <u>AA</u> acucc <u>AGG</u> ctTsT | 529 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUUC 466 | PCSK9: 1105L21 | siRNA (1087C) stab08 | <u>AuAA</u> Acucc <u>AGG</u> ccu <u>AuGAT</u> tsT | 530 |
| 1084 | CACCCUCAUAGGCCUGGAGUUUA 467 | PCSK9: 1102L21 | siRNA (1084C) stab08 | <u>AA</u> cu <u>ccAGG</u> ccu <u>AuGAGG</u> tsT | 531 |
| 1078 | UAGCGGCACCCCUAUAGGCCUGG 468 | PCSK9: 1096L21 | siRNA (1078C) stab08 | <u>AGG</u> ccu <u>AuGAGG</u> GuGccGcTsT | 532 |
| 1081 | CGGCACCCCUAUAGGCCUGGAGU 469 | PCSK9: 1099L21 | siRNA (1081C) stab08 | ucc <u>AGG</u> ccu <u>AuGAGG</u> GuGcTsT | 533 |
| 1092 | UAGGCCUGGAGUUUUAUUCGGAAA 470 | PCSK9: 1110L21 | siRNA (1092C) stab08 | ucc <u>GA</u> au <u>AA</u> acucc <u>AGG</u> ccTsT | 534 |
| 1082 | GGCACCCCUAUAGGCCUGGAGUU 471 | PCSK9: 1100L21 | siRNA (1082C) stab08 | cucc <u>AGG</u> ccu <u>AuGAGG</u> GuGTsT | 535 |
| 1573 | GGCCUGGUUCCCUGAGGACCAGC 472 | PCSK9: 1591L21 | siRNA (1573C) stab08 | u <u>GG</u> ucc <u>ccAGG</u> AA <u>ccAGG</u> tsT | 536 |
| 1093 | AGGCCUGGAGUUUAUCGGAAAA 465 | PCSK9: 1093U21 | siRNA stab09 | B <u>GCC</u> UGGAGUUUAUCGGATT | B 537 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUUC 466 | PCSK9: 1087U21 | siRNA stab09 | B <u>UCA</u> UAGGCCUGGAGUUUAUTT | B 538 |
| 1084 | CACCCUCAUAGGCCUGGAGUUUA 467 | PCSK9: 1084U21 | siRNA stab09 | B <u>CCC</u> CUAUAGGCCUGGAGUUTT | B 539 |
| 1078 | UAGCGGCACCCCUAUAGGCCUGG 468 | PCSK9: 1078U21 | siRNA stab09 | B <u>GCG</u> CACCCCUAUAGGCCUTT | B 540 |
| 1081 | CGGCACCCCUAUAGGCCUGGAGU 469 | PCSK9: 1081U21 | siRNA stab09 | B <u>GCAC</u> CCCUAUAGGCCUGGATT | B 541 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA 470 | PCSK9: 1092U21 | siRNA stab09 | B <u>GGC</u> UGGAGUUUAUCGGATT | B 542 |
| 1082 | GGCACCCCUAUAGGCCUGGAGUU 471 | PCSK9: 1082U21 | siRNA stab09 | B <u>CAC</u> CCCUAUAGGCCUGGAGTT | B 543 |
| 1573 | GGCCUGGUUCCCUGAGGACCAGC 472 | PCSK9: 1573U21 | siRNA stab09 | B <u>CCU</u> GGGUUCCCUGAGGACCATT | B 544 |
| 1093 | AGGCCUGGAGUUUAUCGGAAAA 465 | PCSK9: 1111L21 | siRNA (1093C) stab10 | UUCGAA <u>AA</u> ACUCCAGGCTsT | 545 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUUC 466 | PCSK9: 1105L21 | siRNA (1087C) stab10 | <u>AUAA</u> ACUCCAGGCUAUGATsT | 546 |
| 1084 | CACCCUCAUAGGCCUGGAGUUUA 467 | PCSK9: 1102L21 | siRNA (1084C) stab10 | <u>AACUCCAGG</u> CCUAUGAGGtsT | 547 |
| 1078 | UAGCGGCACCCCUAUAGGCCUGG 468 | PCSK9: 1096L21 | siRNA (1078C) stab10 | <u>AGG</u> CCUAUGAGGUGCCGCTsT | 548 |
| 1081 | CGGCACCCCUAUAGGCCUGGAGU 469 | PCSK9: 1099L21 | siRNA (1081C) stab10 | <u>UCCAGG</u> CCUAUGAGGUGCTsT | 549 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA 470 | PCSK9: 1110L21 | siRNA (1092C) stab10 | <u>UCCGAA</u> AAACUCCAGGCTsT | 550 |
| 1082 | GGCACCCCUAUAGGCCUGGAGUU 471 | PCSK9: 1100L21 | siRNA (1082C) stab10 | <u>CUC</u> CAGGCCUAUGAGGUGTsT | 551 |

TABLE III-continued

| PCSK9 Synthetic Modified siNA constructs | | | | | |
|--|-------------------------|--------|--------|--|--------|
| Target Pos | Target | Seq ID | Cmpd # | Aliases | Seq ID |
| 1573 | GGCCUGGUUCCCUGAGGACCAGC | 472 | PCSK9: | 1591L21 siRNA (1573C) UGGUCCUCAGGGAACCAAGGTsT
stab10 | 552 |
| 1093 | AGGCCUGGAGUUUAUCGGAAA | 465 | PCSK9: | 1111L21 siRNA (1093C) uucc <u>GA</u> au <u>AA</u> Acucc <u>AG</u> gcTT B
stab19 | 553 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC | 466 | PCSK9: | 1105L21 siRNA (1087C) Au <u>AA</u> Acucc <u>AG</u> ccu <u>Au</u> GATT B
stab19 | 554 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA | 467 | PCSK9: | 1102L21 siRNA (1084C) <u>AA</u> cucc <u>AG</u> ccu <u>Au</u> GAGGGTT B
stab19 | 555 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG | 468 | PCSK9: | 1096L21 siRNA (1078C) <u>AG</u> ccu <u>Au</u> GAGGGu <u>Gcc</u> GcTT B
stab19 | 556 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU | 469 | PCSK9: | 1099L21 siRNA (1081C) ucc <u>AG</u> ccu <u>Au</u> GAGGGu <u>Gc</u> TT B
stab19 | 557 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA | 470 | PCSK9: | 1110L21 siRNA (1092C) ucc <u>GA</u> au <u>AA</u> Acucc <u>AG</u> ccTT B
stab19 | 558 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU | 471 | PCSK9: | 1100L21 siRNA (1082C) cucc <u>AG</u> ccu <u>Au</u> GAGGGuGTT B
stab19 | 559 |
| 1573 | GGCCUGGUUCCCUGAGGACCAGC | 472 | PCSK9: | 1591L21 siRNA (1573C) u <u>GG</u> ccuc <u>AG</u> GA <u>Ac</u> <u>AG</u> TT B
stab19 | 560 |
| 1093 | AGGCCUGGAGUUUAUCGGAAA | 465 | PCSK9: | 1111L21 siRNA (1093C) UUCCGAA <u>AA</u> ACUCCAGGCTT B
stab22 | 561 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC | 466 | PCSK9: | 1105L21 siRNA (1087C) AUAAACUCCAGGCCUAUGATT B
stab22 | 562 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA | 467 | PCSK9: | 1102L21 siRNA (1084C) AACUCCAGGCCUAUGAGGGTT B
stab22 | 563 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG | 468 | PCSK9: | 1096L21 siRNA (1078C) AGGCCUAUGAGGGUGCCGCTT B
stab22 | 564 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU | 469 | PCSK9: | 1099L21 siRNA (1081C) UCCAGGCCUAUGAGGGUGCTT B
stab22 | 565 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA | 470 | PCSK9: | 1110L21 siRNA (1092C) UCCGAA <u>AA</u> ACUCCAGGCCTT B
stab22 | 566 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU | 471 | PCSK9: | 1100L21 siRNA (1082C) CUCCAGGCCUAUGAGGGUGTT B
stab22 | 567 |
| 1573 | GGCCUGGUUCCCUGAGGACCAGC | 472 | PCSK9: | 1591L21 siRNA (1573C) UGGUCCUCAGGGAACCAAGGT B
stab22 | 568 |
| 1093 | AGGCCUGGAGUUUAUCGGAAA | 465 | PCSK9: | 1111L21 siRNA (1093C) UU <u>CC</u> <u>GA</u> au <u>AA</u> Acucc <u>AG</u> TsT
stab25 | 569 |
| 1087 | CCUCAUAGGCCUGGAGUUUAUC | 466 | PCSK9: | 1105L21 siRNA (1087C) AUAA <u>Ac</u> cc <u>AG</u> ccu <u>Au</u> GATsT
stab25 | 570 |
| 1084 | CACCUCAUAGGCCUGGAGUUUA | 467 | PCSK9: | 1102L21 siRNA (1084C) AAC <u>CC</u> <u>AG</u> ccu <u>Au</u> GAGGGTsT
stab25 | 571 |
| 1078 | UAGCGGCACCCUCAUAGGCCUGG | 468 | PCSK9: | 1096L21 siRNA (1078C) AGGccu <u>Au</u> GAGGGu <u>Gcc</u> GcTsT
stab25 | 572 |
| 1081 | CGGCACCCUCAUAGGCCUGGAGU | 469 | PCSK9: | 1099L21 siRNA (1081C) UCC <u>AG</u> ccu <u>Au</u> GAGGGu <u>Gc</u> TsT
stab25 | 573 |
| 1092 | UAGGCCUGGAGUUUAUCGGAAA | 470 | PCSK9: | 1110L21 siRNA (1092C) UCC <u>GA</u> au <u>AA</u> Acucc <u>AG</u> ccTsT
stab25 | 574 |
| 1082 | GGCACCCUCAUAGGCCUGGAGUU | 471 | PCSK9: | 1100L21 siRNA (1082C) CU <u>CC</u> <u>AG</u> ccu <u>Au</u> GAGGGu <u>Gt</u> sT
stab25 | 575 |

TABLE III-continued

| PCSK9 Synthetic Modified siNA constructs | | | | | | Seq ID |
|--|------------------------|-----|---|---|----------|--------|
| Target | Seq Cmpd | ID | # | Aliases | Sequence | |
| Pos | Target | | | | | |
| 1573 | GGCCUGGUUCCUGAGGACCAGC | 472 | | PCSK9: 1591L21 siRNA (1573C) UGGuccucAGGGAAccAGGTsT
stab25 | | 576 |

Uppercase = ribonucleotide

u, c = 2'-deoxy-2'-fluoro U, C

T = thymidine

B = inverted deoxy abasic

s = phosphorothioate linkage

A = deoxy Adenosine

G = deoxy Guanosine

G = 2'-O-methyl Guanosine

A = 2'-O-methyl Adenosine

TABLE IV

| Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs | | | | | |
|--|-------------|--------------|----------------|----------------------------|------------|
| Chemistry | pyrimidine | Purine | cap | p = S | Strand |
| "Stab 00" | Ribo | Ribo | TT at 3'-ends | | S/AS |
| "Stab 1" | Ribo | Ribo | — | 5 at 5'-end
1 at 3'-end | S/AS |
| "Stab 2" | Ribo | Ribo | — | All linkages | Usually AS |
| "Stab 3" | 2'-fluoro | Ribo | — | 4 at 5'-end
4 at 3'-end | Usually S |
| "Stab 4" | 2'-fluoro | Ribo | 5' and 3'-ends | — | Usually S |
| "Stab 5" | 2'-fluoro | Ribo | — | 1 at 3'-end | Usually AS |
| "Stab 6" | 2'-O-Methyl | Ribo | 5' and 3'-ends | — | Usually S |
| "Stab 7" | 2'-fluoro | 2'-deoxy | 5' and 3'-ends | — | Usually S |
| "Stab 8" | 2'-fluoro | 2'-O-Methyl | — | 1 at 3'-end | S/AS |
| "Stab 9" | Ribo | Ribo | 5' and 3'-ends | — | Usually S |
| "Stab 10" | Ribo | Ribo | — | 1 at 3'-end | Usually AS |
| "Stab 11" | 2'-fluoro | 2'-deoxy | — | 1 at 3'-end | Usually AS |
| "Stab 12" | 2'-fluoro | LNA | 5' and 3'-ends | | Usually S |
| "Stab 13" | 2'-fluoro | LNA | | 1 at 3'-end | Usually AS |
| "Stab 14" | 2'-fluoro | 2'-deoxy | | 2 at 5'-end
1 at 3'-end | Usually AS |
| "Stab 15" | 2'-deoxy | 2'-deoxy | | 2 at 5'-end
1 at 3'-end | Usually AS |
| "Stab 16" | Ribo | 2'-O-Methyl | 5' and 3'-ends | | Usually S |
| "Stab 17" | 2'-O-Methyl | 2'-O-Methyl | 5' and 3'-ends | | Usually S |
| "Stab 18" | 2'-fluoro | 2'-O-Methyl | 5' and 3'-ends | | Usually S |
| "Stab 19" | 2'-fluoro | 2'-O-Methyl | 3'-end | | S/AS |
| "Stab 20" | 2'-fluoro | 2'-deoxy | 3'-end | | Usually AS |
| "Stab 21" | 2'-fluoro | Ribo | 3'-end | | Usually AS |
| "Stab 22" | Ribo | Ribo | 3'-end | | Usually AS |
| "Stab 23" | 2'-fluoro* | 2'-deoxy* | 5' and 3'-ends | | Usually S |
| "Stab 24" | 2'-fluoro* | 2'-O-Methyl* | — | 1 at 3'-end | S/AS |
| "Stab 25" | 2'-fluoro* | 2'-O-Methyl* | — | 1 at 3'-end | S/AS |
| "Stab 26" | 2'-fluoro* | 2'-O-Methyl* | — | | S/AS |
| "Stab 27" | 2'-fluoro* | 2'-O-Methyl* | 3'-end | | S/AS |
| "Stab 28" | 2'-fluoro* | 2'-O-Methyl* | 3'-end | | S/AS |
| "Stab 29" | 2'-fluoro* | 2'-O-Methyl* | | 1 at 3'-end | S/AS |

TABLE IV-continued

| Non-limiting examples of Stabilization Chemistries for chemically modified siRNA constructs | | | | | |
|---|------------|---------------|----------------|----------------------------|------------|
| Chemistry | pyrimidine | Purine | cap | p = S | Strand |
| "Stab 30" | 2'-fluoro* | 2'-O-Methyl* | | | S/AS |
| "Stab 31" | 2'-fluoro* | 2'-O-Methyl* | 3'-end | | S/AS |
| "Stab 32" | 2'-fluoro | 2'-O-Methyl | | | S/AS |
| "Stab 33" | 2'-fluoro | 2'-deoxy* | 5' and 3'-ends | — | Usually S |
| "Stab 34" | 2'-fluoro | 2'-O-Methyl* | 5' and 3'-ends | | Usually S |
| "Stab 35" | 2'-fluoro | 2'-O-Methyl** | | | Usually AS |
| "Stab 36" | 2'-fluoro | 2'-O-Methyl** | | | Usually AS |
| "Stab 3F" | 2'-OCF3 | Ribo | — | 4 at 5'-end
4 at 3'-end | Usually S |
| "Stab 4F" | 2'-OCF3 | Ribo | 5' and 3'-ends | — | Usually S |
| "Stab 5F" | 2'-OCF3 | Ribo | — | 1 at 3'-end | Usually AS |
| "Stab 7F" | 2'-OCF3 | 2'-deoxy | 5' and 3'-ends | — | Usually S |
| "Stab 8F" | 2'-OCF3 | 2'-O-Methyl | — | 1 at 3'-end | S/AS |
| "Stab 11F" | 2'-OCF3 | 2'-deoxy | — | 1 at 3'-end | Usually AS |
| "Stab 12F" | 2'-OCF3 | LNA | 5' and 3'-ends | | Usually S |
| "Stab 13F" | 2'-OCF3 | LNA | | 1 at 3'-end | Usually AS |
| "Stab 14F" | 2'-OCF3 | 2'-deoxy | | 2 at 5'-end
1 at 3'-end | Usually AS |
| "Stab 15F" | 2'-OCF3 | 2'-deoxy | | 2 at 5'-end
1 at 3'-end | Usually AS |
| "Stab 18F" | 2'-OCF3 | 2'-O-Methyl | 5' and 3'-ends | | Usually S |
| "Stab 19F" | 2'-OCF3 | 2'-O-Methyl | 3'-end | | S/AS |
| "Stab 20F" | 2'-OCF3 | 2'-deoxy | 3'-end | | Usually AS |
| "Stab 21F" | 2'-OCF3 | Ribo | 3'-end | | Usually AS |
| "Stab 23F" | 2'-OCF3* | 2'-deoxy* | 5' and 3'-ends | | Usually S |
| "Stab 24F" | 2'-OCF3* | 2'-O-Methyl* | — | 1 at 3'-end | S/AS |
| "Stab 25F" | 2'-OCF3* | 2'-O-Methyl* | — | 1 at 3'-end | S/AS |
| "Stab 26F" | 2'-OCF3* | 2'-O-Methyl* | — | | S/AS |
| "Stab 27F" | 2'-OCF3* | 2'-O-Methyl* | 3'-end | | S/AS |
| "Stab 28F" | 2'-OCF3* | 2'-O-Methyl* | 3'-end | | S/AS |
| "Stab 29F" | 2'-OCF3* | 2'-O-Methyl* | | 1 at 3'-end | S/AS |
| "Stab 30F" | 2'-OCF3* | 2'-O-Methyl* | | | S/AS |
| "Stab 31F" | 2'-OCF3* | 2'-O-Methyl* | 3'-end | | S/AS |
| "Stab 32F" | 2'-OCF3 | 2'-O-Methyl | | | S/AS |
| "Stab 33F" | 2'-OCF3 | 2'-deoxy* | 5' and 3'-ends | — | Usually S |
| "Stab 34F" | 2'-OCF3 | 2'-O-Methyl* | 5' and 3'-ends | | Usually S |
| "Stab 35F" | 2'-OCF3 | 2'-O-Methyl** | | | Usually AS |

TABLE IV-continued

| Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs | | | | | |
|--|------------|---------------|-----|------------|--------|
| Chemistry | pyrimidine | Purine | cap | p = S | Strand |
| "Stab 36F" | 2'-OCF3 | 2'-O-Methyl** | | Usually AS | |

CAP = any terminal cap, see for example FIG. 10.

All Stab 00-36 chemistries can comprise 3'-terminal thymidine (TT) residues

All Stab 00-36 chemistries typically comprise about 21 nucleotides, but can vary as described herein.

All Stab 00-36 chemistries can also include a single ribonucleotide in the sense or passenger strand at the 11th base paired position of the double stranded nucleic acid duplex as determined from the 5'-end of the antisense or guide strand (see FIG. 6C)

S = sense strand

AS = antisense strand

*Stab 23 has a single ribonucleotide adjacent to 3'-CAP

*Stab 24 and Stab 28 have a single ribonucleotide at 5'-terminus

*Stab 25, Stab 26, and Stab 27 have three ribonucleotides at 5'-terminus

*Stab 29, Stab 30, Stab 31, Stab 33, and Stab 34 any purine at first three nucleotide positions from 5'-terminus are ribonucleotides

p = phosphorothioate linkage

**Stab 35 has 2'-O-methyl U at 3'-overhangs

**Stab 36 has 2'-O-methyl overhangs that are complementary to the target sequence (naturally occurring overhangs)

TABLE V

| Reagent | Equivalents | Amount | Wait Time* | Wait Time* | Wait Time* |
|---|--------------------------------------|----------------------------------|-------------------|---------------------------|--------------------|
| | | | DNA | 2'-O-methyl | RNA |
| A. 2.5 μmol Synthesis Cycle ABI 394 Instrument | | | | | |
| Phosphoramidites | 6.5 | 163 μL | 45 sec | 2.5 min | 7.5 min |
| S-Ethyl Tetrazole | 23.8 | 238 μL | 45 sec | 2.5 min | 7.5 min |
| Acetic Anhydride | 100 | 233 μL | 5 sec | 5 sec | 5 sec |
| N-Methyl Imidazole | 186 | 233 μL | 5 sec | 5 sec | 5 sec |
| TCA | 176 | 2.3 mL | 21 sec | 21 sec | 21 sec |
| Iodine | 11.2 | 1.7 mL | 45 sec | 45 sec | 45 sec |
| Beaucage | 12.9 | 645 μL | 100 sec | 300 sec | 300 sec |
| Acetonitrile | NA | 6.67 mL | NA | NA | NA |
| B. 0.2 μmol Synthesis Cycle ABI 394 Instrument | | | | | |
| Phosphoramidites | 15 | 31 μL | 45 sec | 233 sec | 465 sec |
| S-Ethyl Tetrazole | 38.7 | 31 μL | 45 sec | 233 min | 465 sec |
| Acetic Anhydride | 655 | 124 μL | 5 sec | 5 sec | 5 sec |
| N-Methyl Imidazole | 1245 | 124 μL | 5 sec | 5 sec | 5 sec |
| TCA | 700 | 732 μL | 10 sec | 10 sec | 10 sec |
| Iodine | 20.6 | 244 μL | 15 sec | 15 sec | 15 sec |
| Beaucage | 7.7 | 232 μL | 100 sec | 300 sec | 300 sec |
| Acetonitrile | NA | 2.64 mL | NA | NA | NA |
| C. 0.2 μmol Synthesis Cycle 96 well Instrument | | | | | |
| Reagent | Equivalents:DNA/
2'-O-methyl/Ribo | Amount: DNA/2'-O-
methyl/Ribo | Wait Time*
DNA | Wait Time*
2'-O-methyl | Wait Time*
Ribo |
| Phosphoramidites | 22/33/66 | 40/60/120 μL | 60 sec | 180 sec | 360 sec |
| S-Ethyl Tetrazole | 70/105/210 | 40/60/120 μL | 60 sec | 180 min | 360 sec |
| Acetic Anhydride | 265/265/265 | 50/50/50 μL | 10 sec | 10 sec | 10 sec |
| N-Methyl Imidazole | 502/502/502 | 50/50/50 μL | 10 sec | 10 sec | 10 sec |
| TCA | 238/475/475 | 250/500/500 μL | 15 sec | 15 sec | 15 sec |
| Iodine | 6.8/6.8/6.8 | 80/80/80 μL | 30 sec | 30 sec | 30 sec |
| Beaucage | 34/51/51 | 80/120/120 | 100 sec | 200 sec | 200 sec |
| Acetonitrile | NA | 1150/1150/1150 μL | NA | NA | NA |

Wait time does not include contact time during delivery.

Tandem synthesis utilizes double coupling of linker molecule

TABLE VI

| Lipid Nanoparticle (LNP) Formulations | | |
|---------------------------------------|---|---------------|
| Formulation # | Composition | Molar Ratio |
| L051 | CLinDMA/DSPC/Chol/PEG-n-DMG | 48/40/10/2 |
| L053 | DMOBA/DSPC/Chol/PEG-n-DMG | 30/20/48/2 |
| L054 | DMOBA/DSPC/Chol/PEG-n-DMG | 50/20/28/2 |
| L069 | CLinDMA/DSPC/Cholesterol/PEG-Cholesterol | 48/40/10/2 |
| L073 | pCLinDMA or CLin DMA/DMOBA/DSPC/Chol/PEG-n-DMG | 25/25/20/28/2 |
| L077 | eCLinDMA/DSPC/Cholesterol/2KPEG-Chol | 48/40/10/2 |
| L080 | eCLinDMA/DSPC/Cholesterol/2KPEG-DMG | 48/40/10/2 |
| L082 | pCLinDMA/DSPC/Cholesterol/2KPEG-DMG | 48/40/10/2 |
| L083 | pCLinDMA/DSPC/Cholesterol/2KPEG-Chol | 48/40/10/2 |
| L086 | CLinDMA/DSPC/Cholesterol/2KPEG-DMG/Linoleyl alcohol | 43/38/10/2/7 |
| L061 | DMLBA/Cholesterol/2KPEG-DMG | 52/45/3 |
| L060 | DMOBA/Cholesterol/2KPEG-DMG N/P ratio of 5 | 52/45/3 |
| L097 | DMLBA/DSPC/Cholesterol/2KPEG-DMG | 50/20/28 |
| L098 | DMOBA/Cholesterol/2KPEG-DMG, N/P ratio of 3 | 52/45/3 |
| L099 | DMOBA/Cholesterol/2KPEG-DMG, N/P ratio of 4 | 52/45/3 |
| L100 | DMOBA/DOBA/3% PEG-DMG, N/P ratio of 3 | 52/45/3 |
| L101 | DMOBA/Cholesterol/2KPEG-Cholesterol | 52/45/3 |
| L102 | DMOBA/Cholesterol/2KPEG-Cholesterol, N/P ratio of 5 | 52/45/3 |
| L103 | DMLBA/Cholesterol/2KPEG-Cholesterol | 52/45/3 |
| L104 | CLinDMA/DSPC/Cholesterol/2KPEG-cholesterol/Linoleyl alcohol | 43/38/10/2/7 |
| L105 | DMOBA/Cholesterol/2KPEG-Chol, N/P ratio of 2 | 52/45/3 |
| L106 | DMOBA/Cholesterol/2KPEG-Chol, N/P ratio of 3 | 67/30/3 |
| L107 | DMOBA/Cholesterol/2KPEG-Chol, N/P ratio of 1.5 | 52/45/3 |
| L108 | DMOBA/Cholesterol/2KPEG-Chol, N/P ratio of 2 | 67/30/3 |
| L109 | DMOBA/DSPC/Cholesterol/2KPEG-Chol, N/P ratio of 2 | 50/20/28/2 |
| L110 | DMOBA/Cholesterol/2KPEG-DMG, N/P ratio of 1.5 | 52/45/3 |
| L111 | DMOBA/Cholesterol/2KPEG-DMG, N/P ratio of 1.5 | 67/30/3 |
| L112 | DMLBA/Cholesterol/2KPEG-DMG, N/P ratio of 1.5 | 52/45/3 |
| L113 | DMLBA/Cholesterol/2KPEG-DMG, N/P ratio of 1.5 | 67/30/3 |
| L114 | DMOBA/Cholesterol/2KPEG-DMG, N/P ratio of 2 | 52/45/3 |
| L115 | DMOBA/Cholesterol/2KPEG-DMG, N/P ratio of 2 | 67/30/3 |
| L116 | DMLBA/Cholesterol/2KPEG-DMG, N/P ratio of 2 | 52/45/3 |
| L117 | DMLBA/Cholesterol/2KPEG-DMG, N/P ratio of 2 | 52/45/3 |

N/P ratio = Nitrogen: Phosphorous ratio between cationic lipid and nucleic acid

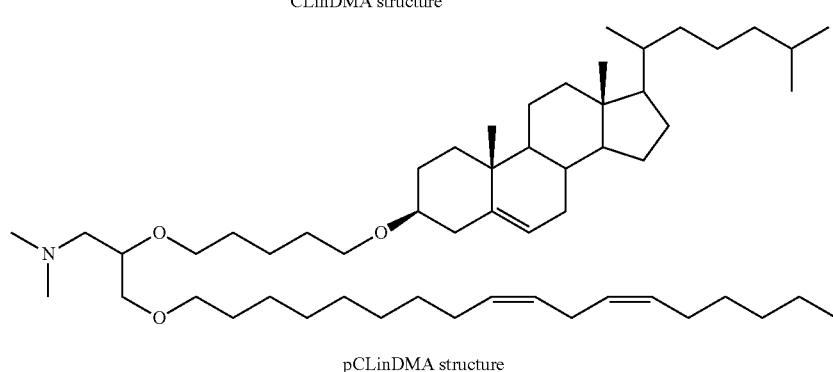
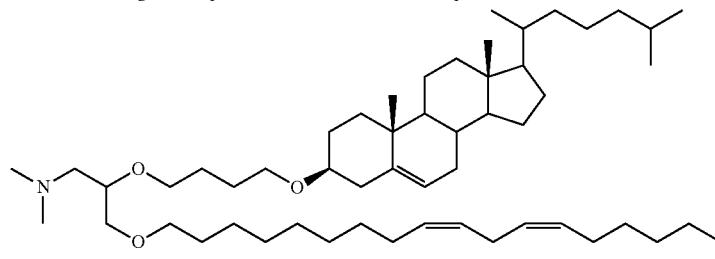


TABLE VI-continued

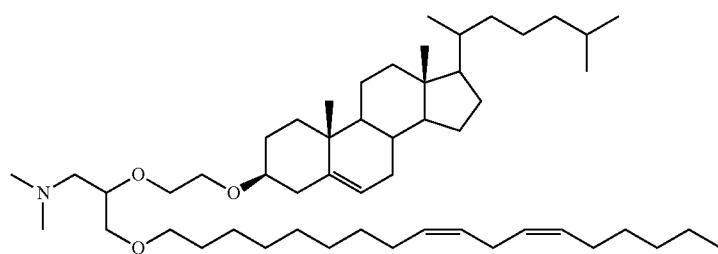
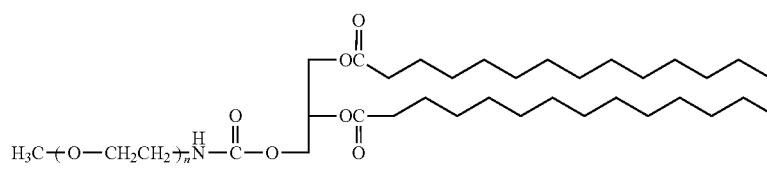
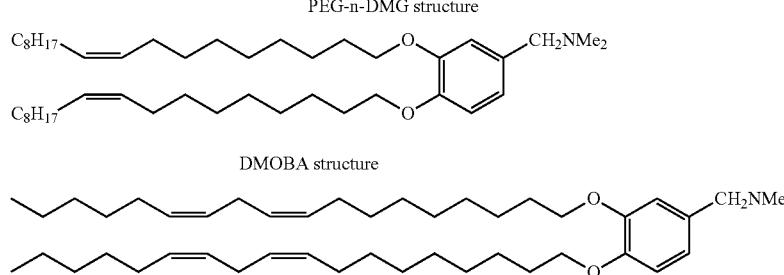
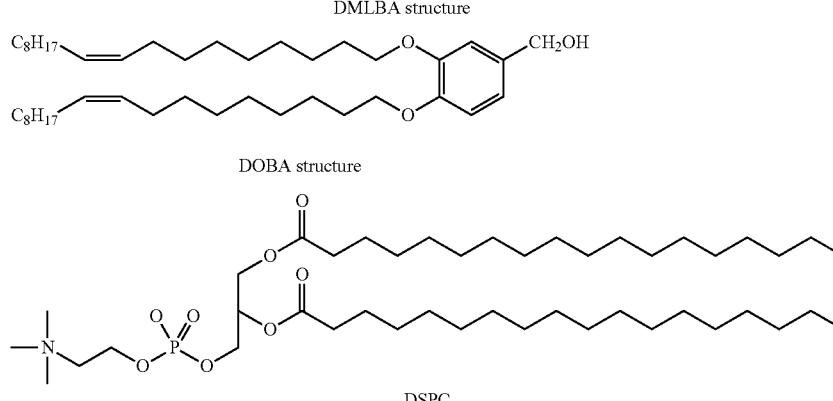
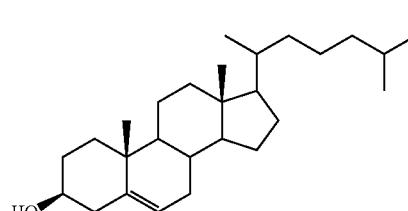
| Lipid Nanoparticle (LNP) Formulations | | |
|---------------------------------------|--|-------------|
| Formulation # | Composition | Molar Ratio |
| |  <p>eCLinDMA structure</p> | |
| |  <p>PEG-n-DMG structure</p> | |
| |  <p>DMOBA structure</p> <p>DMLBA structure</p> | |
| |  <p>DOBA structure</p> <p>DSPC</p> | |
| |  <p>Cholesterol</p> | |

TABLE VI-continued

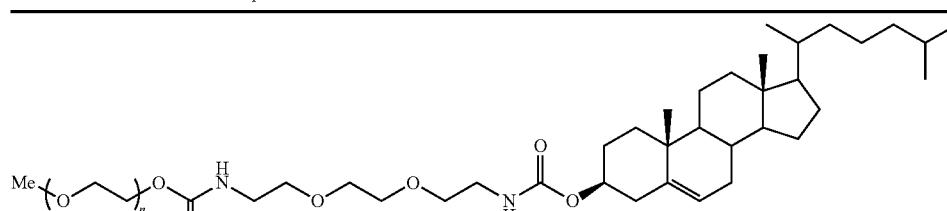
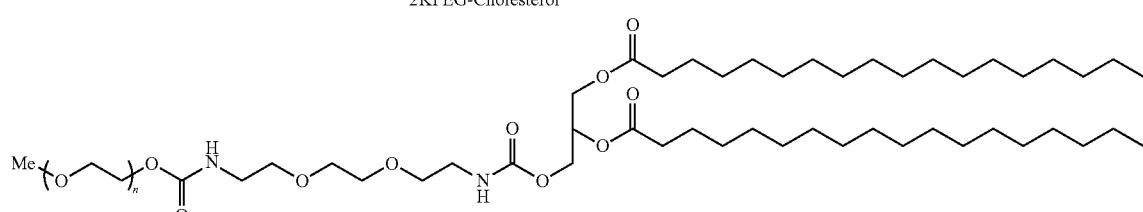
| Lipid Nanoparticle (LNP) Formulations | | |
|---------------------------------------|---|-------------|
| Formulation # | Composition | Molar Ratio |
| |  <p>2KPEG-Cholesterol</p> | |
| |  <p>2KPEG-DMG</p> | |

TABLE VII

Table VII: Sirna algorithm describing patterns with their relative score for predicting hyper-active siRNAs. All the positions given are for the sense strand of 19-mer siRNA.

| Description of pattern | Pattern # | Score |
|--|-----------|-------|
| G or C at position 1 | 1 | 5 |
| A or U at position 19 | 2 | 10 |
| A/U rich between position 15-19 | 3 | 10 |
| String of 4 Gs or 4 Cs (not preferred) | 4 | -100 |
| G/C rich between position 1-5 | 5 | 10 |
| A or U at position 18 | 6 | 5 |
| A or U at position 10 | 7 | 10 |

TABLE VII-continued

Table VII: Sirna algorithm describing patterns with their relative score for predicting hyper-active siRNAs. All the positions given are for the sense strand of 19-mer siRNA.

| Description of pattern | Pattern # | Score |
|----------------------------------|-----------|-------|
| G at position 13 (not preferred) | 8 | -3 |
| A at position 13 | 9 | 3 |
| G at position 9 (not preferred) | 10 | -3 |
| A at position 9 | 11 | 3 |
| A or U at position 14 | 12 | 10 |

SEQUENCE LISTING

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19

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19

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19

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19

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19

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19

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19

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19

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19

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19

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ggcaaggug gugcugccgg 19

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ggcccacaaac gcuuuuuggg 19

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<400> SEQUENCE: 103

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<400> SEQUENCE: 104

cauugccagg ugcugccug 19

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<400> SEQUENCE: 105

guuacccca gccaacugc 19

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<400> SEQUENCE: 106

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<400> SEQUENCE: 107

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19

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19

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19

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19

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19

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Sequence/siNA sense region

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gccugugcug aggccacga 19

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<400> SEQUENCE: 117
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<210> SEQ ID NO 118
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ggaaugcaaa gucaaggag 19

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<400> SEQUENCE: 119

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19

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19

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19

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19

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<400> SEQUENCE: 123

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19

<210> SEQ ID NO 124
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<212> TYPE: RNA
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<400> SEQUENCE: 124

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19

<210> SEQ ID NO 125
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<212> TYPE: RNA
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<220> FEATURE:
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19

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<212> TYPE: RNA
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<400> SEQUENCE: 126

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<400> SEQUENCE: 127

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19

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gacagccguu gcccaucugc

19

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19

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19

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19

<210> SEQ ID NO 134
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19

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<400> SEQUENCE: 135

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19

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<400> SEQUENCE: 136

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19

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<210> SEQ ID NO 137
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<212> TYPE: RNA
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<400> SEQUENCE: 137

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19

<210> SEQ ID NO 138
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<400> SEQUENCE: 138

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19

<210> SEQ ID NO 139
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19

<210> SEQ ID NO 140
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<400> SEQUENCE: 140

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19

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19

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19

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<400> SEQUENCE: 149

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19

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19

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19

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19

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<400> SEQUENCE: 153

ucuccaccaa ggaggcagg

19

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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 154

gauucuuuccc auggauagg

19

<210> SEQ ID NO 155

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19

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19

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<212> TYPE: RNA

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19

<210> SEQ ID NO 160

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<212> TYPE: RNA

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<213> ORGANISM: Artificial Sequence
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19

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cugauuaaug gaggcuuag

19

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guuuucugga uggcaucua

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gcagugugca guggugcau

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ccgcuccacu acccggcag

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ggguaacagu gaggcugggg

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gaaggggaaac acagaccag

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ggaagcucgg ugagugaug

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ggcagaacgca ugccugcag

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ggcauggaac uuuuuccgu

19

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uuaucaccca ggccugauu

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Sequence/siNA sense region

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ucacuggccu ggcggagau 19

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<400> SEQUENCE: 194
cagacauua ucuuuuggg 19

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<400> SEQUENCE: 195

gucuguccuc ucuguugcc

19

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<400> SEQUENCE: 196

cuuuuuuacag ccaacuuuu

19

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<400> SEQUENCE: 197

ucuagaccug uuuugcuuu

19

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uugguaacuug aagauauuu

19

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uauucugggu uuuguagca

19

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aaaaaaaaaa auauugguga

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19

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19

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uggucagcgg ccgggaugc

19

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gccccacccu cauaggccu

19

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<400> SEQUENCE: 206

cggcacccuc auaggccug

19

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<400> SEQUENCE: 207

ggcacccuca uaggccugg

19

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<400> SEQUENCE: 208

gcacccuau aggccugga

19

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cacccuaua ggcuggag

19

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<400> SEQUENCE: 210

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<400> SEQUENCE: 211

cccuauaagg ccuggaguu

19

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cucauaggcc uggaguuua

19

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<400> SEQUENCE: 213

ucauaggccu ggaguuuau

19

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<400> SEQUENCE: 214

cauaggccug gaguuuauu

19

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auagggcugg aguuuauuc

19

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<400> SEQUENCE: 216

uaggccugga guuuauucg

19

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<400> SEQUENCE: 217

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19

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ggccuggagu uuauucgga 19

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<400> SEQUENCE: 219

gccuggaguu uauucgaa 19

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<400> SEQUENCE: 220

gcugccucu acuccccag 19

<210> SEQ ID NO 221
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<400> SEQUENCE: 221

ccugccucua cuccccagc 19

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<400> SEQUENCE: 222

gccuguucc cugaggacc 19

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<220> FEATURE:
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<400> SEQUENCE: 223

ccugguuccc ugaggacca 19

<210> SEQ ID NO 224
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<400> SEQUENCE: 224

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19

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19

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<400> SEQUENCE: 226

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19

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19

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<400> SEQUENCE: 228

ugccaucugc ugccggagc

19

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<400> SEQUENCE: 229

gcacaucugcu gccggagcc

19

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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

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19

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 231

caucugcugc cgagccgg

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 232

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19

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 234

cggcgccccgc cugcaacca

19

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<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<400> SEQUENCE: 235

agaccugaa cugaacggc

19

<210> SEQ ID NO 236

<211> LENGTH: 19

<212> TYPE: RNA

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 236

gcucacuccu ccagguca

19

<210> SEQ ID NO 237
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 237

agccagucuc acugccugg

19

<210> SEQ ID NO 238
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 238

cgcgucccg cccgccccga

19

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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 239

gagccgcugc ugcaacgac

19

<210> SEQ ID NO 240
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 240

auccuggcug ggagecuggg

19

<210> SEQ ID NO 241
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<400> SEQUENCE: 241

cgugaagggg cgcgccgaa

19

<210> SEQ ID NO 242

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<211> LENGTH: 19
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aaguucagga gcagggcgc

19

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aggacugugc aggagcuga

19

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uugagccuug cggugggga

19

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<400> SEQUENCE: 245

guccacgccc gcgccgccc

19

<210> SEQ ID NO 246
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 246

accuagaggc cgugcgcgg

19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 247

ugcuguccug gcgaggaga

19

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<210> SEQ ID NO 248
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 248

gaggggccagg ggagagguu

19

<210> SEQ ID NO 249
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 249

ggagcugacg gugcccaug

19

<210> SEQ ID NO 250
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 250

cggccaccag gaccgcug

19

<210> SEQ ID NO 251
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 251

cagcagcagc aguggcagc

19

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<400> SEQUENCE: 252

acccaggagc agcagcagc

19

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cgcacgggcg cccggggg 19

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Sequence/siNA antisense region
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<400> SEQUENCE: 254

gcccguccucg uccuccugc 19

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<400> SEQUENCE: 255

caccagcucc ucguaguucg 19

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cucggAACgc aaggcuagc 19

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<400> SEQUENCE: 257

uucggccagg ccgguccucc 19

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gguuuccgugc ucgggugcu 19

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Sequence/siNA antisense region
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gggguguaag guggcugug

19

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<400> SEQUENCE: 260

ccacggaucc uuggcgca

19

<210> SEQ ID NO 261
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<400> SEQUENCE: 261

guaggugcca ggcaaccuc

19

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<220> FEATURE:
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cucuuucagc accaccacg

19

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<400> SEQUENCE: 263

cugcgagagg ugguccu

19

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<400> SEQUENCE: 264

gcgggcagug cgcu

19

<210> SEQ ID NO 265
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Sequence/siNA antisense region

<400> SEQUENCE: 265

agccuggggcc ugcaggcg

19

<210> SEQ ID NO 266
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<400> SEQUENCE: 266

gagguaauccc cggcgggca

19

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<220> FEATURE:
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<400> SEQUENCE: 267

gacaugcagg aucuuggug

19

<210> SEQ ID NO 268
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<400> SEQUENCE: 268

aggaagaagg ccauggaag

19

<210> SEQ ID NO 269
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<220> FEATURE:
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<400> SEQUENCE: 269

caucuuucacc aggaaggcca

19

<210> SEQ ID NO 270
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<220> FEATURE:
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<400> SEQUENCE: 270

cuccagcagg ucgccacuc

19

<210> SEQ ID NO 271
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<220> FEATURE:
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gggcaacuuc aaggccagc

19

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<400> SEQUENCE: 272

cucgauguag ucgacaugg

19

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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 273

aaagacagag gaguccucc

19

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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 274

ccacgguaug cucugggca

19

<210> SEQ ID NO 275
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 275

gguaauccgc uccaggguuc

19

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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 276

cgcggguac cguggaggg

19

<210> SEQ ID NO 277
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<220> FEATURE:
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<400> SEQUENCE: 277

ggggggcugg uauucaucc

19

<210> SEQ ID NO 278
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 278

caccaggcug ccuccgucg

19

<210> SEQ ID NO 279
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<220> FEATURE:
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<400> SEQUENCE: 279

gcuuaggaga uacaccucc

19

<210> SEQ ID NO 280
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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 280

gucacucugu augcuggug

19

<210> SEQ ID NO 281
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 281

gcccucgauu ucccgugg

19

<210> SEQ ID NO 282
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 282

gucggugacc augaccug

19

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<210> SEQ ID NO 283
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 283

cucgggcaca uucucgaag

19

<210> SEQ ID NO 284
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<220> FEATURE:
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<400> SEQUENCE: 284

gaagcggguc ccguccucc

19

<210> SEQ ID NO 285
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<220> FEATURE:
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<400> SEQUENCE: 285

cuugcuggcc ugucugugg

19

<210> SEQ ID NO 286
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<212> TYPE: RNA
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<400> SEQUENCE: 286

ggugccauga cugucacac

19

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<400> SEQUENCE: 287

gaccaccccu gccaggugg

19

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<400> SEQUENCE: 288

gccggcaucc cggccgcug

19

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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 289

gcuggcaccc uuggccacg

19

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<400> SEQUENCE: 290

cacgcgcagg cugcgcgaug

19

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<220> FEATURE:
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<400> SEQUENCE: 291

cuuuccuuagg caguugagc

19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 292

ggugccgcua accgugccc

19

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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 293

aaacuccagg ccuaugagg

19

<210> SEQ ID NO 294
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 294

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cagcuggccuu uuuccgaaua 19

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<400> SEQUENCE: 295

uggccccaca ggcuggacc 19

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<212> TYPE: RNA
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Sequence/siNA antisense region
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<400> SEQUENCE: 296

gggcagcagc accaccagu 19

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<212> TYPE: RNA
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Sequence/siNA antisense region
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<400> SEQUENCE: 297

gcuguaccca cccgccagg 19

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<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 298

ggcggeguug aggacgcgg 19

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Sequence/siNA antisense region
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<400> SEQUENCE: 299

ccucgcccagg cgcuggcag 19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 300

gaccagcagc accccagcc

19

<210> SEQ ID NO 301
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 301

gaaguugccg gcageggug

19

<210> SEQ ID NO 302
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 302

gaggcaggca ucgucccg

19

<210> SEQ ID NO 303
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 303

agcugaggcu ggggaguag

19

<210> SEQ ID NO 304
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 304

aacugugaug accucggga

19

<210> SEQ ID NO 305
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 305

uugggcauug guggccca

19

<210> SEQ ID NO 306
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 306

cagggucacc ggcuggugu

19

<210> SEQ ID NO 307

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 307

guuggucccc aaagucccc

19

<210> SEQ ID NO 308

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

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guccacacag cggccaaag

19

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<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 309

cucccccuggg gcaaagagg

19

<210> SEQ ID NO 310

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 310

ggaggcacca augaugucc

19

<210> SEQ ID NO 311

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

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<400> SEQUENCE: 311

gcaggugcug cagucgcug

19

<210> SEQ ID NO 312

<211> LENGTH: 19

<212> TYPE: RNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 312

cccacucugu gacacaaaag

19

<210> SEQ ID NO 313
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 313

ggcagcagcc ugugauugc

19

<210> SEQ ID NO 314
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 314

ugcaaugcca gccacgugg

19

<210> SEQ ID NO 315
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 315

ggcagacacgc aucauggcu

19

<210> SEQ ID NO 316
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 316

caggugugac uccggcucg

19

<210> SEQ ID NO 317
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 317

ucucugccuc aacucggcc

19

<210> SEQ ID NO 318

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 318

ggcagagaag uggaucagu

19

<210> SEQ ID NO 319
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 319

cucauugaug acaucuuug

19

<210> SEQ ID NO 320
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 320

guccucaggg aaccaggcc

19

<210> SEQ ID NO 321
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 321

gggggucagu acccgcgugg

19

<210> SEQ ID NO 322
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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 322

cagggcggcc accagguug

19

<210> SEQ ID NO 323
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 323

cccaugggug cuggggggc

19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 324

aaacagcugc caaccugcc

19

<210> SEQ ID NO 325
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 325

ugaccauaca guccugcaa

19

<210> SEQ ID NO 326
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
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<400> SEQUENCE: 326

uguaggcccc gagugugcu

19

<210> SEQ ID NO 327
<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 327

gacggcugug gccaucgu

19

<210> SEQ ID NO 328
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 328

aucuggggcg cagcgggcg

19

<210> SEQ ID NO 329
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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gcagcucagc agcuccuca 19

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<400> SEQUENCE: 330

acuccuggag aaacuggag 19

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<211> LENGTH: 19
<212> TYPE: RNA
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Sequence/siNA antisense region
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<400> SEQUENCE: 331

cucgccccgc cgcuuccca 19

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<212> TYPE: RNA
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Sequence/siNA antisense region
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<400> SEQUENCE: 332

cccuugggcc uccaugcgc 19

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<212> TYPE: RNA
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Sequence/siNA antisense region
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<400> SEQUENCE: 333

ccggcagacc agcuugccc 19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 334

cccaaaagcg uugugggcc 19

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 335

ggcguagaca cccucaccc

19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 336

caggcagcac cuggcaaug

19

<210> SEQ ID NO 337
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 337

gcaguuggcc uggguuagc

19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 338

uggagcugug uggacgcug

19

<210> SEQ ID NO 339
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 339

caugcuggcc ucagcuggu

19

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<212> TYPE: RNA
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<400> SEQUENCE: 340

gcaguggaca cgggucccc

19

<210> SEQ ID NO 341
<211> LENGTH: 19
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<220> FEATURE:
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Sequence/siNA antisense region

<400> SEQUENCE: 341
gacguggccc uguuggugg 19

<210> SEQ ID NO 342
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<220> FEATURE:
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<400> SEQUENCE: 342
ggagcugcag ccugugagg 19

<210> SEQ ID NO 343
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 343
guccuccacc ucccaagg 19

<210> SEQ ID NO 344
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 344
cgccuugugg gugccaagg 19

<210> SEQ ID NO 345
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<212> TYPE: RNA
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ucguggccuc agcacaggc 19

<210> SEQ ID NO 346
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<400> SEQUENCE: 346
gcacugguug ggcugaccu 19

<210> SEQ ID NO 347
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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ggccuuccug uggcccacg

19

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gcaggaagcg uggaugcug

19

<210> SEQ ID NO 349
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 349

cagaccuggg gcauggcag

19

<210> SEQ ID NO 350
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 350

cuccuugacu uugcaauucc

19

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 351

aggggccggg auuccaugh

19

<210> SEQ ID NO 352
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 352

cacggucacc ugcuccuga

19

<210> SEQ ID NO 353
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 353

ccagccccucc ucgcaggcc

19

<210> SEQ ID NO 354
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 354

acugcagcca gucagggucc

19

<210> SEQ ID NO 355
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 355

ggaggguccca gggaggggca

19

<210> SEQ ID NO 356
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 356

guagggcccc aggacgugg

19

<210> SEQ ID NO 357
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 357

acacguguug ucuacggcg

19

<210> SEQ ID NO 358
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 358

gucccccggcuc cugacuaca

19

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<210> SEQ ID NO 359
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 359

gcugccugua gugcugacg

19

<210> SEQ ID NO 360
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 360

cacggccccu ucgcuggug

19

<210> SEQ ID NO 361
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 361

gcagauggca acggcuguc

19

<210> SEQ ID NO 362
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 362

caggugccgg cuccggcag

19

<210> SEQ ID NO 363
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 363

cuccuggggag gcccugcgcc

19

<210> SEQ ID NO 364
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 364

auggggcugu cacuggagc

19

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<210> SEQ ID NO 365
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 365

ccagacaccc auccuggga

19

<210> SEQ ID NO 366
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 366

cccagcccuu gaccuccc

19

<210> SEQ ID NO 367
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 367

accuuuuuaa agcucagcc

19

<210> SEQ ID NO 368
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 368

agagaggggac aagucggaa

19

<210> SEQ ID NO 369
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 369

ccaggccaug gagggcuga

19

<210> SEQ ID NO 370
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 370

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caucccccauc cccucgugc 19

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<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 371

gccccggaaa ggccgaagc 19

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<212> TYPE: RNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 372

ucaaggggcca ggccagcag 19

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<212> TYPE: RNA
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Sequence/siNA antisense region
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<400> SEQUENCE: 373

gcaaggaggc ugccccacu 19

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<220> FEATURE:
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Sequence/siNA antisense region
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<400> SEQUENCE: 374

agagugagug aguuccagg 19

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<211> LENGTH: 19
<212> TYPE: RNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 375

ccuggggagg aggcacca 19

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 376

agcuuccugg caccuccac

19

<210> SEQ ID NO 377
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 377

ccccacagug agggaggga

19

<210> SEQ ID NO 378
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 378

uguuuugaaug gugaaaugc

19

<210> SEQ ID NO 379
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 379

cccgagcaca gcucgaccu

19

<210> SEQ ID NO 380
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 380

ugggagcagc uggcagcac

19

<210> SEQ ID NO 381
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 381

ccacggacau cggcacauu

19

<210> SEQ ID NO 382
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 382

caauaaaaagu caauucugcc

19

<210> SEQ ID NO 383

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 383

uggcacggaa caagagcuc

19

<210> SEQ ID NO 384

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 384

accugaggau ugaaugccu

19

<210> SEQ ID NO 385

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 385

ccugccuccu ugguggaga

19

<210> SEQ ID NO 386

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 386

ccauccaug ggaagaauc

19

<210> SEQ ID NO 387

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 387

gccccuacccg ccccccuccc

19

<210> SEQ ID NO 388

<211> LENGTH: 19

<212> TYPE: RNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 388

acgauguuug ucccgugcag

19

<210> SEQ ID NO 389
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 389

uuucacacac acccccccaa

19

<210> SEQ ID NO 390
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 390

augaggggcca ucagcacccu

19

<210> SEQ ID NO 391
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 391

cuccacaguu agcuggaga

19

<210> SEQ ID NO 392
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 392

gggagcccc aggggcuuc

19

<210> SEQ ID NO 393
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 393

cuaagccucc auuaaucag

19

<210> SEQ ID NO 394

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 394

uagaugccau ccagaagc

19

<210> SEQ ID NO 395
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 395

cugucuccag ccucuggcu

19

<210> SEQ ID NO 396
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 396

ugaccaccag gggcgcaacc

19

<210> SEQ ID NO 397
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 397

aaacccaaggc acagccugu

19

<210> SEQ ID NO 398
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 398

gaguuaagggu ggcucagga

19

<210> SEQ ID NO 399
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 399

acagccuggc auagagcag

19

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<210> SEQ ID NO 400
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 400

ccuuuggug uugcuagca

19

<210> SEQ ID NO 401
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 401

auggcucccc gcaggcac

19

<210> SEQ ID NO 402
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 402

ccgagucagu ccuagguga

19

<210> SEQ ID NO 403
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 403

augcaccacu gcacacugc

19

<210> SEQ ID NO 404
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 404

gguuggcuga gacagugca

19

<210> SEQ ID NO 405
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 405

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cugccggua guggagcg 19

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<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 406

ggggugcgaa uguguaccc 19

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<210> SEQ ID NO 407
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 407

uucuuccucu gugaaguag 19

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<210> SEQ ID NO 408
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 408

cccccucugg uuccagguu 19

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<210> SEQ ID NO 409
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 409

gugagcuugg caggcacgc 19

```
<210> SEQ ID NO 410
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 410

uggcucaguu ccugcugug 19

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<210> SEQ ID NO 411
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 411

cagcccaauc ugcguuuucu

19

<210> SEQ ID NO 412
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 412

gaggcuuggc uucagagcc

19

<210> SEQ ID NO 413
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 413

agccggguga aguaagaag

19

<210> SEQ ID NO 414
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 414

cguaaaaaug aggagccca

19

<210> SEQ ID NO 415
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 415

cccagccuca cuguuaccc

19

<210> SEQ ID NO 416
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 416

cuggucugug uuccccuuc

19

<210> SEQ ID NO 417
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target

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Sequence/siNA antisense region

<400> SEQUENCE: 417
caucacucac cgagcucc 19

<210> SEQ ID NO 418
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 418
cugcaggcau cguucugcc 19

<210> SEQ ID NO 419
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 419
acggaaaaag uuccaugcc 19

<210> SEQ ID NO 420
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 420
aaucaggccu gggugauaa 19

<210> SEQ ID NO 421
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 421
aucuccgcca ggccaguga 19

<210> SEQ ID NO 422
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 422
cgaccgaugcc uuagaagca 19

<210> SEQ ID NO 423
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 423

guuguuggcc cucuccccc

19

<210> SEQ ID NO 424
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 424

ggugcucaag gagggacag

19

<210> SEQ ID NO 425
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 425

gcuugcuagg guggggcug

19

<210> SEQ ID NO 426
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 426

cccaaaagau aaaugucug

19

<210> SEQ ID NO 427
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 427

ggcaacagag aggacagac

19

<210> SEQ ID NO 428
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 428

aaaaguuggc uguaaaaag

19

<210> SEQ ID NO 429
<211> LENGTH: 19

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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 429

aaagcaaaac agguguaga

19

<210> SEQ ID NO 430
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 430

aaaaaucuuc aaguuacaa

19

<210> SEQ ID NO 431
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 431

ugcuacaaaa cccagaaaa

19

<210> SEQ ID NO 432
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 432

ucaccuaauu aaauaaaaau

19

<210> SEQ ID NO 433
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 433

uguuuuuauu uaaaaaagu

19

<210> SEQ ID NO 434
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<400> SEQUENCE: 434

caucccgccc gcugaccac

19

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<210> SEQ ID NO 435
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 435

gcaucccgcc cgugaccca

19

<210> SEQ ID NO 436
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 436

ggccuaugag ggugccgcu

19

<210> SEQ ID NO 437
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 437

aggccuauga gggugccgc

19

<210> SEQ ID NO 438
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 438

caggccuaug agggugccg

19

<210> SEQ ID NO 439
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 439

ccaggccuaa gagggugucc

19

<210> SEQ ID NO 440
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 440

uccaggccua ugagguguc

19

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<210> SEQ ID NO 441
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 441

cuccaggccu augagggug

19

<210> SEQ ID NO 442
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 442

acuccaggcc uaugagggu

19

<210> SEQ ID NO 443
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 443

aacuccaggc cuauagagg

19

<210> SEQ ID NO 444
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 444

uaaacuccag gccuaugag

19

<210> SEQ ID NO 445
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 445

auaaacucca ggccuauga

19

<210> SEQ ID NO 446
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 446

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aauaaaacucc aggccuaug 19

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<210> SEQ ID NO 447
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 447

gaauaaaacuc caggccuau 19

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<210> SEQ ID NO 448
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 448

cgaaauaaacu ccagggcua 19

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<210> SEQ ID NO 449
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 449

ccgaauaaac uccaggccu 19

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<210> SEQ ID NO 450
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 450

uccgaauaaa cuccaggcc 19

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<210> SEQ ID NO 451
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 451

uuccgaauaa acuccaggc 19

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<210> SEQ ID NO 452
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
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<400> SEQUENCE: 452

cugggggua gaggcaggc

19

<210> SEQ ID NO 453
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 453

gcuggggagu agaggcagg

19

<210> SEQ ID NO 454
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 454

gguccucagg gaaccaggc

19

<210> SEQ ID NO 455
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 455

ugguccucag ggaaccagg

19

<210> SEQ ID NO 456
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 456

cugguccuca gggAACAG

19

<210> SEQ ID NO 457
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 457

gcugguccuc agggAACCA

19

<210> SEQ ID NO 458
<211> LENGTH: 19
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 458

agacacccuc accccccaaa

19

<210> SEQ ID NO 459

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 459

uagacacccu caccccaa

19

<210> SEQ ID NO 460

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 460

gcuccggcag cagauggca

19

<210> SEQ ID NO 461

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 461

ggcuccggca gcagauggc

19

<210> SEQ ID NO 462

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 462

cggcuccggc agcagaugg

19

<210> SEQ ID NO 463

<211> LENGTH: 19

<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 463

ccggcuccgg cagcagaug

19

<210> SEQ ID NO 464

<211> LENGTH: 19

<212> TYPE: RNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region

<400> SEQUENCE: 464

gccggcucccg gcagcagau

19

<210> SEQ ID NO 465
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 465

aggccuggag uuuauucgga aaa

23

<210> SEQ ID NO 466
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 466

ccucauaggc cuggaguuua uuc

23

<210> SEQ ID NO 467
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 467

cacccuauaa ggccuggagu uua

23

<210> SEQ ID NO 468
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 468

uagcggcacc cucauaggcc ugg

23

<210> SEQ ID NO 469
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region

<400> SEQUENCE: 469

cggcacccuc auaggccugg agu

23

<210> SEQ ID NO 470

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<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region

<400> SEQUENCE: 470

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uaggccugga guuuauucgg aaa 23

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<210> SEQ ID NO 471
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region

<400> SEQUENCE: 471

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ggcacccuca uaggeccugga guuu 23

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<210> SEQ ID NO 472
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region

<400> SEQUENCE: 472

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ggccugguuc ccugaggacc agc 23

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<210> SEQ ID NO 473
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence

<400> SEQUENCE: 473

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gccuggaguu uauucggaat t 21

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<210> SEQ ID NO 474
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence

<400> SEQUENCE: 474

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ucauaggccu ggaguuuaut t 21

```

<210> SEQ ID NO 475
<211> LENGTH: 21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
```

```
<400> SEQUENCE: 475
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```
cccucauagg ccuggaguut t
```

21

```
<210> SEQ ID NO 476
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
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```
<400> SEQUENCE: 476
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```
ggggcacccu cauaggccut t
```

21

```
<210> SEQ ID NO 477
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
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<400> SEQUENCE: 477
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```
gcacccuau aggccuggat t
```

21

```
<210> SEQ ID NO 478
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
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<400> SEQUENCE: 478
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```
gcccuggagu uuauucggat t
```

21

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<210> SEQ ID NO 479
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<400> SEQUENCE: 479

cacccuaua ggccuggagt t

21

<210> SEQ ID NO 480
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<400> SEQUENCE: 480

ccugguuccc ugaggaggcat t

21

<210> SEQ ID NO 481
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<400> SEQUENCE: 481

uuccgaauaa acuccaggct t

21

<210> SEQ ID NO 482
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<400> SEQUENCE: 482

auaaacucca ggccuaugat t

21

<210> SEQ ID NO 483
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)

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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence

<400> SEQUENCE: 483

aacuccaggc cuauaggggt t

21

<210> SEQ ID NO 484

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(19)

<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence

<400> SEQUENCE: 484

aggccuauga gggugccgct t

21

<210> SEQ ID NO 485

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(19)

<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence

<400> SEQUENCE: 485

ucccaggccua ugagggugct t

21

<210> SEQ ID NO 486

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(19)

<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence

<400> SEQUENCE: 486

ucccgaaauaaa cuccaggcct t

21

<210> SEQ ID NO 487

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(19)

<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence

<400> SEQUENCE: 487

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cuccaggccu augagggugt t 21

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<210> SEQ ID NO 488
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<400> SEQUENCE: 488

ugguccucag ggaaccaggt t 21

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<210> SEQ ID NO 489
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region (stab04)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<220> FEATURE:
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<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
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<400> SEQUENCE: 489

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<210> SEQ ID NO 490
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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inverted abasic, inverted nucleotide or other terminal cap that is
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

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<400> SEQUENCE: 490

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<210> SEQ ID NO 491
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<222> LOCATION: (1)..(5)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,

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optionally present

<400> SEQUENCE: 491

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<210> SEQ ID NO 492
<211> LENGTH: 21
<212> TYPE: DNA
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<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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optionally present
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

<400> SEQUENCE: 492

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<210> SEQ ID NO 493
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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Sequence/siNA sense region (stab04)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence

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<220> FEATURE:
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<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(16)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 493

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gcacccuau aggcuggat t

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<210> SEQ ID NO 494
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
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<222> LOCATION: (3)..(5)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

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<400> SEQUENCE: 494

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<210> SEQ ID NO 495
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target

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Sequence/siNA sense region (stab04)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
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<222> LOCATION: (3)..(7)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 495
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<210> SEQ ID NO 496
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(18)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

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<400> SEQUENCE: 496

ccuggguuccc ugaggaccat t

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<210> SEQ ID NO 497
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)...(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)...(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)...(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)...(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate 3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 497

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<210> SEQ ID NO 498
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)...(2)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)...(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)...(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)...(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)...(20)

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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 498

auaaacucca ggccuaugat t

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<210> SEQ ID NO 499
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(6)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 499

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<210> SEQ ID NO 500
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 500
aggccuauga gggugccgct t

<210> SEQ_ID NO 501
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 501
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21

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<210> SEQ_ID NO 502
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(14)

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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 502
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uccgaauaaa cuccaggcct t
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<210> SEQ_ID NO 503
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 503
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cuccaggccu augaggugt t
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21

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<210> SEQ_ID NO 504
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab05)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(16)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 504

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<210> SEQ_ID NO 505
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siRNA sense region (stab07)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(8)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(19)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present

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<400> SEQUENCE: 505

gccuggaguu uauucggaa t

21

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<210> SEQ_ID NO 506
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<400> SEQUENCE: 506

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<223> OTHER INFORMATION: 2'-deoxy
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<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<210> SEQ ID NO 509
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<223> OTHER INFORMATION: 2'-deoxy
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-deoxy

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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
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<223> OTHER INFORMATION: 2'-deoxy  
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<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,  
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<400> SEQUENCE: 509
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<210> SEQ ID NO 510  
<211> LENGTH: 21  
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<400> SEQUENCE: 510
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<210> SEQ_ID_NO 511
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER_INFORMATION: Description_of_Artificial_Sequence: Target
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER_INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<223> OTHER_INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER_INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER_INFORMATION: 2'-deoxy
<220> FEATURE:
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<223> OTHER_INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER_INFORMATION: 2'-deoxy
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<223> OTHER_INFORMATION: 2'-deoxy-2'Fluoro
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<220> FEATURE:
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<223> OTHER_INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER_INFORMATION: 2'-deoxy
<220> FEATURE:
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<223> OTHER_INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<400> SEQUENCE: 511
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<210> SEQ_ID_NO 512
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<220> FEATURE:
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<223> OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety,
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<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(5)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<222> LOCATION: (6)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<222> LOCATION: (17)..(18)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,
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      optionally present

<400> SEQUENCE: 512
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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(7)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(18)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 513
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<210> SEQ ID NO 514
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<212> TYPE: DNA
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (3)..(5)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<222> LOCATION: (6)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 514
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: 2'-deoxy
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<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(19)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 515
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
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<400> SEQUENCE: 516

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<210> SEQ ID NO 517
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(16)
<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 517

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21

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<220> FEATURE:
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 518

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21

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<210> SEQ ID NO 519
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<220> FEATURE:

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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

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<400> SEQUENCE: 519

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21

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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<220> FEATURE:

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<400> SEQUENCE: 520

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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<222> LOCATION: (2)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (5)..(8)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 521

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gccuggaguu uauucggaat t

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<210> SEQ ID NO 522
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region (stab18)
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<223> OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (5)..(7)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (8)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (15)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

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<400> SEQUENCE: 522

ucauaggccu ggaguuuaut t

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<210> SEQ ID NO 523
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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Sequence/siNA sense region (stab18)
<220> FEATURE:
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<222> LOCATION: (1)..(1)

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<222> LOCATION: (1)..(5)  
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as  
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<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (8)..(10)  
<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (11)..(13)  
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (14)..(17)  
<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (21)..(21)  
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,  
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<400> SEQUENCE: 523
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cccucauagg ccuggaguu t

21

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<210> SEQ ID NO 524  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target  
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<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(1)  
<223> OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety,  
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<220> FEATURE:  
<221> NAME/KEY: misc_feature  
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<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(19)  
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as  
      described for this sequence  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (2)..(2)  
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature
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<222> LOCATION: (3)..(4)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<400> SEQUENCE: 524

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ggggcacccu cauaggccut t

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<210> SEQ ID NO 525
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<220> FEATURE:
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro

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<223> OTHER INFORMATION: 2'-O-methyl  
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (11)..(13)  
<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (14)..(16)  
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (17)..(19)  
<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (21)..(21)  
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,  
inverted abasic, inverted nucleotide or other terminal cap that is  
optionally present  
  
<400> SEQUENCE: 525
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gcacccuau aggccuggat t

21

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<210> SEQ ID NO 526  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target  
Sequence/siRNA sense region (stab18)  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(1)  
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,  
inverted abasic, inverted nucleotide or other terminal cap that is  
optionally present  
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<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(2)  
<223> OTHER INFORMATION: 2'-O-methyl  
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<222> LOCATION: (1)..(19)  
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as  
described for this sequence  
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (6)..(9)  
<223> OTHER INFORMATION: 2'-O-methyl  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (10)..(12)  
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
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<222> LOCATION: (13)..(13)  
<223> OTHER INFORMATION: 2'-O-methyl  
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<222> LOCATION: (14)..(16)  
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro  
<220> FEATURE:  
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present

<400> SEQUENCE: 526

ggccuggag uuaauucggat t
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21

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<210> SEQ_ID NO 527
<211> LENGTH: 21
<212> TYPE: DNA
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<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
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<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (3)..(7)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present
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<400> SEQUENCE: 527
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<210> SEQ ID NO 528
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
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<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(16)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

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<400> SEQUENCE: 528

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<210> SEQ ID NO 529
<211> LENGTH: 21
<212> TYPE: DNA
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Sequence/siNA antisense region (stab08)
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<222> LOCATION: (5)..(7)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(18)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 529
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uuccgaaauaa acuccaggct t

21

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<211> LENGTH: 21
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<220> FEATURE:
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<222> LOCATION: (6)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 530

auaaacucca ggcuaugat t

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<210> SEQ ID NO 531
<211> LENGTH: 21
<212> TYPE: DNA
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<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 531

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<210> SEQ ID NO 532
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
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<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:

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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 532

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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
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<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 533
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<210> SEQ ID NO 534
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<220> FEATURE:
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<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 534
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<210> SEQ ID NO 535
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
      3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 535
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<212> TYPE: DNA
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<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
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<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:

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<223> OTHER INFORMATION: 2'-O-methyl
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 536

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<210> SEQ ID NO 537
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 537

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<210> SEQ ID NO 538
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<400> SEQUENCE: 538

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<210> SEQ ID NO 539
<211> LENGTH: 21
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<222> LOCATION: (21)...(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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optionally present
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<400> SEQUENCE: 539

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<210> SEQ ID NO 540
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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optionally present
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<222> LOCATION: (1)...(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
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<222> LOCATION: (21)...(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
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<400> SEQUENCE: 540

gcccacccu cauaggccut t

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<210> SEQ ID NO 541
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA sense region (stab09)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(1)
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<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<400> SEQUENCE: 541

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gcacccucau aggccuggat t

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<210> SEQ ID NO 542
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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      optionally present

<400> SEQUENCE: 542

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ggccuggagu uuauucggat t

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<210> SEQ ID NO 543
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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<400> SEQUENCE: 543

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cacccuaua ggccuggagt t 21

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<210> SEQ ID NO 544
<211> LENGTH: 21
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<220> FEATURE:
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<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present
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<400> SEQUENCE: 544

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<210> SEQ ID NO 545
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab10)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 545

uuccgaaaua acuccaggct t 21

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<210> SEQ ID NO 546
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 546

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<210> SEQ ID NO 547
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 547

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| aacuccaggc cuauaggggt t | 21 |
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<210> SEQ ID NO 548
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<212> TYPE: DNA
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 548

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| aggccuauga gggugccgct t | 21 |
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<210> SEQ ID NO 549
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region (stab10)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 549

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| uccaggccua ugagggugct t | 21 |
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<210> SEQ ID NO 550
<211> LENGTH: 21
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 550

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uccgaaauaaa cuccaggcct t

21

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<210> SEQ ID NO 551
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 551

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cuccaggccu augagggugt t

21

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<210> SEQ ID NO 552
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<212> TYPE: DNA
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 552

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ugguccucag ggaaccaggt t

21

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<210> SEQ ID NO 553
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
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<220> FEATURE:
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<222> LOCATION: (5)..(7)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (12)..(15)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

<400> SEQUENCE: 553
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uuccgaaaua acuccaggct t

21

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<212> TYPE: DNA
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (3)..(5)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(9)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxygen-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 554
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21

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<210> SEQ_ID NO 555
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<212> TYPE: DNA
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present

<400> SEQUENCE: 555
aacuccaggc cuaugagggt t

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21

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<210> SEQ_ID NO 556
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target

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Sequence/siNA antisense region (stab19)
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
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<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

<400> SEQUENCE: 556

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aggccuauga gggugccgct t
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21

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<210> SEQ ID NO 557
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
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<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 557
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uccaggccua ugagggugct t

21

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<210> SEQ ID NO 558
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(10)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present

<400> SEQUENCE: 558
uccgaauaaa cuccaggcct t

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<210> SEQ_ID NO 559
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<220> FEATURE:
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<222> LOCATION: (1)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (8)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<222> LOCATION: (13)..(17)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present

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<400> SEQUENCE: 559

cuccaggccu augagggugt t

21

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<210> SEQ_ID NO 560
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target

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Sequence/siNA antisense region (stab19)
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(3)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(14)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(16)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

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<400> SEQUENCE: 560

ugguccucag ggaaccagg t

21

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<210> SEQ ID NO 561
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

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<400> SEQUENCE: 561

uuccgaaaua acuccaggct t

21

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<210> SEQ ID NO 562
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)

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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
      described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
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<400> SEQUENCE: 562

auaaacucca ggccuaugat t

21

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<210> SEQ ID NO 563
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
      Sequence/siRNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
      described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
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<400> SEQUENCE: 563

aacuccagggc cuauaggggt t

21

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<210> SEQ ID NO 564
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
      described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap
      that is optionally present
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<400> SEQUENCE: 564

aggccuauga gggugccgct t

21

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<210> SEQ ID NO 565
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
      Sequence/siRNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
      described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

<400> SEQUENCE: 565

uccaggccua ugagggugct t

21

<210> SEQ ID NO 566
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

<400> SEQUENCE: 566

uccgaauaaa cuccaggcct t

21

<210> SEQ ID NO 567
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

<400> SEQUENCE: 567

cuccaggccu augagggugt t

21

<210> SEQ ID NO 568
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siNA antisense region (stab22)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
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<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
inverted abasic, inverted nucleotide or other terminal cap that is
optionally present

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<400> SEQUENCE: 568
ugguccucag ggaaccagg t

21

<210> SEQ_ID NO 569
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region (stab25)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(7)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(11)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(18)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate 3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 569
uuccgaaauaa acuccaggct t

21

<210> SEQ_ID NO 570
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA antisense region (stab25)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as described for this sequence
<220> FEATURE:
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<222> LOCATION: (4)..(5)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (6)..(9)

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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (13)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 570

auaaacucca ggccuaugat t

21

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<210> SEQ ID NO 571
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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    Sequence/siRNA antisense region (stab25)
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)
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<400> SEQUENCE: 571

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aacuccaggc cuauaggggt t

21

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<210> SEQ ID NO 572
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab25)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
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<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(13)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 572

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aggccuauga gggugccgct t

21

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<210> SEQ ID NO 573
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
Sequence/siRNA antisense region (stab25)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(9)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(16)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 573

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<210> SEQ ID NO 574
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(6)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(10)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(14)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(17)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(19)

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<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 574

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<210> SEQ_ID NO 575
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siNA antisense region (stab25)
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
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<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(7)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (8)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(17)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 575

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cuccaggccu augagggugt t

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<210> SEQ_ID NO 576
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Target
    Sequence/siNA antisense region (stab25)
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
      described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(8)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(14)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(16)
<223> OTHER INFORMATION: 2'-deoxy-2'Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (17)..(19)
<223> OTHER INFORMATION: 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
      3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 576

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ugguccucag ggaaccagg t

21

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<210> SEQ ID NO 577
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA sense
      region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n is any ribonucleotide unmodified or modified
      as described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present

<400> SEQUENCE: 577

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nnnnnnnnnn nnnnnnnnnn n

21

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<210> SEQ ID NO 578
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA
      antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n is any ribonucleotide unmodified or modified
      as described for this sequence

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally absent)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal glyceryl moiety or
    inverted deoxyabasic (optionally present)

<400> SEQUENCE: 578
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21

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<210> SEQ ID NO 579
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA sense
    region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n stands for any ribonucleotide wherein any
    pyrimidine nucleotide present is 2'-Fluoro and any purine
    nucleotide present is 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally absent)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide

<400> SEQUENCE: 579
nnnnnnnnnn nnnnnnnnnn n

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21

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<210> SEQ ID NO 580
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA
    antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n stands for any ribonucleotide wherein any
    pyrimidine nucleotide present is 2'-Fluoro and any purine
    nucleotide present is 2'-O-methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally absent)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal glyceryl moiety or
    inverted deoxyabasic (optionally present)

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<400> SEQUENCE: 580

21

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<210> SEQ ID NO 581
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA sense
      region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n stands for any ribonucleotide wherein any
      pyrimidine nucleotide present is 2'-O-methyl or 2'-Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
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<400> SEQUENCE: 581

21

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<210> SEQ_ID NO 582
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA
    antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n stands for any ribonucleotide wherein any
    pyrimidine nucleotide present is 2'-Fluoro
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally absent)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: attached terminal glyceryl moiety or 3'-3
    attached inverted deoxybasic (optionally present)
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<400> SEQUENCE: 582

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<210> SEQ ID NO 583
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Artificial Sequence: siNA sense
      region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n stands for any ribonucleotide wherein any
      pyrimidine nucleotide present is 2'-Fluoro and any purine
      nucleotide present is 2'-Deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: attached terminal deoxyabasic moiety, 3'-3
      attached inverted abasic, 3'-3 attached inverted nucleotide or
      other terminal cap that is optionally present

<400> SEQUENCE: 583

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nnnnnnnnnn nnnnnnnnnn n

21

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<210> SEQ ID NO 584
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: siNA
      antisense region
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: n stands for any ribonucleotide wherein any
      pyrimidine nucleotide present is 2'-Fluoro and any purine
      nucleotide present is 2'-Deoxy
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
      3'-Internucleotide Linkage (optionally absent)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(21)
<223> OTHER INFORMATION: n stands for any nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: attached terminal glyceryl moiety or 3'-3
      attached inverted deoxyabasic (optionally present)

<400> SEQUENCE: 584

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nnnnnnnnnn nnnnnnnnnn n

21

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<210> SEQ ID NO 585
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,
      inverted abasic, inverted nucleotide or other terminal cap that is
      optionally present
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,
    inverted abasic, inverted nucleotide or other terminal cap that is
    optionally present

<400> SEQUENCE: 585

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aguguuuaau gugaugaaut t

21

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<210> SEQ ID NO 586
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: attached terminal glyceryl moiety or inverted
    deoxyabasic (optionally present)

<400> SEQUENCE: 586

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auucaucaca uuuaacacut t

21

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<210> SEQ ID NO 587
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(8)
<223> OTHER INFORMATION: 2'-O-Methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: 2'-O-Methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(13)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature

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<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: 2'-O-Methyl
<220> FEATURE:
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<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<222> LOCATION: (16)..(17)
<223> OTHER INFORMATION: 2'-O-Methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(19)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)

<400> SEQUENCE: 587
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<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<223> OTHER INFORMATION: 2'-O-Methyl
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<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-Methyl
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<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<222> LOCATION: (7)..(8)
<223> OTHER INFORMATION: 2'-O-Methyl
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<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-O-Methyl
<220> FEATURE:
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<222> LOCATION: (12)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (16)..(19)
<223> OTHER INFORMATION: 2'-O-Methyl
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
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3'-Internucleotide Linkage (optionally present)
<220> FEATURE:
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: attached terminal glyceryl moiety or inverted
    deoxyabasic (optionally present)

<400> SEQUENCE: 588

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<210> SEQ ID NO 589
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety,
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    optionally present
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(10)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(13)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3
<220> FEATURE:
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<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,
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    optionally present

<400> SEQUENCE: 589

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<210> SEQ ID NO 590
<211> LENGTH: 21
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<222> LOCATION: (1)..(19)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence
<220> FEATURE:
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<222> LOCATION: (3)..(4)
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3

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<220> FEATURE:  
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<222> LOCATION: (9)..(9)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (12)..(15)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (20)..(20)  
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate  
    3'-Internucleotide Linkage (optionally present)  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (21)..(21)  
<223> OTHER INFORMATION: attached terminal glyceryl moiety or inverted  
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<400> SEQUENCE: 590

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<210> SEQ ID NO 591  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(19)  
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as  
    described for this sequence  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(4)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (1)..(1)  
<223> OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety,  
    inverted abasic, inverted nucleotide or other terminal cap that is  
    optionally present  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (5)..(8)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (9)..(10)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (11)..(11)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (12)..(13)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (14)..(14)  
<223> OTHER INFORMATION: 2'-deoxy
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<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (15)..(15)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (16)..(17)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (18)..(19)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (21)..(21)  
<223> OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety,  
inverted abasic, inverted nucleotide or other terminal cap that is  
optionally present  
  
<400> SEQUENCE: 591
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<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic  
<220> FEATURE:  
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<222> LOCATION: (1)..(2)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
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<222> LOCATION: (1)..(19)  
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as  
described for this sequence  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (3)..(4)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (5)..(5)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (6)..(6)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (7)..(8)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (9)..(9)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (10)..(11)  
<223> OTHER INFORMATION: 2'-deoxy  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (11)..(15)  
<223> OTHER INFORMATION: 2'-deoxy-2'-Fluoro or 2'-OCF3  
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<222> LOCATION: (16)..(19)  
<223> OTHER INFORMATION: 2'-deoxy
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: Phosphorothioate or Phosphorodithioate
    3'-Internucleotide Linkage (optionally present)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: attached terminal glyceryl moiety or inverted
    deoxyabasic (optionally present)

<400> SEQUENCE: 592

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<210> SEQ ID NO 593
<211> LENGTH: 14
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Target
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<400> SEQUENCE: 593

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14

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<210> SEQ ID NO 594
<211> LENGTH: 14
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
    Complementary Sequence/duplex forming oligonucleotide

<400> SEQUENCE: 594

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14

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<210> SEQ ID NO 595
<211> LENGTH: 23
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Self
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<400> SEQUENCE: 595

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23

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<210> SEQ ID NO 596
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Duplex
    forming oligonucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(22)
<223> OTHER INFORMATION: ribonucleotide unmodified or modified as
    described for this sequence

<400> SEQUENCE: 596

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What we claim is:

- 1.** A chemically modified short interfering nucleic acid molecule that mediates RNA interference against proprotein convertase subtilisin/kexin type 9 (PCSK9) target RNA, wherein:
 - (a) the nucleic acid molecule comprises a sense strand and a separate antisense strand;
 - (b) each strand of the nucleic acid molecule is independently 15 to 30 nucleotides in length;
 - (c) the antisense strand is complementary to PCSK9 target RNA sequence NM_174936;
 - (d) the sense strand includes a terminal cap moiety at its 5' and 3'-ends and the antisense strand includes a terminal cap moiety at its 3'-end; and

(e) the pyrimidine nucleotides of the sense strand and the antisense strand are chemically modified with 2'-deoxy, 2'-O-methyl, or 2'-deoxy-2'-fluoro nucleotides.

2. The short interfering nucleic acid molecule of claim 1, wherein the molecule comprises ~80% modified nucleotides.

3. The short interfering nucleic acid molecule of claim 1, wherein the molecule comprises ~90% modified nucleotides.

4. The short interfering nucleic acid molecule of claim 1, wherein the molecule comprises 100% modified nucleotides.

5. The short interfering nucleic acid molecule of claim 1, comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 phosphorothioate internucleotide linkages.

6. A composition comprising the short interfering nucleic acid molecule of claim 1 and a pharmaceutically acceptable carrier or diluent.

* * * * *