TREATMENT OF APOLIPOPROTEIN-A1 RELATED DISEASES BY INHIBITION OF NATURAL ANTISENSE TRANSCRIPT TO APOLIPOPROTEIN-A1

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims the priority of U.S. provisional patent application No. 61/102,681 filed October 3, 2008, U.S. provisional patent application No. 61/152,236 filed February 12, 2009, and U.S. provisional patent application No. 61/176,267 filed May 7, 2009, each of which is incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

[0002] Embodiments of the invention comprise oligonucleotides modulating expression and/or function of apolipoprotein and associated molecules.

BACKGROUND

[0003] DNA-RNA and RNA-RNA hybridization are important to many aspects of nucleic acid function including DNA replication, transcription, and translation. Hybridization is also central to a variety of technologies that either detect a particular nucleic acid or alter its expression. Antisense nucleotides, for example, disrupt gene expression by hybridizing to target RNA, thereby interfering with RNA splicing, transcription, translation, and replication. Antisense DNA has the added feature that DNA-RNA hybrids serve as a substrate for digestion by ribonuclease H, an activity that is present in most cell types. Antisense molecules can be delivered into cells, as is the case for oligodeoxynucleotides (ODNs), or they can be expressed from endogenous genes as RNA molecules. The FDA recently approved an antisense drug, VITRAVENE™ (for treatment of cytomegalovirus retinitis), reflecting that antisense has therapeutic utility.

SUMMARY

[0004] This Summary is provided to present a summary of the invention to briefly indicate the nature and substance of the invention. It is submitted with the understanding that it will not be used to interpret or limit the scope or meaning of the claims.

[0005] In one embodiment, the invention provides methods for inhibiting the action of a natural antisense transcript by using antisense oligonucleotide(s) targeted to any region of the natural antisense transcript resulting in up-regulation of the corresponding sense gene. It is also contemplated herein that inhibition of the natural antisense transcript can be achieved by

siRNA, ribozymes and small molecules, which are considered to be within the scope of the present invention.

[0006] One embodiment provides a method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro comprising contacting said cells or tissues with an antisense oligonucleotide 5 to 30 nucleotides in length wherein said oligonucleotide has at least 50% sequence identity to a reverse complement of a polynucleotide comprising 5 to 30 consecutive nucleotides within nucleotides 1-932 of SEQ ID NO:2 (Figure 8); thereby modulating function and/or expression of the apolipoprotein (ApoA1) polynucleotide in patient cells or tissues *in vivo* or *in vitro*.

[0007] In another preferred embodiment, an oligonucleotide targets a natural antisense sequence of ApoA1 polynucleotides, for example, polynucleotides set forth as SEQ ID NO: 2 , and any variants, alleles, homologs, mutants, derivatives, fragments and complementary sequences thereto. Examples of antisense oligonucleotides are set forth as SEQ ID NOS: 81-173.

[0008] Another embodiment provides a method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro comprising contacting said cells or tissues with an antisense oligonucleotide 5 to 30 nucleotides in length wherein said oligonucleotide has at least 50% sequence identity to a reverse complement of the an antisense of the apolipoprotein (ApoA1) polynucleotide; thereby modulating function and/or expression of the apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro.

[0009] Another embodiment provides a method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro comprising contacting said cells or tissues with an antisense oligonucleotide 5 to 30 nucleotides in length wherein said oligonucleotide has at least 50% sequence identity to an antisense oligonucleotide to an apolipoprotein (ApoA1) antisense polynucleotide; thereby modulating function and/or expression of the apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro.

[0010] In a preferred embodiment, a composition comprises one or more antisense oligonucleotides which bind to sense and/or antisense apolipoprotein (ApoA1) polynucleotides.

[0011] In another preferred embodiment, the oligonucleotides comprise one or more modified or substituted nucleotides.

[0012] In another preferred embodiment, the oligonucleotides comprise one or more modified bonds.

[0013] In yet another embodiment, the modified nucleotides comprise modified bases comprising phosphorothioate, methylphosphonate, peptide nucleic acids, or locked nucleic acid (LNA) molecules. Preferably, the modified nucleotides are locked nucleic acid molecules, including α-L-LNA.

[0014] In another preferred embodiment, the oligonucleotides are administered to a patient subcutaneously, intra-muscularly, intra- venously or intra-peritoneally.

[0015] In another preferred embodiment, the oligonucleotides are administered in a pharmaceutical composition. A treatment regimen comprises administering the antisense compounds at least once to patient, however, this treatment can be modified to include multiple doses over a period of time. The treatment can be combined with one or more other types of therapies.

[0016] In another preferred embodiment, the oligonucleotides are encapsulated in a liposome.

[0017] Other aspects are described *infra*.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018] Figure 1 is a graph of real time PCR results showing that the levels of ApoA1 mRNA in HepG2 cells are significantly increased 48 h after treatment with some of the antisense oligonucleotides to ApoA1 antisense DA327409ext. Bars RH3-RH597 correspond to samples treated with SEQ ID NOS:81-158.

[0019] Figure 2 is a graph of real time PCR results showing the fold change in ApoA1 mRNA (top panel) and ApoA1 natural antisense DA327409ext RNA (bottom panel) after treatment of HepG2 cells with naked LNA or phosphothioate oligonucleotides over 7 days as compared to control. Bars denoted as #6LNA, #11LNA, #6PS and #11PS represent SEQ ID NOS:159, 160, 161, 162 respectively.

[0020] Figure 3 is a graph of real time PCR results showing the fold change in ApoA1 mRNA (orange bars) and ApoA1 natural antisense DA327409ext RNA (blue bars) after

treatment of HepG2 cells with LNA oligonucleotides. Bars denoted as 6-11 correspond to SEQ ID NOS 159,167-170, 160.

[0021] Figure 4 shows dose dependent increase in ApoA1 mRNA (bottom panel) and protein (top panel) after treatment of HepG2 cells with oligonucleotides. Bars denoted CUR-4806 and CUR-4811 correspond to SEQ ID NOS 159 and 160 respectively.

[0022] Figure 5 is a graph of the real time PCR results showing upregulation of the ApoA1 mRNA in primary African green monkey hepatocytes after treatment with oligonucleotides against natural ApoA1 antisense DA327409ext. Bars denoted CUR-4816 and CUR-4811 correspond to SEQ ID NOS 173 and 160 respectively.

[0023] Figure 6 is a graph showing that ApoA1 mRNA and protein levels increased in monkey liver biopsies after treatment with CUR-962, an oligonucleotide designed to ApoA1 antisense DA327409ext, compared to the baseline levels, as determined by real time PCR and ELISA respectively (right panels). ApoA1 mRNA or protein levels did not change after the same period of time in the control group dosed with an oligonucleotide that showed no effect on ApoA1 levels *in vitro* (CUR-963) (left panels). Bars denoted CUR-962 and CUR-963 correspond to SEQ ID NOS:170 and 171 respectively.

[0024] Figure 7 shows SEQ ID NO 1, ApoA1 mRNA and SEQ ID NO 1a, ApoA1 genomic sequence from the UCSC genome assembly March 2006 (http://genome.ucsc.edu/index.html?org=Human&db=hg18&hgsid=144980821, exons are shown in capital letters, introns in small)

[0025] Figure 8 shows SEQ ID NO: 2.

[0026] Figures 9A-D show SEQ ID NOs: 3-158.

[0027] Figure 10 shows SEQ ID NOs: 159-173. * indicates phosphothioate bond, + indicates LNA modification.

[0028] Figure 11 shows a side-by-side alignment of the human and rhesus ApoA1 natural antisense sequences and the position of some of the oligonucleotides used to target these sequences.

DETAILED DESCRIPTION

[0029] Several aspects of the invention are described below with reference to example applications for illustration. It should be understood that numerous specific details,

relationships, and methods are set forth to provide a full understanding of the invention. One having ordinary skill in the relevant art, however, will readily recognize that the invention can be practiced without one or more of the specific details or with other methods. The present invention is not limited by the illustrated ordering of acts or events, as some acts may occur in different orders and/or concurrently with other acts or events. Furthermore, not all illustrated acts or events are required to implement a methodology in accordance with the present invention.

[0030] All genes, gene names, and gene products disclosed herein are intended to correspond to homologs from any species for which the compositions and methods disclosed herein are applicable. Thus, the terms include, but are not limited to genes and gene products from humans and mice. It is understood that when a gene or gene product from a particular species is disclosed, this disclosure is intended to be exemplary only, and is not to be interpreted as a limitation unless the context in which it appears clearly indicates. Thus, for example, for the genes disclosed herein, which in some embodiments relate to mammalian nucleic acid and amino acid sequences are intended to encompass homologous and/or orthologous genes and gene products from other animals including, but not limited to other mammals, fish, amphibians, reptiles, and birds. In preferred embodiments, the genes or nucleic acid sequences are human.

Definitions

[0031] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting of the invention. As used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the terms "including", "includes", "having", "has", "with", or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term "comprising."

[0032] The term "about" or "approximately" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, i.e., the limitations of the measurement system. For example, "about" can mean within 1 or more than 1 standard deviation, per the practice in the art. Alternatively, "about" can mean a range of up to 20%, preferably up to 10%, more

preferably up to 5%, and more preferably still up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 5-fold, and more preferably within 2-fold, of a value. Where particular values are described in the application and claims, unless otherwise stated the term "about" meaning within an acceptable error range for the particular value should be assumed.

[0033] As used herein, the term "mRNA" means the presently known mRNA transcript(s) of a targeted gene, and any further transcripts which may be elucidated.

[0034] By "antisense oligonucleotides" or "antisense compound" is meant an RNA or DNA molecule that binds to another RNA or DNA (target RNA, DNA). For example, if it is an RNA oligonucleotide it binds to another RNA target by means of RNA-RNA interactions and alters the activity of the target RNA (Eguchi *et al.*, 1991 *Ann. Rev. Biochem.* 60, 631-652). An antisense oligonucleotide can upregulate or downregulate expression and/or function of a particular polynucleotide. The definition is meant to include any foreign RNA or DNA molecule which is useful from a therapeutic, diagnostic, or other viewpoint. Such molecules include, for example, antisense RNA or DNA molecules, interference RNA (RNAi), micro RNA, decoy RNA molecules, siRNA, enzymatic RNA, therapeutic editing RNA and agonist and antagonist RNA, antisense oligomeric compounds, antisense oligonucleotides, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and other oligomeric compounds that hybridize to at least a portion of the target nucleic acid. As such, these compounds may be introduced in the form of single-stranded, double-stranded, partially single-stranded, or circular oligomeric compounds.

[0035] In the context of this invention, the term "oligonucleotide" refers to an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or mimetics thereof. The term "oligonucleotide", also includes linear or circular oligomers of natural and/or modified monomers or linkages, including deoxyribonucleosides, ribonucleosides, substituted and alpha-anomeric forms thereof, peptide nucleic acids (PNA), ed nucleic acids (LNA), phosphorothioate, methylphosphonate, and the like. Oligonucleotides are capable of specifically binding to a target polynucleotide by way of a regular pattern of monomer-to-monomer interactions, such as Watson-Crick type of base pairing, Hoögsteen or reverse Hoögsteen types of base pairing, or the like.

[0036] The oligonucleotide may be "chimeric", that is, composed of different regions. In the context of this invention "chimeric" compounds are oligonucleotides, which contain two

or more chemical regions, for example, DNA region(s), RNA region(s), PNA region(s) etc. Each chemical region is made up of at least one monomer unit, i.e., a nucleotide in the case of an oligonucleotide compound. These oligonucleotides typically comprise at least one region wherein the oligonucleotide is modified in order to exhibit one or more desired properties. The desired properties of the oligonucleotide include, but are not limited, for example, to increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target nucleic acid. Different regions of the oligonucleotide may therefore have different properties. The chimeric oligonucleotides of the present invention can be formed as mixed structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide analogs as described above.

[0037] The oligonucleotide can be composed of regions that can be linked in "register", that is, when the monomers are linked consecutively, as in native DNA, or linked via spacers. The spacers are intended to constitute a covalent "bridge" between the regions and have in preferred cases a length not exceeding about 100 carbon atoms. The spacers may carry different functionalities, for example, having positive or negative charge, carry special nucleic acid binding properties (intercalators, groove binders, toxins, fluorophors etc.), being lipophilic, inducing special secondary structures like, for example, alanine containing peptides that induce alpha-helices.

[0038] As used herein "apolipoprotein" and "apolipoprotein A" are inclusive of all family members, mutants, alleles, fragments, species, coding and noncoding sequences, sense and antisense polynucleotide strands, etc.

[0039] As used herein, the term "oligonucleotide specific for" or "oligonucleotide targets" refers to an oligonucleotide having a sequence (i) capable of forming a stable complex with a portion of the targeted gene, or (ii) capable of forming a stable duplex with a portion of a mRNA transcript of the targeted gene. Stability of the complexes and duplexes can be determined by theoretical calculations and/or *in vitro* assays. Exemplary assays for determining stability of hybridization complexes and duplexes are described in the Examples below.

[0040] As used herein, the term "target nucleic acid" encompasses DNA, RNA (comprising pre-mRNA and mRNA) transcribed from such DNA, and also cDNA derived from such RNA, coding, noncoding sequences, sense or antisense polynucleotides. The specific hybridization of an oligomeric compound with its target nucleic acid interferes with

the normal function of the nucleic acid. This modulation of function of a target nucleic acid by compounds, which specifically hybridize to it, is generally referred to as "antisense". The functions of DNA to be interfered include, for example, replication and transcription. The functions of RNA to be interfered, include all vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity which may be engaged in or facilitated by the RNA. The overall effect of such interference with target nucleic acid function is modulation of the expression of an encoded product or oligonucleotides.

[0041] RNA interference "RNAi" is mediated by double stranded RNA (dsRNA) molecules that have sequence-specific homology to their "target" nucleic acid sequences (Caplen, N. J., *et al., Proc. Natl. Acad. Sci.* USA 98:9742-9747 (2001)). In certain embodiments of the present invention, the mediators are 5-25 nucleotide "small interfering" RNA duplexes (siRNAs). The siRNAs are derived from the processing of dsRNA by an RNase enzyme known as Dicer (Bernstein, E., *et al., Nature* 409:363-366 (2001)). siRNA duplex products are recruited into a multi-protein siRNA complex termed RISC (RNA Induced Silencing Complex). Without wishing to be bound by any particular theory, a RISC is then believed to be guided to a target nucleic acid (suitably mRNA), where the siRNA duplex interacts in a sequence-specific way to mediate cleavage in a catalytic fashion (Bernstein, E., *et al., Nature* 409:363-366 (2001); Boutla, A., *et al., Curr. Biol.* 11:1776-1780 (2001)). Small interfering RNAs that can be used in accordance with the present invention can be synthesized and used according to procedures that are well known in the art and that will be familiar to the ordinarily skilled artisan. Small interfering RNAs for use in the methods of the present invention suitably comprise between about 1 to about 50 nucleotides (nt). In examples of nonlimiting embodiments, siRNAs can comprise about 5 to about 40 nt, about 5 to about 30 nt, about 10 to about 30 nt, about 15 to about 25 nt, or about 20-25 nucleotides.

[0042] Selection of appropriate oligonucleotides is facilitated by using computer programs that automatically align nucleic acid sequences and indicate regions of identity or homology. Such programs are used to compare nucleic acid sequences obtained, for example, by searching databases such as GenBank or by sequencing PCR products. Comparison of nucleic acid sequences from a range of species allows the selection of nucleic acid sequences that display an appropriate degree of identity between species. In the case of genes that have

not been sequenced, Southern blots are performed to allow a determination of the degree of identity between genes in target species and other species. By performing Southern blots at varying degrees of stringency, as is well known in the art, it is possible to obtain an approximate measure of identity. These procedures allow the selection of oligoncueltodes that exhibit a high degree of complementarity to target nucleic acid sequences in a subject to be controlled and a lower degree of complementarity to corresponding nucleic acid sequences in other species. One skilled in the art will realize that there is considerable latitude in selecting appropriate regions of genes for use in the present invention.

[0043] By "enzymatic RNA" is meant an RNA molecule with enzymatic activity (Cech, 1988 *J. American. Med. Assoc*. 260, 3030-3035). Enzymatic nucleic acids (ribozymes) act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA.

[0044] By "decoy RNA" is meant an RNA molecule that mimics the natural binding domain for a ligand. The decoy RNA therefore competes with natural binding target for the binding of a specific ligand. For example, it has been shown that over-expression of HIV trans-activation response (TAR) RNA can act as a "decoy" and efficiently binds HIV tat protein, thereby preventing it from binding to TAR sequences encoded in the HIV RNA (Sullenger *et al*., 1990, *Cell*, 63, 601-608). This is meant to be a specific example. Those in the art will recognize that this is but one example, and other embodiments can be readily generated using techniques generally known in the art.

[0045] As used herein, the term "monomers" typically indicates monomers linked by phosphodiester bonds or analogs thereof to form oligonucleotides ranging in size from a few monomeric units, e.g., from about 3-4, to about several hundreds of monomeric units. Analogs of phosphodiester linkages include: phosphorothioate, phosphorodithioate, methylphosphornates, phosphoroselenoate, phosphoramidate, and the like, as more fully described below.

[0046] In the present context, the terms "nucleobase" and "nucleotides" or "nucleosides" are used interchangeably herein and the terms cover naturally occurring nucleobases as well as non-naturally occurring nucleobases. It should be clear to the person skilled in the art that

various nucleobases which previously have been considered "non-naturally occurring" have subsequently been found in nature. Thus, "nucleobase" includes not only the known purine and pyrimidine heterocycles, but also heterocyclic analogues and tautomers thereof. Illustrative examples of nucleobases are adenine, guanine, thymine, cytosine, uracil, purine, xanthine, diaminopurine, 8-oxo-N^6-methyladenine, 7-deazaxanthine, 7-deazaguanine, N^4,N^4-ethanocytosin, N^6,N^6-ethano-2,6-diaminopurine, 5-methylcytosine, 5-(C^3-C^6)-alkynylcytosine, 5-fluorouracil, 5-bromouracil, pseudoisocytosine, 2-hydroxy-5-methyl-4-triazolopyridin, isocytosine, isoguanin, inosine and the "non-naturally occurring" nucleobases described in Benner *et al.*, U.S. Pat No. 5,432,272. The term "nucleobase" is intended to cover every and all of these examples as well as analogues and tautomers thereof. Especially interesting nucleobases are adenine, guanine, thymine, cytosine, and uracil, which are considered as the naturally occurring nucleobases in relation to therapeutic and diagnostic application in humans. Nucleoside includes the natural nucleosides, including 2'-deoxy and 2'-hydroxyl forms, e.g., as described in Kornberg and Baker, DNA Replication, 2nd Ed. (Freeman, San Francisco, 1992).

[0047] "Analogs" in reference to nucleosides includes synthetic nucleosides having modified base moieties and/or modified sugar moieties, e.g., described generally by Scheit, Nucleotide Analogs, John Wiley, New York, 1980; Freier & Altmann, *Nucl. Acid. Res.*, 1997, 25(22), 4429-4443, Toulmé, J.J., *Nature* Biotechnology 19:17-18 (2001); Manoharan M., *Biochemica et Biophysica Acta* 1489:117-139(1999); Freier S. M., *Nucleic Acid Research*, 25:4429-4443 (1997), Uhlman, E., *Drug Discovery & Development*, 3: 203-213 (2000), Herdewin P., *Antisense & Nucleic Acid Drug Dev.*, 10:297-310 (2000),); 2'-O, 3`-C-linked [3.2.0] bicycloarabinonucleosides (see e.g. N.K Christiensen., *et al*, *J. Am. Chem. Soc.*, 120: 5458-5463 (1998). Such analogs include synthetic nucleosides designed to enhance binding properties, e.g., duplex or triplex stability, specificity, or the like.

[0048] As used herein, "hybridization" means the pairing of substantially complementary strands of oligomeric compounds. One mechanism of pairing involves hydrogen bonding, which may be Watson-Crick, Hoögsteen or reversed Hoögsteen hydrogen bonding, between complementary nucleoside or nucleotide bases (nucleobases) of the strands of oligomeric compounds. For example, adenine and thymine are complementary nucleobases which pair through the formation of hydrogen bonds. Hybridization can occur under varying circumstances.

[0049] An antisense compound is "specifically hybridizable" when binding of the compound to the target nucleic acid interferes with the normal function of the target nucleic acid to cause a modulation of function and/or activity, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target nucleic acid sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and under conditions in which assays are performed in the case of *in vitro* assays.

[0050] As used herein, the phrase "stringent hybridization conditions" or "stringent conditions" refers to conditions under which a compound of the invention will hybridize to its target sequence, but to a minimal number of other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances and in the context of this invention, "stringent conditions" under which oligomeric compounds hybridize to a target sequence are determined by the nature and composition of the oligomeric compounds and the assays in which they are being investigated. In general, stringent hybridization conditions comprise low concentrations (<0.15M) of salts with inorganic cations such as Na^{++} or K^{++} (i.e., low ionic strength), temperature higher than 20°C - 25° C. below the Tm of the oligomeric compound:target sequence complex, and the presence of denaturants such as formamide, dimethylformamide, dimethyl sulfoxide, or the detergent sodium dodecyl sulfate (SDS). For example, the hybridization rate decreases 1.1% for each 1% formamide. An example of a high stringency hybridization condition is 0.1X sodium chloride-sodium citrate buffer (SSC)/0.1% (w/v) SDS at 60° C. for 30 minutes.

[0051] "Complementary," as used herein, refers to the capacity for precise pairing between two nucleobases on one or two oligomeric strands. For example, if a nucleobase at a certain position of an antisense compound is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, said target nucleic acid being a DNA, RNA, or oligonucleotide molecule, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be a complementary position. The oligomeric compound and the further DNA, RNA, or oligonucleotide molecule are complementary to each other when a sufficient number of complementary positions in each molecule are occupied by nucleobases which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of precise pairing or complementarity over a sufficient number of nucleobases such that stable and specific binding occurs between the oligomeric compound and a target nucleic acid.

[0052] It is understood in the art that the sequence of an oligomeric compound need not be 100% complementary to that of its target nucleic acid to be specifically hybridizable. Moreover, an oligonucleotide may hybridize over one or more segments such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure, mismatch or hairpin structure). The oligomeric compounds of the present invention comprise at least about 70%, or at least about 75%, or at least about 80%, or at least about 85%, or at least about 90%, or at least about 95%, or at least about 99% sequence complementarity to a target region within the target nucleic acid sequence to which they are targeted. For example, an antisense compound in which 18 of 20 nucleotides of the antisense compound are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In this example, the remaining noncomplementary nucleotides may be clustered or interspersed with complementary nucleotides and need not be contiguous to each other or to complementary nucleotides. As such, an antisense compound which is 18 nucleotides in length having 4 (four) noncomplementary nucleotides which are flanked by two regions of complete complementarity with the target nucleic acid would have 77.8% overall complementarity with the target nucleic acid and would thus fall within the scope of the present invention. Percent complementarity of an antisense compound with a region of a target nucleic acid can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs known in the art (Altschul *et al.*, *J. Mol. Biol.*, 1990, 215, 403-410; Zhang and Madden, *Genome Res.*, 1997, 7, 649-656). Percent homology, sequence identity or complementarity, can be determined by, for example, the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison Wis.), using default settings, which uses the algorithm of Smith and Waterman (*Adv. Appl. Math.*, 1981, 2, 482-489).

[0053] As used herein, the term "Thermal Melting Point (Tm)" refers to the temperature, under defined ionic strength, pH, and nucleic acid concentration, at which 50% of the oligonucleotides complementary to the target sequence hybridize to the target sequence at equilibrium. As the target sequences are generally present in excess, at Tm, 50% of the oligonucleotides are occupied at equilibrium). Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short oligonucleotides (*e.g.*, 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

[0054] As used herein, "modulation" means either an increase (stimulation) or a decrease (inhibition) in the expression of a gene.

[0055] The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to a wild type gene. This definition may also include, for example, "allelic," "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. Of particular utility in the invention are variants of wild type gene products. Variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes that give rise to variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

[0056] The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs,) or single base mutations in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population with a propensity for a disease state, that is susceptibility versus resistance.

[0057] Derivative polynucleotides include nucleic acids subjected to chemical modification, for example, replacement of hydrogen by an alkyl, acyl, or amino group. Derivatives, e.g., derivative oligonucleotides, may comprise non-naturally-occurring portions, such as altered sugar moieties or inter-sugar linkages. Exemplary among these are phosphorothioate and other sulfur containing species which are known in the art. Derivative nucleic acids may also contain labels, including radionucleotides, enzymes, fluorescent agents, chemiluminescent agents, chromogenic agents, substrates, cofactors, inhibitors, magnetic particles, and the like.

[0058] A "derivative" polypeptide or peptide is one that is modified, for example, by glycosylation, pegylation, phosphorylation, sulfation, reduction/alkylation, acylation, chemical coupling, or mild formalin treatment. A derivative may also be modified to contain a detectable label, either directly or indirectly, including, but not limited to, a radioisotope, fluorescent, and enzyme label.

[0059] As used herein, the term "animal" or "patient" is meant to include, for example, humans, sheep, elks, deer, mule deer, minks, mammals, monkeys, horses, cattle, pigs, goats, dogs, cats, rats, mice, birds, chicken, reptiles, fish, insects and arachnids.

[0060] "Mammal" covers warm blooded mammals that are typically under medical care (e.g., humans and domesticated animals). Examples include feline, canine, equine, bovine, and human, as well as just human.

[0061] "Treating" or "treatment" covers the treatment of a disease-state in a mammal, and includes: (a) preventing the disease-state from occurring in a mammal, in particular, when such mammal is predisposed to the disease-state but has not yet been diagnosed as having it; (b) inhibiting the disease-state, e.g., arresting it development; and/or (c) relieving the disease-state, e.g., causing regression of the disease state until a desired endpoint is reached. Treating also includes the amelioration of a symptom of a disease (e.g., lessen the pain or discomfort), wherein such amelioration may or may not be directly affecting the disease (e.g., cause, transmission, expression, etc.).

Polynucleotide and Oligonucleotide Compositions and Molecules

[0062] High density lipoprotein (HDL) picks up extra cholesterol in the blood and returns it to the liver. Low density lipoprotein (or LDL) is the main transporter of cholesterol in the body. But too much LDL over many years can result in atherosclerosis (the narrowing and hardening of arteries) and lead to heart disease or a heart attack. The ratio is determined by dividing the LDL cholesterol into the HDL cholesterol. For example, if a person has an HDL cholesterol of 50 mg/dL and an LDL cholesterol of 150 mg/dL, the HDL/LDL ratio would be 0.33. The goal is to keep the HDL/LDL ratio above 0.3, with the ideal HDL/LDL ratio being above 0.4.

[0063] *Targets*: In one embodiment, the targets comprise nucleic acid sequences of apolipoprotein (ApoA1), including without limitation sense and/or antisense noncoding and/or coding sequences associated with ApoA. Human apolipoprotein A-I (ApoA-I) is the

major protein constituent of high-density lipoproteins (HDL and lymph chylomicrons. In human plasma four major circulating lipoproteins have been named: chylomicrons (CM), very low-density lipoproteins (VLDL), low-density lipoproteins (LDL), and high-density lipoproteins (HDL). HDL is involved in the removal of cholesterol from peripheral tissues by transporting it to the liver or to other lipoproteins.

[0064] HDL are synthesized *de novo* in both the liver and small intestine as protein-rich disc-shaped particles. The primary apoproteins of HDL are apoA-I, apoA-II, apoC-I, apoC-II, and apoE. Newly formed HDL contain very little cholesterol and cholesteryl esters. HDL are converted from their initial discoidal shape into spherical lipoprotein particles through the accumulation of cholesteryl esters in the neutral core of the lipoprotein particle. Cholesterol is accumulated by HDL from chylomicron remnants VLDL remnants (also called intermediate density Lipoproteins or IDL) and directly from cell surface membranes. The cholesterol is esterfied through the action of an HDL-associated enzyme lecithin:cholesterol acyltransferase ("LCAT"). For LCAT to transfer a fatty acid from lecithin (phosphatidylcholine) to the C-3-OH group of cholesterol, interaction with ApoA-I found on the HDL surface is required. This accumulation of core cholesteryl esters converts nascent HDL to HDL_2 and HDL_3. See R. I. Levy *et al.*, "The structure, function and metabolism of high-density lipoproteins: A status report," Circulation, vol. 62, pp. IV4-8 (1980); and D. I. Silverman *et al.*, "High-density lipoprotein subfractions," *Am. J. Med.*, vol. 94, pp. 636-45 (1993).

[0065] HDL are usually isolated from the plasma by ultracentrifugation. The normal HDL density range is from 1.063 g/mL to 1.21 g/mL, which divides roughly into two ranges HDL_2 (1.063 g/mL to 1.125 g/mL) and HDL3 (1.125 g/mL to 1.21 g/mL). More recently, two major populations of particles in HDL have been identified by two dimensional electrophoresis followed by immunoblotting and enzyme-linked differential antibody immunosorbent assay. One of these populations contains particles with apoA-I alone, and the other contains particles with both apoA-I and apoA-II. The relative proportion of apoA-I particles is highest in the HDL_2 fraction, while HDL_3 is more a combination of apoA-I and apoA-II. See J. C. Fruchart *et al.*, "Apolipoprotein A-containing lipoprotein particles: physiological role, quantification, and clinical significance," *Clin. Chem.*, vol. 38, pp. 793-7 (1992); and B. F. Asztalos *et al.*, "Normolipidemic subjects with low HDL cholesterol levels have altered HDL subpopulations," *Arterioscler. Thromb. Vasc. Biol.*, vol. 17, pp. 1885-1893 (1997).

[0066] Human apolipoprotein A-I (ApoA-I) is the major protein constituent of HDL and lymph chylomicrons. ApoA-I is primarily synthesized in the liver and small intestine as a precursor protein (preproapo A-I). Preproapo A-I is cleaved intracellularly to form proapo A-I, the form secreted into the plasma and lymph. In the plasma, six amino acids are cleaved from proapo A-I to form mature ApoA-I.

[0067] Mature ApoA-I is a single unglycosylated polypeptide composed of 243 amino acids of known sequence. ApoA-I serves as a cofactor of a plasma enzyme (lecithin-cholesterol acyltransferase (LCAT)), responsible for the formation of most cholesterol esters in plasma. Decreased levels of ApoA-I may result in disorders of the plasma lipid transport system and in the development of coronary heart disease. Low levels of both ApoA-I and HDL has been shown to be a strong risk factor for heart attacks and other atherosclerotic vascular diseases. See U.S. Pat. Nos. 5,059,528 and 6,258,596.

[0068] In preferred embodiments, antisense oligonucleotides are used to prevent or treat diseases or disorders associated with apolipoproteins, high density lipoproteins. Examples of diseases which can be treated with the antisense compounds comprise high cholesterol, HDL/LDL ratios, arthritis, heart disease, Tangier disease, systemic non-neuropathic amyloidosis, other amyloid diseases, Alzheimer's disease, Parkinson's disease, diabetes, cardiovascular diseases, cancer, obesity, atherosclerosis, inhibiting tumor growth dependent on angiogenesis, and in decreasing existing blood vessels formed by tumors. It will also be effective in treating non-cancerous diseases which symptoms include an increase in angiogenesis, e.g., psoriasis, retinopathy of prematurity, neovascular glaucoma, diabetic retinopathy, rheumatoid arthritis, obesity, and psoriasis.

[0069] In a preferred embodiment, the oligonucleotides are specific for polynucleotides of ApoA, which includes, without limitation noncoding regions. The ApoA1targets comprise variants of ApoA; mutants of ApoA, including SNPs; noncoding sequences of ApoA; alleles, fragments and the like. Preferably the oligonucleotide is an antisense RNA molecule.

[0070] In accordance with embodiments of the invention, the target nucleic acid molecule is not limited to ApoA1polynucleotides alone but extends to any of the isoforms, receptors, homologs, non-coding regions and the like of ApoA.

[0071] In another preferred embodiment, an oligonucleotide targets a natural antisense sequence (natural antisense to the coding and non-coding regions) of ApoA1targets, including, without limitation, variants, alleles, homologs, mutants, derivatives, fragments and

complementary sequences thereto. Preferably the oligonucleotide is an antisense RNA molecule.

[0072] In another preferred embodiment, the oligomeric compounds of the present invention also include variants in which a different base is present at one or more of the nucleotide positions in the compound. For example, if the first nucleotide is an adenosine, variants may be produced which contain thymidine, guanosine or cytidine at this position. This may be done at any of the positions of the antisense compound. These compounds are then tested using the methods described herein to determine their ability to inhibit expression of a target nucleic acid.

[0073] In some embodiments, homology, sequence identity or complementarity, between the antisense compound and target is from about 50% to about 60%. In some embodiments, homology, sequence identity or complementarity, is from about 60% to about 70%. In some embodiments, homology, sequence identity or complementarity, is from about 70% to about 80%. In some embodiments, homology, sequence identity or complementarity, is from about 80% to about 90%. In some embodiments, homology, sequence identity or complementarity, is about 90%, about 92%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100%.

[0074] An antisense compound is specifically hybridizable when binding of the compound to the target nucleic acid interferes with the normal function of the target nucleic acid to cause a loss of activity, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target nucleic acid sequences under conditions in which specific binding is desired. Such conditions include, i.e., physiological conditions in the case of *in vivo* assays or therapeutic treatment, and conditions in which assays are performed in the case of *in vitro* assays.

[0075] An antisense compound, whether DNA, RNA, chimeric, substituted etc, is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarily to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and in the case of *in vitro* assays, under conditions in which the assays are performed.

[0076] In another preferred embodiment, targeting of ApoA1including without limitation, antisense sequences which are identified and expanded, using for example, PCR, hybridization etc., one or more of the sequences set forth as SEQ ID NOS: 81 to 173, and the like, modulate the expression or function of ApoA. In one embodiment, expression or function is up-regulated as compared to a control. In another preferred embodiment, expression or function is down-regulated as compared to a control.

[0077] In another preferred embodiment, oligonucleotides comprise nucleic acid sequences set forth as SEQ ID NOS: 81 to 173, including antisense sequences which are identified and expanded, using for example, PCR, hybridization etc. These oligonucleotides can comprise one or more modified nucleotides, shorter or longer fragments, modified bonds and the like. Examples of modified bonds or internucleotide linkages comprise phosphorothioate, phosphorodithioate or the like. In another preferred embodiment, the nucleotides comprise a phosphorus derivative. The phosphorus derivative (or modified phosphate group) which may be attached to the sugar or sugar analog moiety in the modified oligonucleotides of the present invention may be a monophosphate, diphosphate, triphosphate, alkylphosphate, alkanephosphate, phosphorothioate and the like. The preparation of the above-noted phosphate analogs, and their incorporation into nucleotides, modified nucleotides and oligonucleotides, *per se*, is also known and need not be described here.

[0078] The specificity and sensitivity of antisense is also harnessed by those of skill in the art for therapeutic uses. Antisense oligonucleotides have been employed as therapeutic moieties in the treatment of disease states in animals and man. Antisense oligonucleotides have been safely and effectively administered to humans and numerous clinical trials are presently underway. It is thus established that oligonucleotides can be useful therapeutic modalities that can be configured to be useful in treatment regimes for treatment of cells, tissues and animals, especially humans.

[0079] In embodiments of the present invention oligomeric antisense compounds, particularly oligonucleotides, bind to target nucleic acid molecules and modulate the expression and/or function of molecules encoded by a target gene. The functions of DNA to be interfered comprise, for example, replication and transcription. The functions of RNA to be interfered comprise all vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity which may be engaged in or facilitated by the RNA. The functions may be up-regulated or inhibited depending on the functions desired.

[0080] The antisense compounds, include, antisense oligomeric compounds, antisense oligonucleotides, external guide sequence (EGS) oligonucleotides, alternate splicers, primers, probes, and other oligomeric compounds that hybridize to at least a portion of the target nucleic acid. As such, these compounds may be introduced in the form of single-stranded, double-stranded, partially single-stranded, or circular oligomeric compounds.

[0081] Targeting an antisense compound to a particular nucleic acid molecule, in the context of this invention, can be a multistep process. The process usually begins with the identification of a target nucleic acid whose function is to be modulated. This target nucleic acid may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target nucleic acid encode apolipoprotein (ApoA1).

[0082] The targeting process usually also includes determination of at least one target region, segment, or site within the target nucleic acid for the antisense interaction to occur such that the desired effect, e.g., modulation of expression, will result. Within the context of the present invention, the term "region" is defined as a portion of the target nucleic acid having at least one identifiable structure, function, or characteristic. Within regions of target nucleic acids are segments. "Segments" are defined as smaller or sub-portions of regions within a target nucleic acid. "Sites," as used in the present invention, are defined as positions within a target nucleic acid.

[0083] In a preferred embodiment, the antisense oligonucleotides bind to the natural antisense sequences of apolipoprotein (ApoA1) and modulate the expression and/or function of apolipoprotein (ApoA1) (SEQ ID NO: 1). Examples of antisense sequences include SEQ ID NOS: 2, 81-173 (ApoA1). Other examples include antisense oliginucleotides comprising the core sequence gctagt (SEQ ID NO: 175) such as the oliginucleotides of SEQ ID NOs 60-69 and 172.

[0084] In another preferred embodiment, the antisense oligonucleotides bind to one or more segments of apolipoprotein (ApoA1) polynucleotides and modulate the expression and/or function of apolipoprotein (ApoA1). The segments comprise at least five consecutive nucleotides of the apolipoprotein (ApoA1) sense or antisense polynucleotides.

[0085] In another preferred embodiment, the antisense oligonucleotides are specific for natural antisense sequences of apolipoprotein (ApoA1) wherein binding of the

oligonucleotides to the natural antisense sequences of apolipoprotein (ApoA1) modulate expression and/or function of apolipoprotein (ApoA1).

[0086] In another preferred embodiment, oligonucleotide compounds comprise sequences set forth as SEQ ID NOS: 3 to 173, antisense sequences which are identified and expanded, using for example, PCR, hybridization etc These oligonucleotides can comprise one or more modified nucleotides, shorter or longer fragments, modified bonds and the like. Examples of modified bonds or internucleotide linkages comprise phosphorothioate, phosphorodithioate or the like. In another preferred embodiment, the nucleotides comprise a phosphorus derivative. The phosphorus derivative (or modified phosphate group) which may be attached to the sugar or sugar analog moiety in the modified oligonucleotides of the present invention may be a monophosphate, diphosphate, triphosphate, alkylphosphate, alkanephosphate, phosphorothioate and the like. The preparation of the above-noted phosphate analogs, and their incorporation into nucleotides, modified nucleotides and oligonucleotides, *per se*, is also known and need not be described here.

[0087] Since, as is known in the art, the translation initiation codon is typically 5'-AUG (in transcribed mRNA molecules; 5'-ATG in the corresponding DNA molecule), the translation initiation codon is also referred to as the "AUG codon," the "start codon" or the "AUG start codon". A minority of genes has a translation initiation codon having the RNA sequence 5'-GUG, 5'-UUG or 5'-CUG; and 5'-AUA, 5'-ACG and 5'-CUG have been shown to function *in vivo*. Thus, the terms "translation initiation codon" and "start codon" can encompass many codon sequences, even though the initiator amino acid in each instance is typically methionine (in eukaryotes) or formylmethionine (in prokaryotes). Eukaryotic and prokaryotic genes may have two or more alternative start codons, any one of which may be preferentially utilized for translation initiation in a particular cell type or tissue, or under a particular set of conditions. In the context of the invention, "start codon" and "translation initiation codon" refer to the codon or codons that are used *in vivo* to initiate translation of an mRNA transcribed from a gene encoding apolipoprotein (ApoA1), regardless of the sequence(s) of such codons. A translation termination codon (or "stop codon") of a gene may have one of three sequences, i.e., 5'-UAA, 5'-UAG and 5'-UGA (the corresponding DNA sequences are 5'-TAA, 5'-TAG and 5'-TGA, respectively).

[0088] The terms "start codon region" and "translation initiation codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation initiation codon. Similarly, the

terms "stop codon region" and "translation termination codon region" refer to a portion of such an mRNA or gene that encompasses from about 25 to about 50 contiguous nucleotides in either direction (i.e., 5' or 3') from a translation termination codon. Consequently, the "start codon region" (or "translation initiation codon region") and the "stop codon region" (or "translation termination codon region") are all regions that may be targeted effectively with the antisense compounds of the present invention.

[0089] The open reading frame (ORF) or "coding region," which is known in the art to refer to the region between the translation initiation codon and the translation termination codon, is also a region which may be targeted effectively. Within the context of the present invention, a targeted region is the intragenic region encompassing the translation initiation or termination codon of the open reading frame (ORF) of a gene.

[0090] Another target region includes the 5' untranslated region (5'UTR), known in the art to refer to the portion of an mRNA in the 5' direction from the translation initiation codon, and thus including nucleotides between the 5' cap site and the translation initiation codon of an mRNA (or corresponding nucleotides on the gene). Still another target region includes the 3' untranslated region (3'UTR), known in the art to refer to the portion of an mRNA in the 3' direction from the translation termination codon, and thus including nucleotides between the translation termination codon and 3' end of an mRNA (or corresponding nucleotides on the gene). The 5' cap site of an mRNA comprises an N7-methylated guanosine residue joined to the 5'-most residue of the mRNA via a 5'-5' triphosphate linkage. The 5' cap region of an mRNA is considered to include the 5' cap structure itself as well as the first 50 nucleotides adjacent to the cap site. Another target region for this invention is the 5' cap region.

[0091] Although some eukaryotic mRNA transcripts are directly translated, many contain one or more regions, known as "introns," which are excised from a transcript before it is translated. The remaining (and therefore translated) regions are known as "exons" and are spliced together to form a continuous mRNA sequence. In one embodiment, targeting splice sites, i.e., intron-exon junctions or exon-intron junctions, is particularly useful in situations where aberrant splicing is implicated in disease, or where an overproduction of a particular splice product is implicated in disease. An aberrant fusion junction due to rearrangement or deletion is another embodiment of a target site. mRNA transcripts produced via the process of splicing of two (or more) mRNAs from different gene sources are known as "fusion

transcripts". Introns can be effectively targeted using antisense compounds targeted to, for example, DNA or pre-mRNA.

[0092] In another preferred embodiment, the antisense oligonucleotides bind to coding and/or non-coding regions of a target polynucleotide and modulate the expression and/or function of the target molecule.

[0093] In another preferred embodiment, the antisense oligonucleotides bind to natural antisense polynucleotides and modulate the expression and/or function of the target molecule.

[0094] In another preferred embodiment, the antisense oligonucleotides bind to sense polynucleotides and modulate the expression and/or function of the target molecule.

[0095] Alternative RNA transcripts can be produced from the same genomic region of DNA. These alternative transcripts are generally known as "variants". More specifically, "pre-mRNA variants" are transcripts produced from the same genomic DNA that differ from other transcripts produced from the same genomic DNA in either their start or stop position and contain both intronic and exonic sequence.

[0096] Upon excision of one or more exon or intron regions, or portions thereof during splicing, pre-mRNA variants produce smaller "mRNA variants". Consequently, mRNA variants are processed pre-mRNA variants and each unique pre-mRNA variant must always produce a unique mRNA variant as a result of splicing. These mRNA variants are also known as "alternative splice variants". If no splicing of the pre-mRNA variant occurs then the pre-mRNA variant is identical to the mRNA variant.

[0097] Variants can be produced through the use of alternative signals to start or stop transcription. Pre-mRNAs and mRNAs can possess more that one start codon or stop codon. Variants that originate from a pre-mRNA or mRNA that use alternative start codons are known as "alternative start variants" of that pre-mRNA or mRNA. Those transcripts that use an alternative stop codon are known as "alternative stop variants" of that pre-mRNA or mRNA. One specific type of alternative stop variant is the "polyA variant" in which the multiple transcripts produced result from the alternative selection of one of the "polyA stop signals" by the transcription machinery, thereby producing transcripts that terminate at unique polyA sites. Within the context of the invention, the types of variants described herein are also embodiments of target nucleic acids.

[0098] The locations on the target nucleic acid to which the antisense compounds hybridize are defined as at least a 5-nucleobase portion of a target region to which an active antisense compound is targeted.

[0099] While the specific sequences of certain exemplary target segments are set forth herein, one of skill in the art will recognize that these serve to illustrate and describe particular embodiments within the scope of the present invention. Additional target segments are readily identifiable by one having ordinary skill in the art in view of this disclosure.

[00100] Target segments 5-100 nucleotides in length comprising a stretch of at least five (5) consecutive nucleotides selected from within the illustrative preferred target segments are considered to be suitable for targeting as well.

[00101] Target segments can include DNA or RNA sequences that comprise at least the 5 consecutive nucleotides from the 5'-terminus of one of the illustrative preferred target segments (the remaining nucleotides being a consecutive stretch of the same DNA or RNA beginning immediately upstream of the 5'-terminus of the target segment and continuing until the DNA or RNA contains about 5 to about 100 nucleotides). Similarly preferred target segments are represented by DNA or RNA sequences that comprise at least the 5 consecutive nucleotides from the 3'-terminus of one of the illustrative preferred target segments (the remaining nucleotides being a consecutive stretch of the same DNA or RNA beginning immediately downstream of the 3'-terminus of the target segment and continuing until the DNA or RNA contains about 5 to about 100 nucleotides). One having skill in the art armed with the target segments illustrated herein will be able, without undue experimentation, to identify further preferred target segments.

[00102] Once one or more target regions, segments or sites have been identified, antisense compounds are chosen which are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give the desired effect.

[00103] In embodiments of the invention the oligonucleotides bind to an antisense strand of a particular target. The oligonucleotides are at least 5 nucleotides in length and can be synthesized so each oligonucleotide targets overlapping sequences such that oligonucleotides are synthesized to cover the entire length of the target polynucleotide. The targets also include coding as well as non coding regions.

[00104] In one embodiment, it is preferred to target specific nucleic acids by antisense oligonucleotides. Targeting an antisense compound to a particular nucleic acid, is a multistep process. The process usually begins with the identification of a nucleic acid sequence whose function is to be modulated. This may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a non coding polynucleotide such as for example, non coding RNA (ncRNA).

[00105] RNAs can be classified into (1) messenger RNAs (mRNAs), which are translated into proteins, and (2) non-protein-coding RNAs (ncRNAs). ncRNAs comprise microRNAs, antisense transcripts and other Transcriptional Units (TU) containing a high density of stop codons and lacking any extensive "Open Reading Frame". Many ncRNAs appear to start from initiation sites in 3' untranslated regions (3'UTRs) of protein-coding loci. ncRNAs are often rare and at least half of the ncRNAs that have been sequenced by the FANTOM consortium seem not to be polyadenylated. Most researchers have for obvious reasons focused on polyadenylated mRNAs that are processed and exported to the cytoplasm. Recently, it was shown that the set of non-polyadenylated nuclear RNAs may be very large, and that many such transcripts arise from so-called intergenic regions (Cheng, J. *et al.* (2005) Transcriptional maps of 10 human chromosomes at 5-nucleotide resolution. *Science* 308 (5725), 1149-1154; Kapranov, P. *et al.* (2005). Examples of the complex architecture of the human transcriptome revealed by RACE and high-density tiling arrays. *Genome Res* 15 (7), 987-997). The most common mechanism by which ncRNAs regulate gene expression is by base-pairing with target transcripts. The RNAs that function by base pairing can be grouped into (1) cis-encoded RNAs that are encoded at the same genetic location, but on the opposite strand to the RNAs they act upon and therefore display perfect complementarity to their target, and (2) trans-encoded RNAs that are encoded at a chromosomal location distinct from the RNAs they act upon and generally do not exhibit perfect base-pairing potential with their targets.

[00106] Without wishing to be bound by theory, perturbation of an antisense polynucleotide by the antisense oligonucleotides described herein, can alter the expression of the corresponding sense messenger RNAs. However, this regulation can either be discordant (antisense knockdown results in sense transcript elevation) or concordant (antisense knockdown results in concomitant sense transcript reduction). In these cases, antisense oligonucleotides can be targeted to overlapping or non-overlapping parts of the antisense strand resulting in knockdown of the target. Coding as well as non-coding antisense can be

targeted in an identical manner and that either category is capable of regulating the corresponding sense transcripts – either in a concordant or disconcordant manner. The strategies that are employed in identifying new oligonucleotides for use against a target can be based on the knockdown of antisense RNA transcripts by antisense oligonucleotides or any other means for modulating the desired target.

[00107] *Strategy 1*: In the case of discordant regulation, knocking down the antisense transcript elevates the expression of the conventional (sense) gene. Should that latter gene encode for a known or putative drug target, then knockdown of its antisense counterpart could conceivably mimic the action of a receptor agonist or an enzyme stimulant.

[00108] *Strategy 2*: In the case of concordant regulation, one could concomitantly knock down both antisense and sense transcripts and thereby achieve synergistic reduction of the conventional (sense) gene expression. If, for example, an antisense oligonucleotide is used to achieve knockdown, then this strategy can be used to apply one antisense oligonucleotide targeted to the sense transcript and another antisense oligonucleotide to the corresponding antisense transcript, or a single energetically symmetric antisense oligonucleotide that simultaneously targets overlapping sense and antisense transcripts.

[00109] According to the present invention, antisense compounds include antisense oligonucleotides, ribozymes, external guide sequence (EGS) oligonucleotides, siRNA compounds, single- or double-stranded RNA interference (RNAi) compounds such as siRNA compounds, and other oligomeric compounds which hybridize to at least a portion of the target nucleic acid and modulate its function. As such, they may be DNA, RNA, DNA-like, RNA-like, or mixtures thereof, or may be mimetics of one or more of these. These compounds may be single-stranded, double-stranded, circular or hairpin oligomeric compounds and may contain structural elements such as internal or terminal bulges, mismatches or loops. Antisense compounds are routinely prepared linearly but can be joined or otherwise prepared to be circular and/or branched. Antisense compounds can include constructs such as, for example, two strands hybridized to form a wholly or partially double-stranded compound or a single strand with sufficient self-complementarity to allow for hybridization and formation of a fully or partially double-stranded compound. The two strands can be linked internally leaving free 3' or 5' termini or can be linked to form a continuous hairpin structure or loop. The hairpin structure may contain an overhang on either the 5' or 3' terminus producing an extension of single stranded character. The double stranded

compounds optionally can include overhangs on the ends. Further modifications can include conjugate groups attached to one of the termini, selected nucleotide positions, sugar positions or to one of the internucleoside linkages. Alternatively, the two strands can be linked via a non-nucleic acid moiety or linker group. When formed from only one strand, dsRNA can take the form of a self-complementary hairpin-type molecule that doubles back on itself to form a duplex. Thus, the dsRNAs can be fully or partially double stranded. Specific modulation of gene expression can be achieved by stable expression of dsRNA hairpins in transgenic cell lines, however, in some embodiments, the gene expression or function is up regulated. When formed from two strands, or a single strand that takes the form of a self-complementary hairpin-type molecule doubled back on itself to form a duplex, the two strands (or duplex-forming regions of a single strand) are complementary RNA strands that base pair in Watson-Crick fashion.

[00110] Once introduced to a system, the compounds of the invention may elicit the action of one or more enzymes or structural proteins to effect cleavage or other modification of the target nucleic acid or may work via occupancy-based mechanisms. In general, nucleic acids (including oligonucleotides) may be described as "DNA-like" (i.e., generally having one or more 2'-deoxy sugars and, generally, T rather than U bases) or "RNA-like" (i.e., generally having one or more 2'-hydroxyl or 2'-modified sugars and, generally U rather than T bases). Nucleic acid helices can adopt more than one type of structure, most commonly the A- and B-forms. It is believed that, in general, oligonucleotides which have B-form-like structure are "DNA-like" and those which have A-form-like structure are "RNA-like." In some (chimeric) embodiments, an antisense compound may contain both A- and B-form regions.

[00111] In another preferred embodiment, the desired oligonucleotides or antisense compounds, comprise at least one of: antisense RNA, antisense DNA, chimeric antisense oligonucleotides, antisense oligonucleotides comprising modified linkages, interference RNA (RNAi), short interfering RNA (siRNA); a micro, interfering RNA (miRNA); a small, temporal RNA (stRNA); or a short, hairpin RNA (shRNA); small RNA-induced gene activation (RNAa); small activating RNAs (saRNAs), or combinations thereof.

[00112] dsRNA can also activate gene expression, a mechanism that has been termed "small RNA-induced gene activation" or RNAa. dsRNAs targeting gene promoters induce potent transcriptional activation of associated genes. RNAa was demonstrated in human cells

using synthetic dsRNAs, termed "small activating RNAs" (saRNAs). It is currently not known whether RNAa is conserved in other organisms.

[00113] Small double-stranded RNA (dsRNA), such as small interfering RNA (siRNA) and microRNA (miRNA), have been found to be the trigger of an evolutionary conserved mechanism known as RNA interference (RNAi). RNAi invariably leads to gene silencing via remodeling chromatin to thereby suppress transcription, degrading complementary mRNA, or blocking protein translation. However, in instances described in detail in the examples section which follows, oligonucleotides are shown to increase the expression and/or function of the apolipoprotein polynucleotides and encoded products thereof. dsRNAs may also act as small activating RNAs (saRNA). Without wishing to be bound by theory, by targeting sequences in gene promoters, saRNAs would induce target gene expression in a phenomenon referred to as dsRNA-induced transcriptional activation (RNAa).

[00114] In a further embodiment, the "preferred target segments" identified herein may be employed in a screen for additional compounds that modulate the expression of apolipoprotein (ApoA1) polynucleotides. "Modulators" are those compounds that decrease or increase the expression of a nucleic acid molecule encoding apolipoprotein (ApoA1) and which comprise at least a 5-nucleotide portion that is complementary to a preferred target segment. The screening method comprises the steps of contacting a preferred target segment of a nucleic acid molecule encoding apolipoprotein (ApoA1) polynucleotides with one or more candidate modulators, and selecting for one or more candidate modulators which decrease or increase the expression of a nucleic acid molecule encoding apolipoprotein (ApoA1) polynucleotides, e.g. SEQ ID NOS: 81-173. Once it is shown that the candidate modulator or modulators are capable of modulating (e.g. either decreasing or increasing) the expression of a nucleic acid molecule encoding apolipoprotein (ApoA1) polynucleotides, the modulator may then be employed in further investigative studies of the function of apolipoprotein (ApoA1) polynucleotides, or for use as a research, diagnostic, or therapeutic agent in accordance with the present invention.

[00115] Targeting the antisense sequence, preferably modulates the function of the target gene. For example, the apolipoprotein A-1 gene (NM_000039; UCSC genome database). In a preferred embodiment, the target is an antisense polynucleotide of the apolipoprotein A-1 gene. In a preferred embodiment, an antisense oligonucleotide targets sense and/or natural antisense sequences of apolipoprotein (ApoA1) polynucleotides (e.g. accession number

NM_000039), variants, alleles, isoforms, homologs, mutants, derivatives, fragments and complementary sequences thereto. Preferably the oligonucleotide is an antisense molecule and the targets include coding and noncoding regions of antisense and/or sense ApoA1polynucleotides.

[00116] The preferred target segments of the present invention may be also be combined with their respective complementary antisense compounds of the present invention to form stabilized double-stranded (duplexed) oligonucleotides.

[00117] Such double stranded oligonucleotide moieties have been shown in the art to modulate target expression and regulate translation as well as RNA processing via an antisense mechanism. Moreover, the double-stranded moieties may be subject to chemical modifications (Fire *et al.*, *Nature*, 1998, 391, 806-811; Timmons and Fire, *Nature* 1998, 395, 854; Timmons *et al.*, *Gene*, 2001, 263, 103-112; Tabara *et al.*, *Science*, 1998, 282, 430-431; Montgomery *et al.*, *Proc. Natl. Acad. Sci.* USA, 1998, 95, 15502-15507; Tuschl *et al.*, *Genes Dev.*, 1999, 13, 3191-3197; Elbashir *et al.*, *Nature*, 2001, 411, 494-498; Elbashir *et al.*, *Genes Dev.* 2001, 15, 188-200). For example, such double-stranded moieties have been shown to inhibit the target by the classical hybridization of antisense strand of the duplex to the target, thereby triggering enzymatic degradation of the target (Tijsterman *et al.*, *Science*, 2002, 295, 694-697).

[00118] In a preferred embodiment, an antisense oligonucleotide targets apolipoprotein (ApoA1) polynucleotides (e.g. accession number NM_000039), variants, alleles, isoforms, homologs, mutants, derivatives, fragments and complementary sequences thereto. Preferably the oligonucleotide is an antisense molecule.

[00119] In accordance with embodiments of the invention, the target nucleic acid molecule is not limited to apolipoprotein (ApoA1) alone but extends to any of the isoforms, receptors, homologs and the like of apolipoprotein (ApoA1) molecules.

[00120] In another preferred embodiment, an oligonucleotide targets a natural antisense sequence of ApoA1polynucleotides, for example, polynucleotides set forth as SEQ ID NOS: 2-165, and any variants, alleles, homologs, mutants, derivatives, fragments and complementary sequences thereto. Examples of antisense oligonucleotides are set forth as SEQ ID NOS: 81 to 173.

[00121] In one embodiment, the oligonucleotides are complementary to or bind to nucleic acid sequences of apolipoprotein (ApoA1) antisense, including without limitation noncoding sense and/or antisense sequences associated with apolipoprotein (ApoA1) polynucleotides and modulate expression and/or function of apolipoprotein (ApoA1) molecules.

[00122] In another preferred embodiment, the oligonucleotides are complementary to or bind to nucleic acid sequences of ApoA1natural antisense, set forth as SEQ ID NOS: 2, 173 and modulate expression and/or function of ApoA1molecules.

[00123] In a preferred embodiment, oligonucleotides comprise sequences of at least 5 consecutive nucleobases of SEQ ID NOS: 81 to 173 and modulate expression and/or function of apolipoprotein (ApoA1) molecules.

[00124] The polynucleotide targets comprise ApoA, including family members thereof, variants of ApoA; mutants of ApoA, including SNPs; noncoding sequences of ApoA; alleles of ApoA; species variants, fragments and the like. Preferably the oligonucleotide is an antisense molecule.

[00125] In another preferred embodiment, the oligonucleotide targeting apolipoprotein (ApoA1) polynucleotides, comprise: antisense RNA, interference RNA (RNAi), short interfering RNA (siRNA); micro interfering RNA (miRNA); a small, temporal RNA (stRNA); or a short, hairpin RNA (shRNA); small RNA-induced gene activation (RNAa); or, small activating RNA (saRNA).

[00126] In another preferred embodiment, targeting of apolipoprotein (ApoA1) polynucleotides, e.g. SEQ ID NOS: 81 to 173, modulates the expression or function of these targets. In one embodiment, expression or function is up-regulated as compared to a control. In another preferred embodiment, expression or function is down-regulated as compared to a control.

[00127] In another preferred embodiment, antisense compounds comprise sequences set forth as SEQ ID NOS: 81 to 173. These oligonucleotides can comprise one or more modified nucleobases, shorter or longer fragments, modified bonds and the like.

[00128] In another preferred embodiment, SEQ ID NOS: 81 to 173 comprise one or more LNA nucleotides.

[00129] The modulation of a desired target nucleic acid can be carried out in several ways known in the art. For example, antisense oligonucleotides, siRNA etc. Enzymatic nucleic

acid molecules (e.g., ribozymes) are nucleic acid molecules capable of catalyzing one or more of a variety of reactions, including the ability to repeatedly cleave other separate nucleic acid molecules in a nucleotide base sequence-specific manner. Such enzymatic nucleic acid molecules can be used, for example, to target virtually any RNA transcript (Zaug *et al.*, 324, *Nature* 429 1986; Cech, 260 *JAMA* 3030, 1988; and Jefferies *et al.*, 17 *Nucleic Acids Research* 1371, 1989).

[00130] Because of their sequence-specificity, trans-cleaving enzymatic nucleic acid molecules show promise as therapeutic agents for human disease (Usman & McSwiggen, 1995 *Ann. Rep. Med. Chem.* 30, 285-294; Christoffersen and Marr, 1995 *J. Med. Chem.* 38, 2023-2037). Enzymatic nucleic acid molecules can be designed to cleave specific RNA targets within the background of cellular RNA. Such a cleavage event renders the mRNA non-functional and abrogates protein expression from that RNA. In this manner, synthesis of a protein associated with a disease state can be selectively inhibited.

[00131] In general, enzymatic nucleic acids with RNA cleaving activity act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

[00132] Several approaches such as *in vitro* selection (evolution) strategies (Orgel, 1979, *Proc. R. Soc.* London, B 205, 435) have been used to evolve new nucleic acid catalysts capable of catalyzing a variety of reactions, such as cleavage and ligation of phosphodiester linkages and amide linkages, (Joyce, 1989, *Gene*, 82, 83-87; Beaudry *et al.*, 1992, *Science* 257, 635-641; Joyce, 1992, Scientific American 267, 90-97; Breaker *et al.*, 1994, *TIBTECH* 12, 268; Bartel *et al.*, 1993, *Science* 261:1411-1418; Szostak, 1993, *TIBS* 17, 89-93; Kumar *et al.*, 1995, *FASEB J.*, 9, 1183; Breaker, 1996, *Curr. Op. Biotech.*, 7, 442).

[00133] The development of ribozymes that are optimal for catalytic activity would contribute significantly to any strategy that employs RNA-cleaving ribozymes for the purpose of regulating gene expression. The hammerhead ribozyme, for example, functions with a

catalytic rate (k_{cat}) of about 1 min^{-1} in the presence of saturating (10 mM) concentrations of Mg^{2+} cofactor. An artificial "RNA ligase" ribozyme has been shown to catalyze the corresponding self-modification reaction with a rate of about 100 min^{-1}. In addition, it is known that certain modified hammerhead ribozymes that have substrate binding arms made of DNA catalyze RNA cleavage with multiple turn-over rates that approach 100 min^{-1}. Finally, replacement of a specific residue within the catalytic core of the hammerhead with certain nucleotide analogues gives modified ribozymes that show as much as a 10-fold improvement in catalytic rate. These findings demonstrate that ribozymes can promote chemical transformations with catalytic rates that are significantly greater than those displayed *in vitro* by most natural self-cleaving ribozymes. It is then possible that the structures of certain self-cleaving ribozymes may be optimized to give maximal catalytic activity, or that entirely new RNA motifs can be made that display significantly faster rates for RNA phosphodiester cleavage.

[00134] Intermolecular cleavage of an RNA substrate by an RNA catalyst that fits the "hammerhead" model was first shown in 1987 (Uhlenbeck, O. C. (1987) *Nature*, 328: 596-600). The RNA catalyst was recovered and reacted with multiple RNA molecules, demonstrating that it was truly catalytic.

[00135] Catalytic RNAs designed based on the "hammerhead" motif have been used to cleave specific target sequences by making appropriate base changes in the catalytic RNA to maintain necessary base pairing with the target sequences (Haseloff and Gerlach, *Natur*e, 334, 585 (1988); Walbot and Bruening, *Nature*, 334, 196 (1988); Uhlenbeck, O. C. (1987) *Nature*, 328: 596-600; Koizumi, M., Iwai, S. and Ohtsuka, E. (1988) *FEBS Lett.*, 228: 228-230). This has allowed use of the catalytic RNA to cleave specific target sequences and indicates that catalytic RNAs designed according to the "hammerhead" model may possibly cleave specific substrate RNAs *in vivo*. (see Haseloff and Gerlach, *Nature*, 334, 585 (1988); Walbot and Bruening, *Nature*, 334, 196 (1988); Uhlenbeck, O. C. (1987) *Nature*, 328: 596-600).

[00136] RNA interference (RNAi) has become a powerful tool for modulating gene expression in mammals and mammalian cells. This approach requires the delivery of small interfering RNA (siRNA) either as RNA itself or as DNA, using an expression plasmid or virus and the coding sequence for small hairpin RNAs that are processed to siRNAs. This system enables efficient transport of the pre-siRNAs to the cytoplasm where they are active and permit the use of regulated and tissue specific promoters for gene expression.

[00137] In a preferred embodiment, an oligonucleotide or antisense compound comprises an oligomer or polymer of ribonucleic acid (RNA) and/or deoxyribonucleic acid (DNA), or a mimetic, chimera, analog or homolog thereof. This term includes oligonucleotides composed of naturally occurring nucleotides, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally occurring portions which function similarly. Such modified or substituted oligonucleotides are often desired over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for a target nucleic acid and increased stability in the presence of nucleases.

[00138] According to the present invention, the oligonucleotides or "antisense compounds" include antisense oligonucleotides (e.g. RNA, DNA, mimetic, chimera, analog or homolog thereof), ribozymes, external guide sequence (EGS) oligonucleotides, siRNA compounds, single- or double-stranded RNA interference (RNAi) compounds such as siRNA compounds, saRNA, aRNA, and other oligomeric compounds which hybridize to at least a portion of the target nucleic acid and modulate its function. As such, they may be DNA, RNA, DNA-like, RNA-like, or mixtures thereof, or may be mimetics of one or more of these. These compounds may be single-stranded, double-stranded, circular or hairpin oligomeric compounds and may contain structural elements such as internal or terminal bulges, mismatches or loops. Antisense compounds are routinely prepared linearly but can be joined or otherwise prepared to be circular and/or branched. Antisense compounds can include constructs such as, for example, two strands hybridized to form a wholly or partially double-stranded compound or a single strand with sufficient self-complementarity to allow for hybridization and formation of a fully or partially double-stranded compound. The two strands can be linked internally leaving free 3' or 5' termini or can be linked to form a continuous hairpin structure or loop. The hairpin structure may contain an overhang on either the 5' or 3' terminus producing an extension of single stranded character. The double stranded compounds optionally can include overhangs on the ends. Further modifications can include conjugate groups attached to one of the termini, selected nucleotide positions, sugar positions or to one of the internucleoside linkages. Alternatively, the two strands can be linked via a non-nucleic acid moiety or linker group. When formed from only one strand, dsRNA can take the form of a self-complementary hairpin-type molecule that doubles back on itself to form a duplex. Thus, the dsRNAs can be fully or partially double stranded. Specific modulation of gene expression can be achieved by stable expression of dsRNA hairpins in transgenic cell lines (Hammond *et al.*, *Nat. Rev. Genet.*, 1991, 2, 110-119; Matzke *et al.*, *Curr.*

Opin. Genet. Dev., 2001, 11, 221-227; Sharp, *Genes Dev.*, 2001, 15, 485-490). When formed from two strands, or a single strand that takes the form of a self-complementary hairpin-type molecule doubled back on itself to form a duplex, the two strands (or duplex-forming regions of a single strand) are complementary RNA strands that base pair in Watson-Crick fashion.

[00139] Once introduced to a system, the compounds of the invention may elicit the action of one or more enzymes or structural proteins to effect cleavage or other modification of the target nucleic acid or may work via occupancy-based mechanisms. In general, nucleic acids (including oligonucleotides) may be described as "DNA-like" (i.e., generally having one or more 2'-deoxy sugars and, generally, T rather than U bases) or "RNA-like" (i.e., generally having one or more 2'-hydroxyl or 2'-modified sugars and, generally U rather than T bases). Nucleic acid helices can adopt more than one type of structure, most commonly the A- and B-forms. It is believed that, in general, oligonucleotides which have B-form-like structure are "DNA-like" and those which have A-form-like structure are "RNA-like." In some (chimeric) embodiments, an antisense compound may contain both A- and B-form regions.

[00140] The antisense compounds in accordance with this invention can comprise an antisense portion from about 5 to about 80 nucleotides (i.e. from about 5 to about 80 linked nucleosides) in length. This refers to the length of the antisense strand or portion of the antisense compound. In other words, a single-stranded antisense compound of the invention comprises from 5 to about 80 nucleotides, and a double-stranded antisense compound of the invention (such as a dsRNA, for example) comprises an antisense strand or portion of 5 to about 80 nucleotides in length. One of ordinary skill in the art will appreciate that this comprehends antisense portions of 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, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 80 nucleotides in length, or any range therewithin.

[00141] In one embodiment, the antisense compounds of the invention have antisense portions of 10 to 50 nucleotides in length. One having ordinary skill in the art will appreciate that this embodies oligonucleotides having antisense portions of 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, or any range therewithin. In some embodiments, the oligonucleotides are 15 nucleotides in length.

[00142] In one embodiment, the antisense or oligonucleotide compounds of the invention have antisense portions of 12 or 13 to 30 nucleotides in length. One having ordinary skill in the art will appreciate that this embodies antisense compounds having antisense portions of 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 nucleotides in length, or any range therewithin.

[00143] In a preferred embodiment, administration of at least one oligonucleotide targeting any one or more polynucleotides of apolipoprotein (ApoA1), prevents or treats diseases associated with abnormal expression or function of apolipoprotein (ApoA1) polynucleotides and encoded products thereof, or other related diseases. Examples of diseases which can be treated with the antisense oligonucleotides comprise: high cholesterol, cardiovascular diseases, heart disease, Tangier's Disease, arthritis, inflammation, autoimmunity, inflammatory diseases, neurological diseases or disorders (e.g. Alzheimer's Disease, Parkinson's Diseases); neurodegeneration, cancer, diseases or disorders caused by foreign organisms such as viral, bacterial, parasitic, fungal, and the like.

[00144] In another preferred embodiment, the oligomeric compounds of the present invention also include variants in which a different base is present at one or more of the nucleotide positions in the compound. For example, if the first nucleotide is an adenosine, variants may be produced which contain thymidine, guanosine or cytidine at this position. This may be done at any of the positions of the antisense or dsRNA compounds. These compounds are then tested using the methods described herein to determine their ability to inhibit expression of a target nucleic acid.

[00145] In some embodiments, homology, sequence identity or complementarity, between the antisense compound and target is from about 40% to about 60%. In some embodiments, homology, sequence identity or complementarity, is from about 60% to about 70%. In some embodiments, homology, sequence identity or complementarity, is from about 70% to about 80%. In some embodiments, homology, sequence identity or complementarity, is from about 80% to about 90%. In some embodiments, homology, sequence identity or complementarity, is about 90%, about 92%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99% or about 100%.

[00146] In another preferred embodiment, the antisense oligonucleotides, such as for example, nucleic acid molecules set forth in SEQ ID NOS:3 to 172 comprise one or more

substitutions or modifications. In one embodiment, the nucleotides are substituted with locked nucleic acids (LNA).

[00147] In another preferred embodiment, the oligonucleotides target one or more regions of the nucleic acid molecules sense and/or antisense of coding and/or noncoding sequences associated with ApoA1and the sequences set forth as SEQ ID NOS: 1, 2. The oligonucleotides are also targeted to overlapping regions of SEQ ID NOS: 1, 2.

[00148] Certain preferred oligonucleotides of this invention are chimeric oligonucleotides. "Chimeric oligonucleotides" or "chimeras," in the context of this invention, are oligonucleotides which contain two or more chemically distinct regions, each made up of at least one nucleotide. These oligonucleotides typically contain at least one region of modified nucleotides that confers one or more beneficial properties (such as, for example, increased nuclease resistance, increased uptake into cells, increased binding affinity for the target) and a region that is a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of antisense modulation of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art. In one preferred embodiment, a chimeric oligonucleotide comprises at least one region modified to increase target binding affinity, and, usually, a region that acts as a substrate for RNAse H. Affinity of an oligonucleotide for its target (in this case, a nucleic acid encoding ras) is routinely determined by measuring the T_m of an oligonucleotide/target pair, which is the temperature at which the oligonucleotide and target dissociate; dissociation is detected spectrophotometrically. The higher the T_m, the greater the affinity of the oligonucleotide for the target.

[00149] Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such; compounds have also been referred to in the art as hybrids or gapmers. Representative United States patents that teach the preparation of such hybrid structures comprise, but are not limited to, US patent nos.

5,013,830; 5,149,797; 5, 220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; and 5,700,922, each of which is herein incorporated by reference.

[00150] In another preferred embodiment, the region of the oligonucleotide which is modified comprises at least one nucleotide modified at the 2' position of the sugar, most preferably a 2'-O-alkyl, 2'-O-alkyl-O-alkyl or 2'-fluoro-modified nucleotide. In other preferred embodiments, RNA modifications include 2'-fluoro, 2'-amino and 2' O-methyl modifications on the ribose of pyrimidines, abasic residues or an inverted base at the 3' end of the RNA. Such modifications are routinely incorporated into oligonucleotides and these oligonucleotides have been shown to have a higher T_m (i.e., higher target binding affinity) than; 2'-deoxyoligonucleotides against a given target. The effect of such increased affinity is to greatly enhance RNAi oligonucleotide inhibition of gene expression. RNAse H is a cellular endonuclease that cleaves the RNA strand of RNA:DNA duplexes; activation of this enzyme therefore results in cleavage of the RNA target, and thus can greatly enhance the efficiency of RNAi inhibition. Cleavage of the RNA target can be routinely demonstrated by gel electrophoresis. In another preferred embodiment, the chimeric oligonucleotide is also modified to enhance nuclease resistance. Cells contain a variety of exo- and endo-nucleases which can degrade nucleic acids. A number of nucleotide and nucleoside modifications have been shown to make the oligonucleotide into which they are incorporated more resistant to nuclease digestion than the native oligodeoxynucleotide. Nuclease resistance is routinely measured by incubating oligonucleotides with cellular extracts or isolated nuclease solutions and measuring the extent of intact oligonucleotide remaining over time, usually by gel electrophoresis. Oligonucleotides which have been modified to enhance their nuclease resistance survive intact for a longer time than unmodified oligonucleotides. A variety of oligonucleotide modifications have been demonstrated to enhance or confer nuclease resistance. Oligonucleotides which contain at least one phosphorothioate modification are presently more preferred. In some cases, oligonucleotide modifications which enhance target binding affinity are also, independently, able to enhance nuclease resistance. Some desirable modifications can be found in De Mesmaeker *et al. Acc. Chem. Res.* 1995, 28:366-374.

[00151] Specific examples of some preferred oligonucleotides envisioned for this invention include those comprising modified backbones, for example, phosphorothioates, phosphotriesters, methyl phosphonates, short chain alkyl or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar linkages. Most preferred are

oligonucleotides with phosphorothioate backbones and those with heteroatom backbones, particularly CH_2 --NH--O--CH_2, CH,--N(CH_3)--O--CH_2 [known as a methylene(methylimino) or MMI backbone], CH_2 --O--N (CH_3)--CH_2, CH_2 --N (CH_3)--N (CH_3)--CH_2 and O--N (CH_3)--CH_2 --CH_2 backbones, wherein the native phosphodiester backbone is represented as O--P--O--CH,). The amide backbones disclosed by De Mesmaeker *et al. Acc. Chem. Res.* 1995, 28:366-374) are also preferred. Also preferred are oligonucleotides having morpholino backbone structures (Summerton and Weller, U.S. Pat. No. 5,034,506). In other preferred embodiments, such as the peptide nucleic acid (PNA) backbone, the phosphodiester backbone of the oligonucleotide is replaced with a polyamide backbone, the nucleotides being bound directly or indirectly to the aza nitrogen atoms of the polyamide backbone (Nielsen *et al. Science* 1991, 254, 1497). Oligonucleotides may also comprise one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH, SH, SCH_3, F, OCN, OCH_3 OCH_3, OCH_3 $O(CH_2)_n$ CH_3, $O(CH_2)_n$ NH_2 or $O(CH_2)_n$ CH_3 where n is from 1 to about 10; C_1 to C_{10} lower alkyl, alkoxyalkoxy, substituted lower alkyl, alkaryl or aralkyl; Cl; Br; CN; CF_3 ; OCF_3; O--, S--, or N-alkyl; O--, S--, or N-alkenyl; $SOCH_3$; SO_2 CH_3; ONO_2; NO_2; N_3; NH_2; heterocycloalkyl; heterocycloalkaryl; aminoalkylamino; polyalkylamino; substituted silyl; an RNA cleaving group; a reporter group; an intercalator; a group for improving the pharmacokinetic properties of an oligonucleotide; or a group for improving the pharmacodynamic properties of an oligonucleotide and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy [2'-O-CH_2 CH_2 OCH_3, also known as 2'-O-(2-methoxyethyl)] (Martin *et al., Helv. Chim. Acta*, 1995, 78, 486). Other preferred modifications include 2'-methoxy (2'-O--CH_3), 2'-propoxy (2'-OCH_2 CH_2CH_3) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyls in place of the pentofuranosyl group.

[00152] Oligonucleotides may also include, additionally or alternatively, nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include adenine (A), guanine (G), thymine (T), cytosine (C) and uracil (U). Modified nucleobases include nucleobases found only infrequently or transiently in natural nucleic acids, e.g., hypoxanthine, 6-methyladenine, 5-Me pyrimidines, particularly 5-methylcytosine (also referred to as 5-methyl-2' deoxycytosine and often referred to in the art as 5-Me-C), 5-hydroxymethylcytosine (HMC), glycosyl HMC and

gentobiosyl HMC, as well as synthetic nucleobases, e.g., 2-aminoadenine, 2-(methylamino)adenine, 2-(imidazolylalkyl)adenine, 2-(aminoalklyamino)adenine or other heterosubstituted alkyladenines, 2-thiouracil, 2-thiothymine, 5-bromouracil, 5-hydroxymethyluracil, 8-azaguanine, 7-deazaguanine, N_6 (6-aminohexyl)adenine and 2,6-diaminopurine. Kornberg, A., DNA Replication, W. H. Freeman & Co., San Francisco, 1980, pp75-77; Gebeyehu, G., *et al.* Nucl. Acids Res. 1987, 15:4513). A "universal" base known in the art, e.g., inosine, may be included. 5-Me-C substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C. (Sanghvi, Y. S., in Crooke, S. T. and Lebleu, B., eds., Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are presently preferred base substitutions.

[00153] Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates which enhance the activity or cellular uptake of the oligonucleotide. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety, a cholesteryl moiety (Letsinger *et al.*, *Proc. Natl. Acad. Sci.* USA 1989, 86, 6553), cholic acid (Manoharan *et al. Bioorg. Med. Chem. Let.* 1994, 4, 1053), a thioether, e.g., hexyl-S-tritylthiol (Manoharan *et al. Ann. N.Y. Acad. Sci.* 1992, 660, 306; Manoharan *et al. Bioorg. Med. Chem. Let.* 1993, 3, 2765), a thiocholesterol (Oberhauser *et al.*, *Nucl. Acids Res.* 1992, 20, 533), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras *et al. EMBO J.* 1991, 10, 111; Kabanov *et al. FEBS Lett.* 1990, 259, 327; Svinarchuk *et al. Biochimie* 1993, 75, 49), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan *et al. Tetrahedron Lett.* 1995, 36, 3651; Shea *et al. Nucl. Acids Res.* 1990, 18, 3777), a polyamine or a polyethylene glycol chain (Manoharan *et al. Nucleosides & Nucleotides* 1995, 14, 969), or adamantane acetic acid (Manoharan *et al. Tetrahedron Lett.* 1995, 36, 3651). Oligonucleotides comprising lipophilic moieties, and methods for preparing such oligonucleotides are known in the art, for example, U.S. Pat. Nos. 5,138,045, 5,218,105 and 5,459,255.

[00154] It is not necessary for all positions in a given oligonucleotide to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single oligonucleotide or even at within a single nucleoside within an oligonucleotide. The present invention also includes oligonucleotides which are chimeric oligonucleotides as hereinbefore defined.

[00155] In another embodiment, the nucleic acid molecule of the present invention is conjugated with another moiety including but not limited to abasic nucleotides, polyether, polyamine, polyamides, peptides, carbohydrates, lipid, or polyhydrocarbon compounds. Those skilled in the art will recognize that these molecules can be linked to one or more of any nucleotides comprising the nucleic acid molecule at several positions on the sugar, base or phosphate group.

[00156] The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including Applied Biosystems. Any other means for such synthesis may also be employed; the actual synthesis of the oligonucleotides is well within the talents of one of ordinary skill in the art. It is also well known to use similar techniques to prepare other oligonucleotides such as the phosphorothioates and alkylated derivatives. It is also well known to use similar techniques and commercially available modified amidites and controlled-pore glass (CPG) products such as biotin, fluorescein, acridine or psoralen-modified amidites and/or CPG (available from Glen Research, Sterling VA) to synthesize fluorescently labeled, biotinylated or other modified oligonucleotides such as cholesterol-modified oligonucleotides.

[00157] In accordance with the invention, use of modifications such as the use of LNA monomers to enhance the potency, specificity and duration of action and broaden the routes of administration of oligonucleotides comprised of current chemistries such as MOE, ANA, FANA, PS etc (ref: Recent advances in the medical chemistry of antisense oligonucleotide by Uhlman, Current Opinions in Drug Discovery & Development 2000 Vol 3 No 2). This can be achieved by substituting some of the monomers in the current oligonucleotides by LNA monomers. The LNA modified oligonucleotide may have a size similar to the parent compound or may be larger or preferably smaller. It is preferred that such LNA-modified oligonucleotides contain less than about 70%, more preferably less than about 60%, most preferably less than about 50% LNA monomers and that their sizes are between about 5 and 25 nucleotides, more preferably between about 12 and 20 nucleotides.

[00158] Preferred modified oligonucleotide backbones comprise, but not limited to, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates comprising 3'alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates comprising 3'-amino

phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included.

[00159] Representative United States patents that teach the preparation of the above phosphorus-containing linkages comprise, but are not limited to, US patent nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5, 177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455, 233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563, 253; 5,571,799; 5,587,361; and 5,625,050, each of which is herein incorporated by reference.

[00160] Preferred modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These comprise those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts.

[00161] Representative United States patents that teach the preparation of the above oligonucleosides comprise, but are not limited to, US patent nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264, 562; 5, 264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596, 086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623, 070; 5,663,312; 5,633,360; 5,677,437; and 5,677,439, each of which is herein incorporated by reference.

[00162] In other preferred oligonucleotide mimetics, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds,

the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds comprise, but are not limited to, US patent nos. 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference . Further teaching of PNA compounds can be found in o Nielsen *et al.*, *Science*, 1991, 254, 1497-1500.

[00163] In another preferred embodiment of the invention the oligonucleotides with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular-CH_2-NH-O-CH_2-,-CH_2-N (CH_3)-O-CH_2-known as a methylene (methylimino) or MMI backbone,-CH_2-O-N (CH_3)-CH_2-,-CH_2N(CH_3)-N(CH_3) CH_2-and-O-N(CH_3)-CH_2-CH_2- wherein the native phosphodiester backbone is represented as-O-P-O-CH_2- of the above referenced US patent no. 5,489,677, and the amide backbones of the above referenced US patent no. 5,602,240. Also preferred are oligonucleotides having morpholino backbone structures of the above-referenced US patent no. 5,034,506.

[00164] Modified oligonucleotides may also contain one or more substituted sugar moieties. Preferred oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S-or N-alkynyl; or O alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C to CO alkyl or C_2 to CO alkenyl and alkynyl. Particularly preferred are O $(CH_2)_n$ O_mCH_3, $O(CH_2)_n$,OCH_3, $O(CH_2)_nNH_2$, $O(CH_2)$nCH_3, $O(CH_2)_nONH_2$, and $O(CH_{2n}ON(CH_2)$n$CH_3)_2$ where n and m can be from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: C to CO, (lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification comprises 2'-methoxyethoxy (2'-O-$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification comprises 2'-dimethylaminooxyethoxy, i.e. , a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as

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

[00165] Other preferred modifications comprise 2'-methoxy (2'-O CH_3), 2'-aminopropoxy (2'-O $CH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative United States patents that teach the preparation of such modified sugar structures comprise, but are not limited to, US patent nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514, 785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646, 265; 5,658,873; 5,670,633; and 5,700,920, each of which is herein incorporated by reference.

[00166] Oligonucleotides may also comprise nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases comprise the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases comprise other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudo-uracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylquanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine.

[00167] Further, nucleobases comprise those disclosed in United States Patent No. 3,687,808, those disclosed in 'The Concise Encyclopedia of Polymer Science And Engineering', pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, 1990, those disclosed by Englisch *et al.*, 'Angewandle Chemie, International Edition', 1991, 30, page 613, and those disclosed by Sanghvi, Y.S., Chapter 15, 'Antisense Research and Applications', pages 289-302, Crooke, S.T. and Lebleu, B. ea., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the

invention. These comprise 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, comprising 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds, 'Antisense Research and Applications', CRC Press, Boca Raton, 1993, pp. 276-278) and are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

[00168] Representative United States patents that teach the preparation of the above noted modified nucleobases as well as other modified nucleobases comprise, but are not limited to, US patent nos. 3,687,808, as well as 4,845,205; 5,130,302; 5,134,066; 5,175, 273; 5, 367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,596,091; 5,614,617; 5,750,692, and 5,681,941, each of which is herein incorporated by reference.

[00169] Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates, which enhance the activity, cellular distribution, or cellular uptake of the oligonucleotide.

[00170] Such moieties comprise but are not limited to, lipid moieties such as a cholesterol moiety (Letsinger *et al.*, *Proc. Natl. Acad. Sci.* USA, 1989, 86, 6553-6556), cholic acid (Manoharan *et al.*, *Bioorg. Med. Chem. Let.*, 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan *et al.*, *Ann. N. Y. Acad. Sci.*, 1992, 660, 306-309; Manoharan *et al.*, *Bioorg. Med. Chem. Let.*, 1993, 3, 2765-2770), a thiocholesterol (Oberhauser *et al.*, *Nucl. Acids Res.*, 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Kabanov *et al.*, *FEBS Lett.*, 1990, 259, 327-330; Svinarchuk *et al.*, *Biochimie*, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36, 3651-3654; Shea *et al.*, *Nucl. Acids Res.*, 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Mancharan *et al.*, *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantane acetic acid (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36, 3651-3654), a palmityl moiety (Mishra *et al.*, *Biochim. Biophys. Acta*, 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-t oxycholesterol moiety (Crooke *et al.*, *J. Pharmacol. Exp. Ther.*, 1996, 277, 923-937).

[00171] Representative United States patents that teach the preparation of such oligonucleotide conjugates comprise, but are not limited to, US patent nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552, 538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486, 603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762, 779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082, 830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5, 245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391, 723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5, 565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599, 928 and 5,688,941, each of which is herein incorporated by reference.

[00172] *Drug discovery*: The compounds of the present invention can also be applied in the areas of drug discovery and target validation. The present invention comprehends the use of the compounds and preferred target segments identified herein in drug discovery efforts to elucidate relationships that exist between apolipoprotein (ApoA1) polynucleotides and a disease state, phenotype, or condition. These methods include detecting or modulating apolipoprotein (ApoA1) polynucleotides comprising contacting a sample, tissue, cell, or organism with the compounds of the present invention, measuring the nucleic acid or protein level of apolipoprotein (ApoA1) polynucleotides and/or a related phenotypic or chemical endpoint at some time after treatment, and optionally comparing the measured value to a non-treated sample or sample treated with a further compound of the invention. These methods can also be performed in parallel or in combination with other experiments to determine the function of unknown genes for the process of target validation or to determine the validity of a particular gene product as a target for treatment or prevention of a particular disease, condition, or phenotype.

Assessing Up-regulation or Inhibition of Gene Expression:

[00173] Transfer of an exogenous nucleic acid into a host cell or organism can be assessed by directly detecting the presence of the nucleic acid in the cell or organism. Such detection can be achieved by several methods well known in the art. For example, the presence of the exogenous nucleic acid can be detected by Southern blot or by a polymerase chain reaction (PCR) technique using primers that specifically amplify nucleotide sequences associated with the nucleic acid. Expression of the exogenous nucleic acids can also be measured using conventional methods including gene expression analysis. For instance, mRNA produced from an exogenous nucleic acid can be detected and quantified using a Northern blot and reverse transcription PCR (RT-PCR).

[00174] Expression of an RNA from the exogenous nucleic acid can also be detected by measuring an enzymatic activity or a reporter protein activity. For example, antisense modulatory activity can be measured indirectly as a decrease or increase in target nucleic acid expression as an indication that the exogenous nucleic acid is producing the effector RNA. Based on sequence conservation, primers can be designed and used to amplify coding regions of the target genes. Initially, the most highly expressed coding region from each gene can be used to build a model control gene, although any coding or non coding region can be used. Each control gene is assembled by inserting each coding region between a reporter coding region and its poly(A) signal. These plasmids would produce an mRNA with a reporter gene in the upstream portion of the gene and a potential RNAi target in the 3' non-coding region. The effectiveness of individual antisense oligonucleotides would be assayed by modulation of the reporter gene. Reporter genes useful in the methods of the present invention include acetohydroxyacid synthase (AHAS), alkaline phosphatase (AP), beta galactosidase (LacZ), beta glucoronidase (GUS), chloramphenicol acetyltransferase (CAT), green fluorescent protein (GFP), red fluorescent protein (RFP), yellow fluorescent protein (YFP), cyan fluorescent protein (CFP), horseradish peroxidase (HRP), luciferase (Luc), nopaline synthase (NOS), octopine synthase (OCS), and derivatives thereof. Multiple selectable markers are available that confer resistance to ampicillin, bleomycin, chloramphenicol, gentamycin, hygromycin, kanamycin, lincomycin, methotrexate, phosphinothricin, puromycin, and tetracycline. Methods to determine modulation of a reporter gene are well known in the art, and include, but are not limited to, fluorometric methods (e.g. fluorescence spectroscopy, Fluorescence Activated Cell Sorting (FACS), fluorescence microscopy), antibiotic resistance determination.

Kits, Research Reagents, Diagnostics, and Therapeutics

[00175] The compounds of the present invention can be utilized for diagnostics, therapeutics, and prophylaxis, and as research reagents and components of kits. Furthermore, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used by those of ordinary skill to elucidate the function of particular genes or to distinguish between functions of various members of a biological pathway.

[00176] For use in kits and diagnostics and in various biological systems, the compounds of the present invention, either alone or in combination with other compounds or therapeutics, are useful as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion or the entire complement of genes expressed within cells and tissues.

[00177] As used herein the term "biological system" or "system" is defined as any organism, cell, cell culture or tissue that expresses, or is made competent to express products of the apolipoprotein (ApoA1) genes. These include, but are not limited to, humans, transgenic animals, cells, cell cultures, tissues, xenografts, transplants and combinations thereof.

[00178] As one nonlimiting example, expression patterns within cells or tissues treated with one or more antisense compounds are compared to control cells or tissues not treated with antisense compounds and the patterns produced are analyzed for differential levels of gene expression as they pertain, for example, to disease association, signaling pathway, cellular localization, expression level, size, structure or function of the genes examined. These analyses can be performed on stimulated or unstimulated cells and in the presence or absence of other compounds that affect expression patterns.

[00179] Examples of methods of gene expression analysis known in the art include DNA arrays or microarrays (Brazma and Vilo, *FEBS Lett.*, 2000 480, 17-24; Celis, *et al.*, *FEBS Lett.*, 2000 480, 2-16), SAGE (serial analysis of gene expression)(Madden, *et al.*, *Drug Discov. Today*, 2000, 5, 415-425), READS (restriction enzyme amplification of digested cDNAs) (Prashar and Weissman, *Methods Enzymol.*, 1999, 303, 258-72), TOGA (total gene expression analysis) (Sutcliffe, *et al.*, *Proc. Natl. Acad. Sci.* U.S.A., 2000, 97, 1976-81), protein arrays and proteomics (Celis, *et al.*, *FEBS Lett.*, 2000, 480, 2-16; Jungblut, *et al.*, *Electrophoresis*, 1999, 20, 2100-10), expressed sequence tag (EST) sequencing (Celis, *et al.*, *FEBS Lett.*, 2000, 480, 2-16; Larsson, *et al.*, *J. Biotechnol.*, 2000, 80, 143-57), subtractive RNA fingerprinting (SuRF) (Fuchs, *et al.*, *Anal. Biochem.*, 2000, 286, 91-98; Larson, *et al.*,

Cytometry, 2000, 41, 203-208), subtractive cloning, differential display (DD) (Jurecic and Belmont, *Curr. Opin. Microbiol.*, 2000, 3, 316-21), comparative genomic hybridization (Carulli, *et al.*, *J. Cell Biochem.* Suppl., 1998, 31, 286-96), FISH (fluorescent *in situ* hybridization) techniques (Going and Gusterson, *Eur. J. Cancer*, 1999, 35, 1895-904) and mass spectrometry methods (To, *Comb. Chem. High Throughput Screen*, 2000, 3, 235-41).

[00180] The compounds of the invention are useful for research and diagnostics, because these compounds hybridize to nucleic acids encoding apolipoprotein (ApoA1). For example, oligonucleotides that hybridize with such efficiency and under such conditions as disclosed herein as to be effective apolipoprotein (ApoA1) modulators are effective primers or probes under conditions favoring gene amplification or detection, respectively. These primers and probes are useful in methods requiring the specific detection of nucleic acid molecules encoding apolipoprotein (ApoA1) and in the amplification of said nucleic acid molecules for detection or for use in further studies of apolipoprotein (ApoA1). Hybridization of the antisense oligonucleotides, particularly the primers and probes, of the invention with a nucleic acid encoding apolipoprotein (ApoA1) can be detected by means known in the art. Such means may include conjugation of an enzyme to the oligonucleotide, radiolabeling of the oligonucleotide, or any other suitable detection means. Kits using such detection means for detecting the level of apolipoprotein (ApoA1) in a sample may also be prepared.

[00181] The specificity and sensitivity of antisense are also harnessed by those of skill in the art for therapeutic uses. Antisense compounds have been employed as therapeutic moieties in the treatment of disease states in animals, including humans. Antisense oligonucleotide drugs have been safely and effectively administered to humans and numerous clinical trials are presently underway. It is thus established that antisense compounds can be useful therapeutic modalities that can be configured to be useful in treatment regimes for the treatment of cells, tissues and animals, especially humans.

[00182] For therapeutics, an animal, preferably a human, suspected of having a disease or disorder which can be treated by modulating the expression of apolipoprotein (ApoA1) polynucleotides is treated by administering antisense compounds in accordance with this invention. For example, in one non-limiting embodiment, the methods comprise the step of administering to the animal in need of treatment, a therapeutically effective amount of an apolipoprotein (ApoA1) modulator. The apolipoprotein (ApoA1) modulators of the present invention effectively modulate the activity of the apolipoprotein (ApoA1) protein or modulate

the expression of the apolipoprotein (ApoA1) protein. In one embodiment, the activity or expression of apolipoprotein (ApoA1) in an animal is inhibited by about 10% as compared to a control. Preferably, the activity or expression of apolipoprotein (ApoA1) in an animal is inhibited by about 30%. More preferably, the activity or expression of apolipoprotein (ApoA1) in an animal is inhibited by 50% or more. Thus, the oligomeric compounds modulate expression of apolipoprotein (ApoA1) mRNA by at least 10%, by at least 50%, by at least 25%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, by at least 75%, by at least 80%, by at least 85%, by at least 90%, by at least 95%, by at least 98%, by at least 99%, or by 100% as compared to a control.

[00183] In one embodiment, the activity or expression of apolipoprotein (ApoA1) and/or in an animal is increased by about 10% as compared to a control. Preferably, the activity or expression of apolipoprotein (ApoA1) in an animal is increased by about 30%. More preferably, the activity or expression of apolipoprotein (ApoA1) in an animal is increased by 50% or more. Thus, the oligomeric compounds modulate expression of apolipoprotein (ApoA1) mRNA by at least 10%, by at least 50%, by at least 25%, by at least 30%, by at least 40%, by at least 50%, by at least 60%, by at least 70%, by at least 75%, by at least 80%, by at least 85%, by at least 90%, by at least 95%, by at least 98%, by at least 99%, or by 100% as compared to a control.

[00184] For example, the reduction of the expression of apolipoprotein (ApoA1) may be measured in serum, blood, adipose tissue, liver or any other body fluid, tissue or organ of the animal. Preferably, the cells contained within said fluids, tissues or organs being analyzed contain a nucleic acid molecule encoding apolipoprotein (ApoA1) peptides and/or the apolipoprotein (ApoA1) protein itself.

[00185] The compounds of the invention can be utilized in pharmaceutical compositions by adding an effective amount of a compound to a suitable pharmaceutically acceptable diluent or carrier. Use of the compounds and methods of the invention may also be useful prophylactically.

Conjugates

[00186] Another modification of the oligonucleotides of the invention involves chemically linking to the oligonucleotide one or more moieties or conjugates that enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. These moieties or conjugates can include conjugate groups covalently bound to functional groups such as primary or

secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugate groups include cholesterols, lipids, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve uptake, enhance resistance to degradation, and/or strengthen sequence-specific hybridization with the target nucleic acid. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve uptake, distribution, metabolism or excretion of the compounds of the present invention. Representative conjugate groups are disclosed in International Patent Application No. PCT/US92/09196, filed Oct. 23, 1992, and U.S. Pat. No. 6,287,860, which are incorporated herein by reference. Conjugate moieties include, but are not limited to, lipid moieties such as a cholesterol moiety, cholic acid, a thioether, e.g., hexyl-5-tritylthiol, a thiocholesterol, an aliphatic chain, e.g., dodecandiol or undecyl residues, a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety. Oligonucleotides of the invention may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

[00187] Representative United States patents that teach the preparation of such oligonucleotide conjugates include, but are not limited to, U.S. Pat. Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941.

Formulations

[00188] The compounds of the invention may also be admixed, encapsulated, conjugated or otherwise associated with other molecules, molecule structures or mixtures of compounds, as for example, liposomes, receptor-targeted molecules, oral, rectal, topical or other formulations, for assisting in uptake, distribution and/or absorption. Representative United States patents that teach the preparation of such uptake, distribution and/or absorption-assisting formulations include, but are not limited to, U.S. Pat. Nos. 5,108,921; 5,354,844; 5,416,016; 5,459,127; 5,521,291; 5,543,165; 5,547,932; 5,583,020; 5,591,721; 4,426,330; 4,534,899; 5,013,556; 5,108,921; 5,213,804; 5,227,170; 5,264,221; 5,356,633; 5,395,619; 5,416,016; 5,417,978; 5,462,854; 5,469,854; 5,512,295; 5,527,528; 5,534,259; 5,543,152; 5,556,948; 5,580,575; and 5,595,756, each of which is herein incorporated by reference.

[00189] Although, the antisense oligonucleotides do not need to be administered in the context of a vector in order to modulate a target expression and/or function, embodiments of the invention relates to expression vector constructs for the expression of antisense oligonucleotides, comprising promoters, hybrid promoter gene sequences and possess a strong constitutive promoter activity, or a promoter activity which can be induced in the desired case.

[00190] In an embodiment, invention practice involves administering at least one of the foregoing antisense oligonucleotides with a suitable nucleic acid delivery system. In one embodiment, that system includes a non-viral vector operably linked to the polynucleotide. Examples of such non-viral vectors include the oligonucleotide alone (e.g. any one or more of SEQ ID NOS: 81 to173) or in combination with a suitable protein, polysaccharide or lipid formulation.

[00191] Additionally suitable nucleic acid delivery systems include viral vector, typically sequence from at least one of an adenovirus, adenovirus-associated virus (AAV), helper-dependent adenovirus, retrovirus, or hemagglutinatin virus of Japan-liposome (HVJ) complex. Preferably, the viral vector comprises a strong eukaryotic promoter operably linked to the polynucleotide e.g., a cytomegalovirus (CMV) promoter.

[00192] Additionally preferred vectors include viral vectors, fusion proteins and chemical conjugates. Retroviral vectors include Moloney murine leukemia viruses and HIV-based viruses. One preferred HIV-based viral vector comprises at least two vectors wherein the gag and pol genes are from an HIV genome and the *env* gene is from another virus. DNA viral vectors are preferred. These vectors include pox vectors such as orthopox or avipox vectors,

herpesvirus vectors such as a herpes simplex I virus (HSV) vector [Geller, A.I. *et al.*, *J. Neurochem*, 64: 487 (1995); Lim, F., *et al.*, in DNA Cloning: Mammalian Systems, D. Glover, Ed. (Oxford Univ. Press, Oxford England) (1995); Geller, A.I. *et al.*, *Proc Natl. Acad. Sci.*: U.S.A.:90 7603 (1993); Geller, A.I., *et al.*, *Proc Natl. Acad. Sci* USA: 87:1149 (1990)], Adenovirus Vectors [LeGal LaSalle *et al.*, *Science*, 259:988 (1993); Davidson, *et al.*, *Nat. Genet.* 3: 219 (1993); Yang, *et al.*, *J. Virol.* 69: 2004 (1995)] and Adeno-associated Virus Vectors [Kaplitt, M.G., *et al.*, *Nat. Genet.* 8:148 (1994)].

[00193] The antisense compounds of the invention encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other compound which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof.

[00194] The term "pharmaceutically acceptable salts" refers to physiologically and pharmaceutically acceptable salts of the compounds of the invention: i.e., salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto. For oligonucleotides, preferred examples of pharmaceutically acceptable salts and their uses are further described in U.S. Pat. No. 6,287,860, which is incorporated herein by reference.

[00195] The present invention also includes pharmaceutical compositions and formulations that include the antisense compounds of the invention. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical (including ophthalmic and to mucous membranes including vaginal and rectal delivery), pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal), oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration. Oligonucleotides with at least one 2'-O-methoxyethyl modification are believed to be particularly useful for oral administration. Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful.

[00196] The pharmaceutical formulations of the present invention, which may conveniently be presented in unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

[00197] The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels, suppositories, and enemas. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances that increase the viscosity of the suspension including, for example, sodium carboxymethylcellulose, sorbitol and/or dextran. The suspension may also contain stabilizers.

[00198] Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, foams and liposome-containing formulations. The pharmaceutical compositions and formulations of the present invention may comprise one or more penetration enhancers, carriers, excipients or other active or inactive ingredients.

[00199] Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter. Emulsions may contain additional components in addition to the dispersed phases, and the active drug that may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Microemulsions are included as an embodiment of the present invention. Emulsions and their uses are well known in the art and are further described in U.S. Pat. No. 6,287,860.

[00200] Formulations of the present invention include liposomal formulations. As used in the present invention, the term "liposome" means a vesicle composed of amphiphilic lipids arranged in a spherical bilayer or bilayers. Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior that contains the composition to be delivered. Cationic liposomes are positively charged liposomes that are believed to interact with negatively charged DNA molecules to form a stable complex. Liposomes that are pH-sensitive or negatively-charged are believed to entrap

DNA rather than complex with it. Both cationic and noncationic liposomes have been used to deliver DNA to cells.

[00201] Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids. When incorporated into liposomes, these specialized lipids result in liposomes with enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome comprises one or more glycolipids or is derivatized with one or more hydrophilic polymers, such as a polyethylene glycol (PEG) moiety. Liposomes and their uses are further described in U.S. Pat. No. 6,287,860.

[00202] The pharmaceutical formulations and compositions of the present invention may also include surfactants. The use of surfactants in drug products, formulations and in emulsions is well known in the art. Surfactants and their uses are further described in U.S. Pat. No. 6,287,860, which is incorporated herein by reference.

[00203] In one embodiment, the present invention employs various penetration enhancers to effect the efficient delivery of nucleic acids, particularly oligonucleotides. In addition to aiding the diffusion of non-lipophilic drugs across cell membranes, penetration enhancers also enhance the permeability of lipophilic drugs. Penetration enhancers may be classified as belonging to one of five broad categories, i.e., surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants. Penetration enhancers and their uses are further described in U.S. Pat. No. 6,287,860, which is incorporated herein by reference.

[00204] One of skill in the art will recognize that formulations are routinely designed according to their intended use, i.e. route of administration.

[00205] Preferred formulations for topical administration include those in which the oligonucleotides of the invention are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Preferred lipids and liposomes include neutral (e.g. dioleoyl-phosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearolyphosphatidyl choline) negative (e.g. dimyristoylphosphatidyl glycerol DMPG) and cationic (e.g. dioleoyltetramethylaminopropyl DOTAP and dioleoyl-phosphatidyl ethanolamine DOTMA).

[00206] For topical or other administration, oligonucleotides of the invention may be encapsulated within liposomes or may form complexes thereto, in particular to cationic liposomes. Alternatively, oligonucleotides may be complexed to lipids, in particular to cationic lipids. Preferred fatty acids and esters, pharmaceutically acceptable salts thereof, and their uses are further described in U.S. Pat. No. 6,287,860.

[00207] Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. Preferred oral formulations are those in which oligonucleotides of the invention are administered in conjunction with one or more penetration enhancers surfactants and chelators. Preferred surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Preferred bile acids/salts and fatty acids and their uses are further described in U.S. Pat. No. 6,287,860, which is incorporated herein by reference. Also preferred are combinations of penetration enhancers, for example, fatty acids/salts in combination with bile acids/salts. A particularly preferred combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. Oligonucleotides of the invention may be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. Oligonucleotide complexing agents and their uses are further described in U.S. Pat. No. 6,287,860, which is incorporated herein by reference.

[00208] Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions that may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

[00209] Certain embodiments of the invention provide pharmaceutical compositions containing one or more oligomeric compounds and one or more other chemotherapeutic agents that function by a non-antisense mechanism. Examples of such chemotherapeutic agents include but are not limited to cancer chemotherapeutic drugs such as daunorubicin, daunomycin, dactinomycin, doxorubicin, epirubicin, idarubicin, esorubicin, bleomycin, mafosfamide, ifosfamide, cytosine arabinoside, bis-chloroethyl-nitrosurea, busulfan, mitomycin C, actinomycin D, mithramycin, prednisone, hydroxyprogesterone, testosterone,

tamoxifen, dacarbazine, procarbazine, hexamethylmelamine, pentamethylmelamine, mitoxantrone, amsacrine, chlorambucil, methylcyclohexylnitrosurea, nitrogen mustards, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-azacytidine, hydroxyurea, deoxycoformycin, 4-hydroxyperoxycyclo-phosphoramide, 5-fluorouracil (5-FU), 5-fluorodeoxyuridine (5-FUdR), methotrexate (MTX), colchicine, taxol, vincristine, vinblastine, etoposide (VP-16), trimetrexate, irinotecan, topotecan, gemcitabine, teniposide, cisplatin and diethylstilbestrol (DES). When used with the compounds of the invention, such chemotherapeutic agents may be used individually (e.g., 5-FU and oligonucleotide), sequentially (e.g., 5-FU and oligonucleotide for a period of time followed by MTX and oligonucleotide), or in combination with one or more other such chemotherapeutic agents (e.g., 5-FU, MTX and oligonucleotide, or 5-FU, radiotherapy and oligonucleotide). Anti-inflammatory drugs, including but not limited to nonsteroidal anti-inflammatory drugs and corticosteroids, and antiviral drugs, including but not limited to ribivirin, vidarabine, acyclovir and ganciclovir, may also be combined in compositions of the invention. Combinations of antisense compounds and other non-antisense drugs are also within the scope of this invention. Two or more combined compounds may be used together or sequentially.

[00210] In another related embodiment, compositions of the invention may contain one or more antisense compounds, particularly oligonucleotides, targeted to a first nucleic acid and one or more additional antisense compounds targeted to a second nucleic acid target. For example, the first target may be a particular antisense sequence of apolipoprotein (ApoA1), and the second target may be a region from another nucleotide sequence. Alternatively, compositions of the invention may contain two or more antisense compounds targeted to different regions of the same apolipoprotein (ApoA1) nucleic acid target. Numerous examples of antisense compounds are illustrated herein and others may be selected from among suitable compounds known in the art. Two or more combined compounds may be used together or sequentially.

Dosing:

[00211] The formulation of therapeutic compositions and their subsequent administration (dosing) is believed to be within the skill of those in the art. Dosing is dependent on severity and responsiveness of the disease state to be treated, with the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug

accumulation in the body of the patient. Persons of ordinary skill can easily determine optimum dosages, dosing methodologies and repetition rates. Optimum dosages may vary depending on the relative potency of individual oligonucleotides, and can generally be estimated based on EC_{50s} found to be effective in *in vitro* and *in vivo* animal models. In general, dosage is from 0.01 μg to 100 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state, wherein the oligonucleotide is administered in maintenance doses, ranging from 0.01 μg to 100 g per kg of body weight, once or more daily, to once every 20 years.

[00212] While various embodiments of the present invention have been described above, it should be understood that they have been presented by way of example only, and not limitation. Numerous changes to the disclosed embodiments can be made in accordance with the disclosure herein without departing from the spirit or scope of the invention. Thus, the breadth and scope of the present invention should not be limited by any of the above described embodiments.

[00213] All documents mentioned herein are incorporated herein by reference. All publications and patent documents cited in this application are incorporated by reference for all purposes to the same extent as if each individual publication or patent document were so individually denoted. By their citation of various references in this document, Applicants do not admit any particular reference is "prior art" to their invention. Embodiments of inventive compositions and methods are illustrated in the following examples.

EXAMPLES

[00214] The following non-limiting Examples serve to illustrate selected embodiments of the invention. It will be appreciated that variations in proportions and alternatives in elements of the components shown will be apparent to those skilled in the art and are within the scope of embodiments of the present invention.

Example 1: Design of antisense oligonucleotides specific for a nucleic acid molecule antisense and/or sense strand of an apolipoprotein (ApoA1) polynucleotide

[00215] As indicated above the term "oligonucleotide specific for" or "oligonucleotide targets" refers to an oligonucleotide having a sequence (i) capable of forming a stable complex with a portion of the targeted gene, or (ii) capable of forming a stable duplex with a portion of a mRNA transcript of the targeted gene.

[00216] Selection of appropriate oligonucleotides is facilitated by using computer programs that automatically align nucleic acid sequences and indicate regions of identity or homology. Such programs are used to compare nucleic acid sequences obtained, for example, by searching databases such as GenBank or by sequencing PCR products. Comparison of nucleic acid sequences from a range of species allows the selection of nucleic acid sequences that display an appropriate degree of identity between species. In the case of genes that have not been sequenced, Southern blots are performed to allow a determination of the degree of identity between genes in target species and other species. By performing Southern blots at varying degrees of stringency, as is well known in the art, it is possible to obtain an approximate measure of identity. These procedures allow the selection of oligoncueltodes that exhibit a high degree of complementarity to target nucleic acid sequences in a subject to be controlled and a lower degree of complementarity to corresponding nucleic acid sequences in other species. One skilled in the art will realize that there is considerable latitude in selecting appropriate regions of genes for use in the present invention.

[00217] An antisense compound is "specifically hybridizable" when binding of the compound to the target nucleic acid interferes with the normal function of the target nucleic acid to cause a modulation of function and/or activity, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target nucleic acid sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and under conditions in which assays are performed in the case of *in vitro* assays

[00218] The hybridization properties of the oliginucleotides described herein can be determined by one or more *in vitro* assays as known iin the art. For example, the properties of the oligonucleotides desccribed herein can be obtained by determination of binding strength between the target natural antisense and a potential drug molecules using melting curve assay

[00219] The binding strength between the target natural antisense and a potential drug molecule (Molecule) can be estimated using any of the established methods of measuring the strength of intermolecular interactions, for example, a melting curve assay.

[00220] Melting curve assay determines the temperature at which a rapid transition from doublestranded to singlestranded conformation occurs for the natural antisense/Molecule complex. This temperature is widely accepted as a reliable measure of the interaction strength between the two molecules.

[00221] A melting curve assay can be performed using a cDNA copy of the actual natural antisense RNA molecule or a synthetic DNA or RNA nucleotide corresponding to the binding site of the Molecule. Multiple kits containing all necessary reagents to perform this assay are available (e.g. Applied Biosystems Inc. MeltDoctor kit). These kits include a suitable buffer solution containing one of the double strand DNA (dsDNA) binding dyes (such as ABI HRM dyes, SYBR Green, SYTO, etc.). The properties of the dsDNA dyes are such that they emit almost no fluorescence in free form, but are highly fluorescent when bound to dsDNA.

[00222] To perform the assay the cDNA or a corresponding oligonucleotide are mixed with Molecule in concentrations defined by the particular manufacturer's protocols. The mixture is heated to 95 °C to dissociate all pre-formed dsDNA complexes, then slowly cooled to room temperature or other lower temperature defined by the kit manufacturer to allow the DNA molecules to anneal. The newly formed complexes are then slowly heated to 95 °C with simultaneous continuous collection of data on the amount of fluorescence that is produced by the reaction. The fluorescence intensity is inversely proportional to the amounts of dsDNA present in the reaction. The data can be collected using a real time PCR instrument compatible with the kit (e.g.ABI's StepOne Plus Real Time PCR System or LightTyper instrument, Roche Diagnostics, Lewes, UK).

[00223] Melting peaks are constructed by plotting the negative derivative of fluorescence with respect to temperature (-d(Fluorescence)/dT) on the y-axis) against temperature (x-axis) using appropriate software (for example LightTyper (Roche) or SDS Dissociation Curve, ABI). The data is analyzed to identify the temperature of the rapid transition from dsDNA complex to single strand molecules. This temperature is called Tm and is directly proportional to the strength of interaction between the two molecules. Typically, Tm will exceed 40 °C.

Example 2: Modulation of ApoA1 polynucleotides

Materials and Methods:

[00224] Cells were treated with either of the following methods:

Method 1: *Treatment of HepG2 cells with naked antisense oligonucleotides:*

[00225] HepG2 cells from ATCC (cat# HB-8065) were grown in growth media (MEM/EBSS (Hyclone cat #SH30024, or Mediatech cat # MT-10-010-CV) +10% FBS (Mediatech cat# MT35-011-CV)+ penicillin/streptomycin (Mediatech cat# MT30-002-CI)) at 37°C and 5% CO_2. One day before the experiment the cells were replated at the density of 0.5×10^4/ml into 6 well plates and incubated at 37°C and 5% CO_2. On the day of the experiment the media in the 6 well plates was replaced with 1.5 ml/well of fresh growth media.

All antisense oligonucleotides were diluted in water to the concentration of 20 μM. 2 μl of this solution was mixed with 400 μl of fresh growth media and applied to each well of the 6 well plates with HepG2 cells. Similar mixture including 2 μl of water instead of the oligonucleotide solution was used for the mock-treated controls. After 3-18 h of incubation at 37°C and 5% CO_2 the media was changed to fresh growth media. 72 h after addition of antisense oligonucleotides the cells were redosed as described in above. 48-72 h after second dosing the media was removed and RNA was extracted from the cells using SV Total RNA Isolation System from Promega (cat # Z3105) or RNeasy Total RNA Isolation kit from Qiagen (cat# 74181) following the manufacturers' instructions. 600 ng of RNA was added to the reverse transcription reaction performed using Verso cDNA kit from Thermo Scientific (cat#AB1453B) as described in the manufacturer's protocol. The cDNA from this reverse transcription reaction was used to monitor gene expression by real time PCR using ABI Taqman Gene Expression Mix (cat#4369510) and primers/probes designed by ABI (for 18S cat# 4319413E, for ApoA1 Hs00163641_m1, Applied Biosystems Inc., Foster City CA). The following PCR cycle was used: 50°C for 2 min, 95°C for 10 min, 40 cycles of (95°C for 15 seconds, 60°C for 1 min) using Mx4000 thermal cycler (Stratagene). Fold change in gene expression after treatment with antisense oligonucleotides was calculated based on the difference in 18S-normalized dCt values between treated and mock-transfected samples.

Method Two: *Treatment of HepG2 cells with antisense oligonucleotides*:

[00226] HepG2 cells from ATCC (cat# HB-8065) were grown in growth media (MEM/EBSS (Hyclone cat #SH30024, or Mediatech cat # MT-10-010-CV) +10% FBS (Mediatech cat# MT35-011-CV)+ penicillin/streptomycin (Mediatech cat# MT30-002-CI)) at 37°C and 5% CO_2. One day before the experiment the cells were replated at the density of 1.5×10^5/ml into 6 well plates and incubated at 37°C and 5% CO_2. On the day of the experiment the media in the 6 well plates was changed to fresh growth media. All antisense oligonucleotides were diluted to the concentration of 20 μM. 2 μl of this solution was incubated with 400 μl of Opti-MEM media (Gibco cat#31985-070) and 4 μl of Lipofectamine 2000 (Invitrogen cat# 11668019) at room temperature for 20 min and applied to each well of the 6 well plates with HepG2 cells. Similar mixture including 2 μl of water instead of the oligonucleotide solution was used for the mock-transfected controls. After 3-18 h of incubation at 37°C and 5% CO_2 the media was changed to fresh growth media. 48 h after addition of antisense oligonucleotides the media was removed and RNA was extracted from the cells using SV Total RNA Isolation System from Promega (cat # Z3105) or RNeasy Total RNA Isolation kit from Qiagen (cat# 74181) following the manufacturers' instructions.

600 ng of RNA was added to the reverse transcription reaction performed using Verso cDNA kit from Thermo Scientific (cat#AB1453B) as described in the manufacturer's protocol. The cDNA from this reverse transcription reaction was used to monitor gene expression by real time PCR using ABI Taqman Gene Expression Mix (cat#4369510) and primers/probes designed by ABI (for 18S cat# 4319413E, for ApoA1 Hs00163641_m1, Applied Biosystems Inc., Foster City CA). The following PCR cycle was used: 50°C for 2 min, 95°C for 10 min, 40 cycles of (95°C for 15 seconds, 60°C for 1 min) using Mx4000 thermal cycler (Stratagene). Fold change in gene expression after treatment with antisense oligonucleotides was calculated based on the difference in 18S-normalized dCt values between treated and mock-transfected samples.

Results:

[00227] Real time PCR results show that the levels of ApoA1 mRNA in HepG2 cells are significantly increased in HepG2 cells 48 h after treatment with antisense oligonucleotides to ApoA1 antisense DA327409ext (Fig 1).

Example 3: Modulation of ApoA1 Gene Expression

Materials and Methods

[00228] Cells were treated with either of the following methods:

Method 1: *Treatment of HepG2 cells with naked antisense oligonucleotides:*

[00229] HepG2 cell were grown in MEM/EBSS (Hyclone cat #SH30024) +10% FBS+ penicillin+streptomycin at 37°C and 5% CO_2. One day before the experiment the cells were replated at the density of 1.5×10^4/ml into 6 well plates and left at 37°C and 5% CO_2. On the day of the experiment the media in the 6 well plates was changed to fresh MEM/EBSS +10% FBS. All antisense oligonucleotides manufactured by IDT were diluted to the concentration of 20 μM. 2 μl of this solution was incubated with 400 μl of Opti-MEM media (Gibco cat#31985-070) and applied to each well of the 6 well plates with HepG2 cells. Similar mixture including 2 μl of water instead of the oligonucleotide solution was used for the mock-transfected controls. 72 h after addition of antisense oligonucleotides the media was removed and the dosing procedure was repeated as described in above.

48-72 h after repeated dosing RNA was extracted from the cells using SV Total RNA Isolation System from Promega (cat # Z3105) or RNeasy Total RNA Isolation kit from Qiagen (cat# 74181) following the manufacturers' instructions. 600 ng of RNA was added to the reverse transcription reaction performed using Verso cDNA kit from Thermo Scientific (cat#AB1453B) as described in the manufacturer's protocol. The cDNA from this reverse transcription reaction was used to monitor gene expression by real time PCR using ABI Taqman Gene Expression Mix (cat#4369510) and primers/probes designed by ABI (for 18S cat# 4319413E, for ApoA1 Hs00163641_m1, and a custom designed assay for ApoA1 antisense DA327409ext, all by Applied Biosystems Inc., Foster City CA). The following PCR cycle was used: 50°C for 2 min, 95°C for 10 min, 40 cycles of (95°C for 15 seconds, 60°C for 1 min) using Mx4000 thermal cycler (Stratagene).

Fold change in gene expression after treatment with antisense oligonucleotides was calculated based on the difference in 18S-normalized dCt values between treated and mock-transfected samples.

Primers and probe for the custom designed Taqman assay for the ApoA1 natural antisense DA327409ext. Capital letters indicate unmodified deoxyribonucleotides

Forward Primer Seq. CTCCTCCTGCCACTTCTTCTG (SEQ ID NO: 163)

Reverse Primer Seq. CTGGTGGATGAAGAAGGTTTGC (SEQ ID NO: 164)

Probe sequence (FAM labeled) TTTGGATCTGGACGACTTC (SEQ ID NO: 165)

Method Two: *Treatment of HepG2 cells with antisense oligonucleotides*:

[00230] HepG2 cells from ATCC (cat# HB-8065) were grown in growth media (MEM/EBSS (Hyclone cat #SH30024, or Mediatech cat # MT-10-010-CV) +10% FBS (Mediatech cat# MT35-011-CV)+ penicillin/streptomycin (Mediatech cat# MT30-002-CI)) at 37°C and 5% CO_2. One day before the experiment the cells were replated at the density of 1.5×10^5/ml into 6 well plates and incubated at 37°C and 5% CO_2. On the day of the experiment the media in the 6 well plates was changed to fresh growth media. All antisense oligonucleotides were diluted to the concentration of 20 μM. 2 μl of this solution was incubated with 400 μl of Opti-MEM media (Gibco cat#31985-070) and 4 μl of Lipofectamine 2000 (Invitrogen cat# 11668019) at room temperature for 20 min and applied to each well of the 6 well plates with HepG2 cells. Similar mixture including 2 μl of water instead of the oligonucleotide solution was used for the mock-transfected controls. After 3-18 h of incubation at 37°C and 5% CO_2 the media was changed to fresh growth media. 48 h after addition of antisense oligonucleotides the media was removed and RNA was extracted from the cells using SV Total RNA Isolation System from Promega (cat # Z3105) or RNeasy Total RNA Isolation kit from Qiagen (cat# 74181) following the manufacturers' instructions.

600 ng of RNA was added to the reverse transcription reaction performed using Verso cDNA kit from Thermo Scientific (cat#AB1453B) as described in the manufacturer's protocol. The cDNA from this reverse transcription reaction was used to monitor gene expression by real time PCR using ABI Taqman Gene Expression Mix (cat#4369510) and primers/probes designed by ABI (for 18S cat# 4319413E, for ApoA1 Hs00163641_m1, and a custom designed assay for ApoA1 antisense DA327409ext, all by Applied Biosystems Inc., Foster City CA). The following PCR cycle was used: 50°C for 2 min, 95°C for 10 min, 40 cycles of (95°C for 15 seconds, 60°C for 1 min) using Mx4000 thermal cycler (Stratagene). Fold change in gene expression after treatment with antisense oligonucleotides was calculated based on the difference in 18S-normalized dCt values between treated and mock-transfected samples.

Primers and probe for the custom designed Taqman assay for the ApoA1 natural antisense DA327409ext. Capital letters indicate unmodified deoxyribonucleotides

Forward Primer Seq. CTCCTCCTGCCACTTCTTCTG (SEQ ID NO: 163)

Reverse Primer Seq. CTGGTGGATGAAGAAGGTTTGC (SEQ ID NO: 164)

Probe sequence (FAM labeled) TTTGGATCTGGACGACTTC (SEQ ID NO: 165)

[00231] *Treatment of primary monkey hepatocytes.* Primary monkey hepatocytes were introduced into culture by RxGen Inc. and plated in 6 well plates. They were treated with oligonucleotides as follows. The media in the 6 well plates was changed to fresh growth media consisting of William's Medium E (Sigma cat#W4128) supplemented with 5% FBS, 50 U/ml penicillin and 50 ug/ml streptomycin, 4 ug/ml insulin, 1 uM dexamethasone, 10 ug/ml Fungin (InVivogen, San Diego CA). All antisense oligonucleotides were diluted to the concentration of 20 μM. 2 μl of this solution was incubated with 400 μl of Opti-MEM media (Gibco cat#31985-070) and 4 μl of Lipofectamine 2000 (Invitrogen cat# 11668019) at room temperature for 20 min and applied to each well of the 6 well plates with cells. Similar mixture including 2 μl of water instead of the oligonucleotide solution was used for the mock-transfected controls. After 3-18 h of incubation at 37°C and 5% CO_2 the media was changed to fresh growth media. 48 h after addition of antisense oligonucleotides the media was removed and RNA was extracted from the cells using SV Total RNA Isolation System from Promega (cat # Z3105) or RNeasy Total RNA Isolation kit from Qiagen (cat# 74181) following the manufacturers' instructions.

600 ng of RNA was added to the reverse transcription reaction performed using Verso cDNA kit from Thermo Scientific (cat#AB1453B) as described in the manufacturer's protocol. The cDNA from this reverse transcription reaction was used to monitor gene expression by real time PCR using ABI Taqman Gene Expression Mix (cat#4369510) and primers/probes designed by ABI (for 18S cat# 4319413E, for ApoA1 Hs00163641_m1, and a custom designed assay for ApoA1 antisense DA327409ext, all by Applied Biosystems Inc., Foster City CA). The following PCR cycle was used: 50°C for 2 min, 95°C for 10 min, 40 cycles of (95°C for 15 seconds, 60°C for 1 min) using Mx4000 thermal cycler (Stratagene). Fold change in gene expression after treatment with antisense oligonucleotides was calculated based on the difference in 18S-normalized dCt values between treated and mock-transfected samples.

ELISA was conducted using MabTech Inc. ApoA1 ELISA kit cat# 3710-11-6 according to manufacturer's instructions.

[00232] The results are shown in Figures 2, 3, 4 and 5. Figure 2 shows that both oligonucleotides with the phosphothioate backbone, i.e. internucleotide linkages and LNA oligonucleotides were effective in modulating the target gene expression as measured by ApoA1 mRNA (top panel) and ApoA1 antisense DA327409ext RNA (bottom panel) amounts

detected. Figure 3 shows the levels of ApoA1 mRNA (orange bars) and ApoA1 antisense DA327409ext RNA (blue bars) in HepG2 cells treated with oligonucleotides designed against DA327409ext. Figure 4 shows dose dependent upregulation of ApoA1 mRNA (bottom panel) and protein (top panel) in HepG2 cultures treated with oligonucleotides designed against DA327409ext. Figure 5 shows upregulation of ApoA1 mRNA in primary African green monkey hepatocytes after treatment with oligonucleotides designed against DA327409ext.

Example 4: Efficacy and Duration of Action Study of CUR-962 in the African Green Monkey

[00233] The objective of this study was to assess and compare the effect of antisense knockdown of the discordant noncoding antisense sequences that regulate the APOA1 genes following intravenous administration in a nonhuman primate model. The antisense oligonucleotide test articles designed to inhibit the APOA1 regulatory sequences were designated as CUR-962.

[00234] CUR-962: +G*+C*T* A*G*T* C*T*G* +T*+T*+G (SEQ ID NO: 170).

[00235]

CUR-963 (control): +G*+T*C* T*G*A* T*G*G* +A*+G*+A (SEQ ID NO: 171).

REGULATORY TEST GUIDELINES

[00236] This study was designed in accordance with accepted toxicological principles and to comply with International Conference of Harmonization (ICH) Harmonized Tripartite Guidelines (Non-Clinical Safety Studies for the Conduct of Human Clinical Trials for Pharmaceuticals ICH M3(m), 2000 November 9), and generally accepted procedures for the testing of therapeutic agents.

TEST AND CONTROL ARTICLES

Test Article Identity and Preparation

[00237] The test article, CUR-962, is a chemically stabilized antisense oligonucleotide. The vehicle for intravenous delivery is phosphate-buffered saline (PBS).

Vehicle characterization

[00238] For the PBS vehicle, the composition, batch number, expiry date and storage conditions (temperature and light/dark) was obtained from the supplier.

Test Article Storage and Handling

[00239] The test substance and vehicle were stored according to the received storage conditions supplied by the Sponsor and manufacturer, accordingly.

Analysis of the Test Article Formulations

[00240] Samples of the test article formulation will be cryopreserved for analysis of the concentration, stability and homogeneity of the test substance formulations.

TEST SYSTEM RATIONALE

[00241] The primate is a suitable non rodent species, acceptable to regulatory authorities as an indicator of potential hazards, and for which extensive background data are available. The African green monkey specifically is a highly clinically relevant model of multiple human physiologic and disease states.

[00242] The intravenous route of administration corresponds to a possible human therapeutic route. The dose of the test articles was based on the results of the dose finding studies of analogous compounds previously performed in the African green monkey.

[00243] African green monkey were chosen as the primate of choice as the test substances' target sequence are conserved across species with 100 % homology in primates. Additionally, the test substance is a synthetic oligonucleotide. Consequently, dosing in primates allows for a superior assessment of the efficacy of these compounds that would be more reflective of the uptake likely to be seen in humans than in any other species.

ANIMALS

Species

Chlorocebus sabaeus, non-human primate

Breed

[00244] African green monkey indigenous to St. Kitts.

Source

[00245] RxGen, Lower Bourryeau, St. Kitts, West Indies.

Expected Age

[00246] The test animals were adults.

Expected Body Weight

[00247] The monkeys weigh approximately 3-4 kg. The actual range may vary but will be documented in the data.

Sex

[00248] The test animals were adult females.

Number of Animals

[00249] Ten animals were screened to ensure identification of 8 animals appropriate for enrollment in the study.

Number on Study

[00250] Females: 8

Justification for Number on Study

[00251] This study was designed to use the fewest number of animals possible, consistent with the primary objective of evaluating the therapeutic efficacy of the test article in the African green monkey and prior studies of the systemic administration of this type of oligonucleotide in this species.

Animal Specification

[00252] Ten adult African Green monkeys in the weight range of 3 to 4 kg, were employed in the study. The monkeys were drug-naïve adult animals humanely trapped from the feral population that inhabits the island. Trapped monkeys were treated with antihelminthics to eliminate any possible intestinal parasite burden and were observed in quarantine for a minimum of 4 weeks prior to screening for study enrollment. The age of trapped monkeys were estimated by size and dentation, with the exclusion of older animals from the study. Prior to study enrollment, a clinical exam was performed on each monkey, including evaluation of locomotion and dexterity. Blood samples were taken and sent to Antech Diagnostics (Memphis, TN) for comprehensive clinical chemistries and a complete blood count and lipid profiles (see sections 9.2 and 319567928 for specifications). Monkeys with abnormal lab values, as determined by comparison to the established normal range for monkeys in the St. Kitts colony, wre excluded from the study. In order to identify 8 monkeys that satisfy this criterion, 10 monkeys were screened, with the screening of additional animals as needed. Before study initiation, the selected monkeys will be transferred to individual

cages to acclimate to individual housing for a one-week period. Only animals deemed suitable for experimentation will be enrolled in the study. The actual (or estimated) age and weight ranges at the start of the study will be detailed in the raw data and final report.

Animal Health and Welfare

[00253] The highest standards of animal welfare were followed and adhered to guidelines stipulated by the St. Kitts Department of Agriculture and the U.S. Department of Health and Human Services. All studies will be conducted in accordance with these requirements and all applicable codes of practice for the care and housing of laboratory animals. All applicable standards for veterinary care, operation, and review as contained in the NIH Guide for the Care and Use of Animals. The St. Kitts facility maintains an animal research committee that reviews the protocols and inspects the facilities as required by the Guide. The Foundation has an approved assurance filed with the Office of Laboratory Animal Welfare, as required by the Guide, #A4384-01 (Axion Research Foundation/St. Kitts Biomedical Foundation). There are no special nonhuman primate veterinary care issues and biohazard issues raised by the research specified in this study.

Housing and Environment

[00254] To allow detection of any treatment-related clinical signs, the animals were housed individually prior to surgery and postoperatively until sacrifice. The primate building in which the individual cages were situated were illuminated entirely by ambient light, which at 17 degrees north latitude approximates a 12hr:12hr light-dark cycle as recommended in the U.S. D.H.H.S guidelines. The RxGen primate building was completely ventilated to the outside. Additional air movement was assured by ceiling fans to maintain a constant target temperature of 23-35°C, as is typical of St. Kitts throughout the year. Twenty-four hour extremes of temperature and relative humidity (which also will not be controlled) were measured daily. During the study, the cages were cleaned at regular intervals.

Diet and Water

[00255] Each animal was offered approximately 90 grams per day of a standard monkey chow diet (TekLad, Madison, WI). The specific nutritional composition of the diet was recorded. The water was periodically analyzed for microbiological purity. The criteria for acceptable levels of contaminants in stock diet and water supply were within the analytical specifications established by the diet manufacturer and the periodic facility water evaluations,

respectively. The water met all criteria necessary for certification as acceptable for human consumption.

EXPERIMENTAL DESIGN

Animal Identification and Randomization

[00256] Allocation was done by means of a stratified randomization procedure based on bodyweight and plasma cholesterol profiles. Prior to and after allocation to a group, each animal was identified by a tattoo on the abdomen. Tattoos are placed on all colony animals as a means of identification in the course of routine health inspections. A cage plan was drawn up to identify the individuals housed within, and individual monkeys were further identified by a labeled tag attached to their respective cage.

Group sizes, doses and identification numbers

[00257] The animals were assigned to 2 treatment groups, comprised of 4 monkeys in each group. Specific animal identification numbers were provided to each monkey according to the facility numbering system. This system uniquely identifies each monkey by a letter followed by a three-digit number, e.g. Y032.

Route and Frequency of Administration

[00258] Animals were dosed once daily on Days 1, 3, and 5 delivered intravenously by manual infusion over ~10 min. The infusion rate will be 24 mL/kg/h. The animals were sedated with ketamine and xylazine prior to and during the dosing procedure. A venous catheter (Terumo mini vein infusion set, 20 gauge needle, or similar appropriate infusion set) was inserted into the saphenous vein. Dosing took place in each monkey between 8:00 and 10:00 a.m. shortly after the animals wake and prior to feeding. A blood sample to assess plasma cholesterol and other lipid levels as described in Blood Chemistry section below, was collected just prior to each infusion. Blood collection preceded feeding at both sampling intervals to minimize dietary effects on cholesterol measurements.

Clinical Observations

[00259] All visible signs of reaction to treatment were recorded on each day of dosing. In addition, the animals were examined at least once each week for physical attributes such as appearance and general condition.

Body Weights

[00260] Body weights were recorded at weekly intervals during the treatment and post-treatment periods.

Food Consumption

[00261] Individual food consumption was not be quantified. Feeding patterns, however, werebe monitored and a note made of any major changes.

Mortality and Morbidity

[00262] Mortality and morbidity will be recorded. Any decision regarding premature sacrifice will be made after consultation with the Study Director and with the Sponsor's Monitoring Scientist, if possible. Animals that are found dead or killed prematurely will be subjected to necropsy with collection of liver, kidney, heart and spleen lung tissues for histopathology. In the event of premature sacrifice a blood sample will also be taken (if possible) and the parameters determined. Animals that are found dead after regular working hours will be refrigerated overnight and necropsies performed at the start of the next working day. If the condition of an animal requires premature sacrifice, it will be euthanized by intravenous overdose of sodium pentobarbital. All research is governed by the Principles for Use of Animals. RxGen is required by law to comply with the U.S. Department of Health and Human Services standards for primate facility, which dictates the levels of severity that the procedures within this study, specified as mild, must abide.

CLINICAL LABORATORY STUDIES

Blood Samples

[00263] Three blood samples were obtained from all animals prior to treatment, to establish a plasma cholesterol baseline. Blood samples were collected post treatment and were taken via superficial venipuncture. The volume collected at any one sampling time point was not to exceed 8 ml, which represents approximately 4% total blood volume of an adult monkey.

[00264] Animals had blood drawn at two baseline time points and on study days 1, 3, 5, 7, 9, 11, 13 and 15, with continued ~weekly collection thereafter until total plasma cholesterol normalizes in group 1 (APOA1), if a perturbation is appreciated. Eight milliliters of blood were collected on days 1, 6 and 11 to allow for assessment of clinical chemistries, lipid profiles and coagulation profiles. On all other days only 5 mls of blood were collected, sufficient for clinical chemistries and lipid profiles.

[00265] Blood samples were split into three parts on days on which both chemistry and hematology measures will be made. One sample was collected into plasma collection tubes containing 25µl of heparin and labeled with the study number, dose level, day number, date, unique animal identification number. Following separation 1ml of plasma was removed to a sterile cryotube carrying the above details and stored appropriately until shipment, for blood chemistry analysis. One aliquot of the plasma (0.5 ml) was removed to a sterile cryotube labeled with the details described above and stored appropriately until shipment for plasma cholesterol distribution and apolipoprotein analysis. An additional 1ml and 0.5ml aliquot of plasma was flash frozen and stored in liquid nitrogen to serve as back-up samples for potential additional analyses.

[00266] Two additional whole blood sample aliquots (2.5ml each) were treated with acid citrate dextrose (ACD) anticoagulant and labeled, and stored at 4°C until shipped for coagulation and CBC measures detailed below.

[00267] The samples were shipped to arrive within 24 h of sampling, or stored under stable conditions for shipment at a time determined appropriate.

[00268] Repeat samples were taken only if the method of sampling or the method of assay was thought to be outside normal quality limits. Samples were taken into labeled tubes.

Hematology

[00269] A complete blood count (CBC), Prothrombin Time, PTT, Fibrinogen and D-Dimer were measured on all samples collected on days 1, 6 and 11 (and on additional days if perturbations are detected at any of these time points). Blood counts were assessed on 1 ml of whole blood collected in vacutainers containing EDTA. Coagulation profile determinations were performed on approximately 2.0 mL blood collected in vacutainers containing acid citrate dextrose (ACD) anticoagulant.

Blood Chemistry

[00270] Glucose, Blood Urea Nitrogen, Creatinine, Total protein, Albumin, Total bilirubin, Alkaline Phosphatase, Alanine aminotransferase (ALT), Aspartate aminotransferase (AST), Cholesterol, Calcium, Phosphorus, Sodium, Potassium, Chloride, A/G ratio, BUN/Creatine (calculated) Globulins (calculated),Lipase, Amylase, Triglycerides, CPK, Lactate dehydrogenase, Gamma glutamyl transferase (GGT), Magnesium ,Total Cholesterol LDL, VLDL, HDL, ApoA1, ApoA2, ApoB, ApoE, ApoLp(a). Superchemistries and LDL and

HDL measures were made on every plasma sample. Apolipoprotein measures were made on select samples after assessment of the LDL and HDL data.

[00271] Determinations were performed on approximately 1.0 mL plasma for the superchemistry and 0.5ml plasma for the cholesterol distribution and apolipoprotein measures. An additional aliquot of plasma was collected and stored for possible future analyses.

Liver Biopsies

[00272] A percutaneous liver biopsy was performed on all monkeys at baseline and on days 7 and 17. A 14 gauge biopsy needle (INRAD) will be employed to obtain 2 core biopsies (~1.0 cm in length) from both the right and left lobe of the liver. Successful biopsy was confirmed by visual inspection of the biopsy sample on the biopsy needle prior to subdividing as indicated below.

[00273] The samples were pooled and then split in the following manner. Half of one biopsy (~0.5 cm) from the left lobe was immersed in paraformaldehyde for sectioning for histopathology and *in situ* analysis. The remaining half of each of the divided biopsies, as well the other two intact biopsies were immediately immersed in a labeled cryotube containing 2 mls of RNAlater (Qiagen) and incubated at 4°C overnight, following which the RNAlater was aspirated and the sample tube flash frozen in liquid nitrogen. Following transportation in liquid nitrogen total RNA was isolated employing the Trizol or TriReagent method, with an expected yield of ~40 μg per 1.0 cm 14 g core biopsy (~80-100 μg total for the pooled RNA derived from all 4 pooled core biopsies from a single monkey, absent the component saved for histopathology and in situ). 5μg of the RNA fraction were used for target-specific real-time qPCR (TaqMan miRNA assay, ABI). The remaining RNA fraction was reserved for possible genome wide expression analysis.

[00274] The fixed tissue was processed for paraffin embedding. Sections were stained for H&E and histopathological findings reported under Gross Histological findings. All slides generated in this work carried a label with the study number, dose level, day number, date, unique animal identification number.

STATISTICAL ANALYSIS

Statistics

[00275] Descriptive statistics on hematology, clinical chemistries and lipid profiles were performed. Appropriate bioinformatic analyses was conducted on expression data.

Sample Size

[00276] Sample size determinations were made on the basis of prior experiments administering modified anti-sense oligonucleotides to African green monkeys and resulting clinical chemistry and lipid profile changes and associated variability. The total number of subjects for efficacy evaluation were twenty enrolled animals, with four animals per treatment group, and four additional screened animals.

Results:

[00277] The results are shown in the following figures. Figure 6: ApoA1 mRNA (top panels) and protein (bottom panels) levels increased in monkey liver biopsies after treatment with CUR-962, an oligonucleotide designed to ApoA1 antisense DA327409ext, compared to the baseline levels, as determined by real time PCR and ELISA respectively (two left panels). ApoA1 mRNA and protein levels did not change after the same period of time in the control group dosed with an oligonucleotide that showed no effect on ApoA1 levels in vitro (CUR-963, two right panels).

[00278] Although the invention has been illustrated and described with respect to one or more implementations, equivalent alterations and modifications will occur to others skilled in the art upon the reading and understanding of this specification and the annexed drawings. In addition, while a particular feature of the invention may have been disclosed with respect to only one of several implementations, such feature may be combined with one or more other features of the other implementations as may be desired and advantageous for any given or particular application.

[00279] The Abstract of the disclosure will allow the reader to quickly ascertain the nature of the technical disclosure. It is submitted with the understanding that it will not be used to interpret or limit the scope or meaning of the following claims.

CLAIMS

What is claimed is:

1. A method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro comprising:

contacting said cells or tissues with an antisense oligonucleotide 5 to 30 nucleotides in length wherein said oligonucleotide has at least 50% sequence identity to a reverse complement of polynucleotide comprising 5 to 30 consecutive nucleotides within nucleotides 1-932 of SEQ ID NO:2 (Figure 8); thereby modulating function and/or expression of the apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro.

2. A method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro comprising:

contacting said cells or tissues with an antisense oligonucleotide 5 to 30 nucleotides in length wherein said oligonucleotide has at least 50% sequence identity to a reverse complement of the an antisense of the apolipoprotein (ApoA1) polynucleotide; thereby modulating function and/or expression of the apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro.

3. A method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro comprising:

contacting said cells or tissues with an antisense oligonucleotide 5 to 30 nucleotides in length wherein said oligonucleotide has at least 50% sequence identity to an antisense oligonucleotide to an apolipoprotein (ApoA1) polynucleotide; thereby modulating function and/or expression of the apolipoprotein (ApoA1) polynucleotide in patient cells or tissues in vivo or in vitro.

4. A method of modulating function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues *in vivo* or *in vitro* comprising:

contacting said cells or tissues with an antisense oligonucleotide that targets a region of the natural antisense of a apolipoprotein (ApoA1) polynucleotide; thereby modulating

function and/or expression of an apolipoprotein (ApoA1) polynucleotide in patient cells or tissues *in vivo* or *in vitro*.

5. The method of claim4, wherein the expression and/or function of the apolipoprotein (ApoA1) is increased *in vivo* or *in vitro* with respect to a control.

6. The method of claim4, wherein the antisense oligonucleotide targets a natural antisense sequence of an apolipoprotein (ApoA1) polynucleotide.

7. The method of claim4, wherein the antisense oligonucleotide targets a nucleic acid sequence comprising coding and/or non-coding nucleic acid sequences of an apolipoprotein (ApoA1) polynucleotide.

8. The method of claim4, wherein the antisense oligonucleotides target overlapping and/or non-overlapping sequences of apolipoprotein (ApoA1) polynucleotides.

9. The method of claim4, wherein the antisense oligonucleotides comprise one or more modifications comprising: a modified sugar moiety, a modified internucleoside linkage, a modified nucleotide and/or combinations thereof.

10. The method of claim 9, wherein the modified sugar moiety comprises a 2'-O-methoxyethyl modified sugar moiety, a 2'-methoxy modified sugar moiety, a 2'-O-alkyl modified sugar moiety, or a bicyclic sugar moiety.

11. The method of claim 9, wherein modified internucleoside linkages comprise a phosphorothioate, 2'- O-methoxyethyl (MOE), 2'-fluoro, alkylphosphonate, phosphorodithioate, alkylphosphonothioate, phosphoramidate, carbamate, carbonate, phosphate triester, acetamidate, carboxymethyl ester, and/or combinations thereof.

12. The method of claim 9, wherein the oligonucleotides optionally having at least one modified nucleotides comprising, peptide nucleic acids, locked nucleic acid (LNA) molecules, arabino-nucleic acid (FANA), peptide nucleic acids (PNAs), analogues or derivatives thereof.

13. The method of claim 1 wherein the antisense oligonucleotide comprises the core sequence gctagt (SEQ ID NO: 172).

14. The method of claim 1, wherein the oligonucleotides comprises at least one oligonucleotide sequence set forth as SEQ ID NOS: 81to 173.

15. A method of modulating an apolipoprotein (ApoA1) gene expression and/or function in mammalian cells or tissues *in vivo* or *in vitro* comprising:

contacting said cells or tissues with a short interfering RNA (siRNA) oligonucleotide 5 to 30 nucleotides in length specific for an antisense polynucleotide of an apolipoprotein (ApoA1) polynucleotide wherein said oligonucleotide has at least 50% sequence identity to a complementary sequence of at least about five consecutive nucleic acids of the antisense and/or sense nucleic acid molecule of the apolipoprotein (ApoA1) polynucleotide; and,

modulating an apolipoprotein (ApoA1) gene expression and/or function in mammalian cells or tissues *in vivo* or *in vitro*.

16, The method of claim 15, wherein said oligonucleotide has at least 80% sequence identity to a complementary sequence of at least about five consecutive nucleic acids of the antisense and/or sense nucleic acid molecule of the apolipoprotein (ApoA1) polynucleotide.

17. A method of modulating an apolipoprotein (ApoA1) gene expression and/or function in mammalian cells or tissues *in vivo* or *in vitro* comprising:

contacting said cells or tissues with an antisense oligonucleotide of about 5 to 30 nucleotides in length specific for noncoding and/or coding sequences of a sense and/or natural antisense strand of a polynucleotide encoding an apolipoprotein (ApoA1) molecule wherein an antisense oligonucleotide has at least 50% sequence identity to at least one nucleic acid sequence set forth as SEQ ID NOS: 81 to 173; and,

modulating an apolipoprotein (ApoA1) gene expression and/or function in mammalian cells or tissues *in vivo* or *in vitro*..

18. A synthetic, modified oligonucleotide comprising at least one modification wherein the modification comprises at least one internucleotide linkage of: alkylphosphonate, phosphorothioate, phosphorodithioate, alkylphosphonothioate, phosphoramidate, carbamate, carbonate, phosphate triester, acetamidate, carboxymethyl ester, or combinations thereof, wherein said oligonucleotide is an antisense compound which hybridizes to and modulates expression and/or function of apolipoprotein (ApoA1) molecules *in vivo* or *in vitro* as compared to a normal control.

19. The oligonucleotide of claim 18, comprising combinations of phosphorothioate internucleotide linkages and at least one internucleotide linkage selected from the group consisting of: alkylphosphonate, phosphorodithioate, alkylphosphonothioate, phosphoramidate, carbamate, carbonate, phosphate triester, acetamidate, carboxymethyl ester, and/or combinations thereof.

20. The oligonucleotide of claim 18, wherein said oligonucleotide comprises at least one phosphorothioate internucleotide linkage.

21. The oligonucleotide of claim 18, wherein said oligonucleotide comprising a backbone of phosphorothioate internucleotide linkages.

22. The oligonucleotide of claim 18, wherein the oligonucleotide optionally comprises at least one modified nucleotide comprising, peptide nucleic acids, locked nucleic acid (LNA) molecules, analogues, derivatives and/or combinations thereof.

23. The oligonucleotide of claim 18, wherein the oligonucleotide comprises a modified sugar moiety comprising a 2'-O-methoxyethyl modified sugar moiety, a 2'-methoxy modified sugar moiety, a 2'-O-alkyl modified sugar moiety, or a bicyclic sugar moiety.

24. The oligonucleotide of claim 18, wherein the antisense oligonucleotide is of at least about 5 to 30 nucleotides in length and hybridizes to an antisense and/or sense strand of an apolipoprotein (ApoA1) polynucleotide wherein said oligonucleotide has at least about 20% sequence identity to a complementary sequence of at least about five consecutive nucleic acids of the antisense and/or sense coding and/or noncoding nucleic acid sequences of the apolipoprotein (ApoA1) polynucleotide.

25. The oligonucleotide of claim 18, wherein the oligonucleotide is at least about 80% sequence identity to a complementary sequence of at least about five consecutive nucleic acids of the antisense and/or sense coding and/or noncoding nucleic acid sequences of the apolipoprotein (ApoA1) polynucleotide.

26. The oligonucleotide of claim 18, wherein said oligonucleotide hybridizes to and modulates expression and/or function of at least one apolipoprotein (ApoA1) polynucleotide *in vivo* or *in vitro*, as compared to a normal control.

27. The oligonucleotide of claim 18 wherein the oligonucleotides comprises the core sequence gctagt (SEQ ID NO: 172).

28. The oligonucleotide of claim 18, wherein the oligonucleotides comprise the sequences set forth as SEQ ID NOS: 81 to 173.

29. A composition comprising one or more oligonucleotides specific for apolipoprotein (ApoA1) polynucleotides said polynucleotides comprising antisense sequences, complementary sequences, alleles, homologs, isoforms, variants, derivatives, mutants or fragments thereof.

30. The composition of claim 29, wherein the oligonucleotides comprise a nucleotide sequence identity of at least about 40% as compared to any one of the nucleotide sequences set forth as SEQ ID NOS: 81 to 173.

31. The composition of claim 29, wherein the oligonucleotides comprise nucleotide sequences set forth as SEQ ID NOS: 1 to 173.

32. The composition of claim 28, wherein the oligonucleotides set forth as SEQ ID NOS: 81 to 173, comprise one or more modified or substituted nucleotides.

33. The composition of claim 29, wherein the modified nucleotides comprise modified bases comprising phosphorthiorate, methylphosphonate, peptide nucleic acids, locked nucleic acid (LNA) molecules.

34. A method of preventing or treating diseases associated with apolipoprotein (ApoA1) polynucleotides and/or encoded products thereof, comprising:

administering to a patient a therapeutically effective dose of at least one antisense oligonucleotide that binds to a natural antisense sequence of apolipoprotein (ApoA1) polynucleotide and modulates expression of said apolipoprotein (ApoA1) polynucleotides; thereby preventing or treating diseases associated with apolipoprotein (ApoA1) polynucleotides and/or encoded products thereof.

35. The method of claim 34, wherein a disease associated with apolipoprotein (ApoA1) polynucleotides comprise: cardiovascular disorders, cholesterol, diabetes, heart disease,

arthritis, inflammation, neurological diseases or disorders, autoimmune diseases, cancer, or obesity.

36. A method of identifying and selecting oligonucleotides for *in vivo* administration comprising selecting a target polynucleotide associated with a disease state;

identifying oligonucleotides comprising at least five consecutive nucleotides which are complementary to, or in an antisense orientation to the identified polynucleotide; and,

measuring the thermal melting point between binding of the antisense oligonucleotide and target polynucleotide under stringent hybridization conditions; and,

identifying and selecting oligonucleotides for *in vivo* administration.