ANGIOTENSINOGEN (AGT) iRNA COMPOSITIONS AND METHODS OF USE THEREOF

Cross-Reference to Related Applications

This application claims the benefit of priority to U.S. Provisional Application No. 62/001,731, filed on May 22, 2014, and U.S. Provisional Application No. 62/047978, filed on September 9, 2014. The entire contents of each of the foregoing applications are hereby incorporated herein by reference.

Sequence Listing

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incoroporated by reference in its entirety. The ASCII copy, created on May 18, 2015, is named 121301-01320_SL.txt and is 318,688 bytes in size.

Background of the Invention

The renin-angiotensin-aldosterone system (RAAS) plays a crucial role in the regulation of blood pressure. The RAAS cascade begins with the release of renin by the juxtaglomerular cells of the kidney into the circulation. Renin secretion is stimulated by several factors, including Na+ load in the distal tubule, β-sympathetic stimulation, and/or reduced renal perfusion. Active renin in the plasma cleaves angiotensinogen (produced by the liver) to angiotensin I, which is then converted by circulating and locally expressed angiotensin-converting enzyme (ACE) to angiotensin II. Most of the effects of angiotensin II on the RAAS are exerted by its binding to angiotensin II type 1 receptors (AT_1R), leading to arterial vasoconstriction, tubular and glomerular effects, such as enhanced Na+ reabsorption or modulation of glomerular filtration rate. In addition, together with other stimuli such as adrenocorticotropin, anti-diuretic hormone, catecholamines, endothelin, serotonin, and levels of Mg2+ and K+, AT_1R stimulation leads to aldosterone release which, in turn, promotes Na+ and K+ excretion in the renal distal convoluted tubule.

Dysregulation of the RAAS leading to, for example, excessive angiotensin II production and/or AT_1R stimulation results in hypertension which can lead to, *e.g.,* increased oxidative stress, promotion of inflammation, hypertrophy, and fibrosis in the heart, kidneys, and arteries, and result in, *e.g.,* left ventricular fibrosis, arterial remodeling, and glomerulosclerosis.

Hypertension is the most prevalent, controllable disease in developed countries, affecting 20–50% of adult populations. It is a major risk factor for various diseases, disorders and conditions such as, shortened life expectancy, chronic kidney disease, stroke, myocardial

infarction, heart failure, aneurysms (*e.g.* aortic aneurysm), peripheral artery disease, heart damage (*e.g.*, heart enlargement or hypertrophy) and other cardiovascular related diseases, disorders and/or conditions. In addition, hypertension has been shown to be an important risk factor for cardiovascular morbidity and mortality accounting for, or contributing to, 62% of all strokes and 49% of all cases of heart disease.

Despite the number of anti-hypertensive drugs available for treating hypertension, more than two-thirds of subjects are not controlled with one anti-hypertensive agent and require two or more anti-hypertensive agents selected from different drug classes. This further reduces the number of subjects with controlled blood pressure as compliance and side-effects increase with increasing medication.

Accordingly, there is a need in the art for alternative therapies and combination therapies for subjects having an angiotensinogen-associated disease.

Summary of the Invention

The present invention provides iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of an angiotensinogen (AGT) gene. The AGT gene may be within a cell, *e.g.,* a cell within a subject, such as a human.

The present invention also provides methods and therapies for treating a subject having a disorder that would benefit from inhibiting or reducing the expression of an AGT gene, *e.g.,* an angiotensinogen-associated disease, such as hypertension, using iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of an AGT gene for inhibiting the expression of an AGT gene.

Accordingly, in one aspect, the present invention provides double-stranded ribonucleic acid (RNAi) agents for inhibiting expression of angiotensinogen (AGT), which comprise a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:2, wherein substantially all of the nucleotides of the sense strand and substantially all of the nucleotides of the antisense strand are modified nucleotides, and wherein the sense strand is conjugated to a ligand attached at the 3'-terminus. In one embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand are modified nucleotides.

In another aspect, the present invention provides double-stranded ribonucleic acid (RNAi) agents for inhibiting expression of angiotensinogen (AGT), which comprise a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand

comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101; 803-843; 834-859; 803-859; 803-875; 834-875; 847-875; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1892-1914; 1894-1914;1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2078-2107; 2078-2011; 2080-2098; 2081-2099; 2081-2104; 2081-2011; 2082-2100; 2084-2102; 2084-2011; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2291-2311; 2291-2318; 2291-2315; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2304-2329; 2306-2324; 2307-2325; 2309-2327; 2309-2329; 2309-2342; 2309-2350; 2309-2358; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2 such that the antisense strand is substantially complementary to the at least 15 contiguous nucleotides in the sense strand. In certain embodiments, substantially all of the nucleotides of the sense strand are modified nucleotides. In other embodiments, substantially all of the nucleotides of the antisense strand are modified nucleotides. In yet other embodiments, substantially all of the nucleotides of both strands are modified nucleotides. In one embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand are modified nucleotides. In one embodiment, the sense strand is conjugated to a ligand attached at the 3'-terminus. In one embodiment, the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2 such that the antisense strand is substantially complementary to the at least 15 contiguous nucleotides in the sense strand.

In one aspect, the present invention provides double-stranded ribonucleic acid (RNAi) agents for inhibiting expression of angiotensinogen (AGT), which comprise a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides from nucleotides 803-843; 834-859; 803-859; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2080-2098; 2081-2099; 2082-2100; 2084-2102; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2306-2324; 2307-2325; 2309-2327; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleoides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2 such that the antisense strand is substantially complementary to the at least 15 contiguous nucleotides in the sense strand. In certain embodiments, substantially all of the nucleotides of the sense strand are modified nucleotides. In other embodiments, substantially all of the nucleotides of the antisense strand are modified nucleotides. In yet other embodiments, substantially all of the nucleotides of both strands are modified nucleotides. In one embodiment, the sense strand is conjugated to a ligand attached at the 3'-terminus.

In one embodiment, the sense strand and the antisense strand comprise a region of complementarity which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the antisense sequences listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15. For example, in certain embodiments, the sense strand and the antisense strand comprise a region of complementarity which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the antisense sequences of the duplexes AD-52433.1, AD-52438.1, AD-52439.1, AD-52445.1, AD-52449.1, AD-52451.1, AD-52456.1, AD-52457.1, AD-52462.1, AD-52463.1, AD-52469.1, AD-52474.1, AD-55976.1, AD-55978.1, AD-55979.1, AD-55980.1, AD-55981.1, AD-55982.1, AD-

55983.1, AD-55984.1, AD-55987.1, AD-55988.1, AD-55989.1, AD-55990.1, AD-55991.1, AD-55994.1, AD-55995.1, AD-55996.1, AD-55999.1, AD-56000.1, AD-56001.1, AD-56002.1, AD-56003.1, AD-56006.1, AD-56007.1, AD-56008.1, AD-56009.1, AD-56011.1, AD-56012.1, AD-56013.1, AD-56016.1, AD-56017.1, AD-56019.1, AD-56020.1, AD-56021.1, AD-56022.1, AD-56024.1, AD-56026.1, AD-56027.1, AD-56029.1, AD-56030.1, AD-56031.1, AD-56032.1, AD-56035.1, AD-56039.1, AD-56041.1, AD-56043.1, AD-56044.1, AD-56047.1, AD-56048.1, AD-56051.1, AD-56053.1, AD-56054.1, AD-56059.1, AD-56062.1, AD-56065.1, AD-56066.1, AD-60770.1, AD-60771.1, AD-60776.1, AD-60777.1, AD-60778.1, AD-60779.1, AD-60780.1, AD-60781.1, AD-60783.1, AD-60784.1, AD-60785.1, AD-60788.1, AD-60789.1, AD-60791.1, AD-60793.1, AD-60795.1, AD-60798.1, AD-60801.1, AD-67903.1, AD-67906.1, AD-67923.1, AD-67924.1, AD-67925.1, AD-67926.1, AD-67935.1, AD-67965.1, AD-67994.1, AD-67995.1, AD-67996.1, AD-68017.1, AD-68022.1, AD-68035.1, AD-68036.1, AD-68037.1, AD-68084.2, AD-68085.2, AD-68086.2, AD-68087.2, AD-68090.2, AD-68091.2, AD-68092.2, AD-68093.2, AD-68116.1, AD-68117.1, AD-68118.1, AD-68124.1, AD-68125.1, or AD-68126.1. In certain embodiments, the sense strand and the antisense strand comprise a region of complementarity which comprises at least 15 contiguous nucleotides of the region of complementarity of any one of duplexes AD-52433.1, AD-52438.1, AD-52439.1, AD-52445.1, AD-52449.1, AD-52451.1, AD-52456.1, AD-52457.1, AD-52462.1, AD-52463.1, AD-52469.1, AD-52474.1, AD-55976.1, AD-55978.1, AD-55979.1, AD-55980.1, AD-55981.1, AD-55982.1, AD-55983.1, AD-55984.1, AD-55987.1, AD-55988.1, AD-55989.1, AD-55990.1, AD-55991.1, AD-55994.1, AD-55995.1, AD-55996.1, AD-55999.1, AD-56000.1, AD-56001.1, AD-56002.1, AD-56003.1, AD-56006.1, AD-56007.1, AD-56008.1, AD-56009.1, AD-56011.1, AD-56012.1, AD-56013.1, AD-56016.1, AD-56017.1, AD-56019.1, AD-56020.1, AD-56021.1, AD-56022.1, AD-56024.1, AD-56026.1, AD-56027.1, AD-56029.1, AD-56030.1, AD-56031.1, AD-56032.1, AD-56035.1, AD-56039.1, AD-56041.1, AD-56043.1, AD-56044.1, AD-56047.1, AD-56048.1, AD-56051.1, AD-56053.1, AD-56054.1, AD-56059.1, AD-56062.1, AD-56065.1, AD-56066.1, AD-60770.1, AD-60771.1, AD-60776.1, AD-60777.1, AD-60778.1, AD-60779.1, AD-60780.1, AD-60781.1, AD-60783.1, AD-60784.1, AD-60785.1, AD-60788.1, AD-60789.1, AD-60791.1, AD-60793.1, AD-60795.1, AD-60798.1, AD-60801.1, AD-67903.1, AD-67906.1, AD-67923.1, AD-67924.1, AD-67925.1, AD-67926.1, AD-67935.1, AD-67965.1, AD-67994.1, AD-67995.1, AD-67996.1, AD-68017.1, AD-68022.1, AD-68035.1, AD-68036.1, AD-68037.1, AD-68084.2, AD-68085.2, AD-68086.2, AD-68087.2, AD-68090.2, AD-68091.2, AD-68092.2, AD-68093.2, AD-68116.1, AD-68117.1, AD-68118.1, AD-68124.1, AD-68125.1, or AD-68126.1.

In one embodiment, the antisense strand comprises a region of complementarity which comprises at least 15 contiguous unmodified nucleotides differing by no more than 3

nucleotides from the antisense nucleotide sequence of AD-67327 (5'-AUUAGAAGAAAAGGUGGGAGACU-3'; SEQ ID NO:537). In another embodiment, the region of complementarity consists of the antisense unmodified nucleotide sequence of AD-67327 (5'- AUUAGAAGAAAAGGUGGGAGACU-3'; SEQ ID NO:537). In one embodiment, the dsRNA comprises a sense strand consisting of the nucleotide sequence of 5'-UCUCCCACCUUUUCUUCUAAU-3' (SEQ ID NO:499), and an antisense strand consisting of the nucleotide sequence of 5'-UUAGAAGAAAAGGUGGGAGACU-3' (SEQ ID NO:537). In one embodiment, the double-stranded RNAi agent comprises the modified nucleotide sequence of AD-67327 (5'-uscsucccAfcCfUfUfuucuucuaau-3'; SEQ ID NO:1037 and 5'-asUfsuagAfagaaaagGfuGfggagascsu-3'; SEQ ID NO:1038.

In some embodiments, the modified nucleotide(s) is independently selected from the group consisting of a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a nucleotide comprising a 5'-phosphorothioate group, and a terminal nucleotide linked to a cholesteryl derivative or a dodecanoic acid bisdecylamide group. In further embodiments, the modified nucleotide is selected from the group consisting of a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide a conformationally restricted nucleotide, a contrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-alkyl-modified nucleotide, a 2'-O-allyl modified nucleotide, a 2'-C-allyl modified nucleotide, a 2'-hydroxyl modified nucleotide, a morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide.

In another embodiment of the double-stranded RNAi agent, at least one strand comprises a 3' overhang of at least 1 nucleotide. In another embodiment, at least one strand comprises a 3' overhang of at least 2 nucleotides.

In another aspect, the present invention provides RNAi agents, *e.g.*, double-stranded ribonucleic acid (RNAi) agents capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein the double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein the antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein the double-stranded RNAi agent is represented by formula (III):

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

antisense: $3'\ n_p'\text{-}N_a'\text{-}(X'X'X')_k\text{-}N_b'\text{-}Y'Y'Y'\text{-}N_b'\text{-}(Z'Z'Z')_l\text{-}N_a'\text{-}n_q'\ 5'$ (III)

wherein:

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

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

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each

sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

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

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides;

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y′; and

wherein the sense strand is conjugated to at least one ligand.

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

In one embodiment, XXX is complementary to X′X′X′, YYY is complementary to Y′Y′Y′, and ZZZ is complementary to Z′Z′Z′.

In one embodiment, the YYY motif occurs at or near the cleavage site of the sense strand.

In another embodiment, the Y′Y′Y′ motif occurs at the 11, 12 and 13 positions of the antisense strand from the 5'-end.

In one embodiment, Y′ is 2′-O-methyl.

In one embodiment, formula (III) is represented by formula (IIIa):

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

antisense: 3' $n_{p'}$-$N_{a'}$- Y′Y′Y′- $N_{a'}$- $n_{q'}$ 5' (IIIa).

In another embodiment, formula (III) is represented by formula (IIIb):

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

antisense: 3' $n_{p'}$-$N_{a'}$- Y′Y′Y′-$N_{b'}$-Z′Z′Z′- $N_{a'}$- $n_{q'}$ 5' (IIIb)

wherein each N_b and N_b' independently represents an oligonucleotide sequence comprising 1-5 modified nucleotides.

In yet another embodiment, formula (III) is represented by formula (IIIc):

sense: 5' n_p -N_a –X X X -N_b -Y Y Y -N_a - n_q 3'

antisense: 3' $n_{p'}$-$N_{a'}$- X′X′X′-$N_{b'}$- Y′Y′Y′- $N_{a'}$- $n_{q'}$ 5' (IIIc)

wherein each N_b and N_b' independently represents an oligonucleotide sequence comprising 1-5 modified nucleotides.

In a further embodiment, formula (III) is represented by formula (IIId):

sense: 5' n_p -N_a –X X X- N_b -Y Y Y -N_b -Z Z Z -N_a - n_q 3'

antisense: 3' $n_{p'}$-$N_{a'}$- X′X′X′- $N_{b'}$-Y′Y′Y′-$N_{b'}$-Z′Z′Z′- $N_{a'}$- $n_{q'}$ 5'

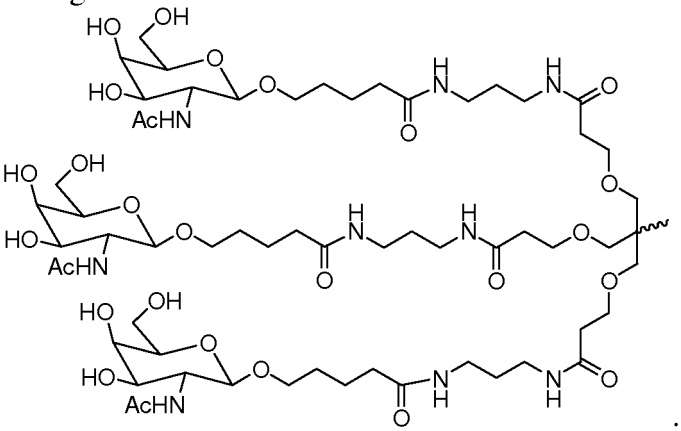
(IIId)

wherein each N_b and N_b' independently represents an oligonucleotide sequence comprising 1-5 modified nucleotides and each N_a and N_a' independently represents an oligonucleotide sequence comprising 2-10 modified nucleotides.

In one embodiment, the double-stranded region is 15-30 nucleotide pairs in length. In another embodiment, the double-stranded region is 17-23 nucleotide pairs in length. In yet another embodiment, the double-stranded region is 17-25 nucleotide pairs in length. In a further embodiment, the double-stranded region is 23-27 nucleotide pairs in length. In another embodiment, the double-stranded region is 19-21 nucleotide pairs in length. In another embodiment, the double-stranded region is 19-23 nucleotide pairs in length. In another embodiment, the double-stranded region is 21-23 nucleotide pairs in length. In yet another embodiment, each strand has 15-30 nucleotides. In yet another embodiment, each strand has 19-30 nucleotides.

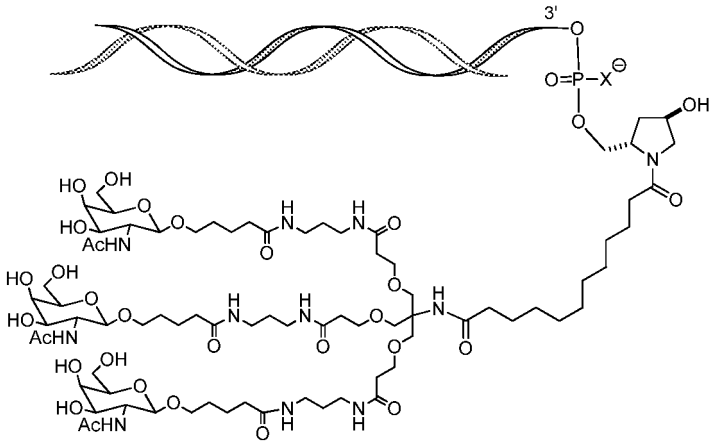
In one embodiment, the modifications on the nucleotides are selected from the group consisting of LNA, UNA, CRN, cEt, HNA, CeNA, 2′-methoxyethyl, 2′-O-alkyl, 2′-O-allyl, 2′-C- allyl, 2′-fluoro, 2′-deoxy, 2'-hydroxyl, and combinations thereof. In another embodiment, the modifications on the nucleotides are 2′-O-methyl or 2′-fluoro modifications.

In one embodiment, the ligand the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker. In another embodiment, the ligand is



In one embodiment, the ligand is attached to the 3′ end of the sense strand.

In another embodiment, the RNAi agent is conjugated to the ligand as shown in the following schematic



wherein X is O or S. In a specific embodiment, X is O.

In one embodiment, the agent further comprises at least one phosphorothioate or methylphosphonate internucleotide linkage.

In a further embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 3'-terminus of one strand. In another embodiment, the strand is the antisense strand. In another embodiment, the strand is the sense strand.

In one embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand. In another embodiment, the strand is the antisense strand. In a further embodiment, the strand is the sense strand.

In one embodiment, the phosphorothioate or methylphosphonate internucleotide linkage is at the both the 5'- and 3'-terminus of one strand. In another embodiment, the strand is the antisense strand.

In another embodiment, the double-stranded RNAi agent comprises 6-8 phosphorothioate internucleotide linkages. In a further embodiment, the antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and the sense strand comprises at least two phosphorothioate internucleotide linkages at either the 5'-terminus or the 3'-terminus of the sense strand.

In one embodiment, the base pair at the 1 position of the 5′-end of the antisense strand of the duplex is an AU base pair. In another embodiment, the Y nucleotides contain a 2′-fluoro modification. In a further embodiment, the Y′ nucleotides contain a 2′-O-methyl modification.

In one embodiment, p′>0. In another embodiment, p′=2. In a further embodiment, q'=0, p=0, q=0, and p' overhang nucleotides are complementary to the target mRNA. In yet a further embodiment, q'=0, p=0, q=0, and p' overhang nucleotides are non-complementary to the target mRNA.

In one embodiment, the sense strand has a total of 21 nucleotides and the antisense strand has a total of 23 nucleotides.

In another embodiment, at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage. In a further embodiment, all n_p' are linked to neighboring nucleotides via phosphorothioate linkages.

In another embodiment, the RNAi agent is selected from the group of RNAi agents listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15.

In one aspect, the present invention provides double-stranded ribonucleic acid (RNAi) agents for inhibiting expression of angiotensinogen (AGT). The double-stranded RNAi agents include a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:1and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:2, wherein substantially all of the nucleotides of the sense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification wherein the sense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus, wherein substantially all of the nucleotides of the antisense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification,wherein the antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and wherein the sense strand is conjugated to one or more GalNAc derivatives attached through a branched bivalent or trivalent linker at the 3'-terminus.

In one embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand comprise a modification.

In another aspect, the present invention provides RNAi agents, *e.g.*, double-stranded ribonucleic acid (RNAi) agents capable of inhibiting the expression of AGT (angiotensinogen) in a cell, wherein the double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein the antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein the double-stranded RNAi agent is represented by formula (III):

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

antisense: $3'\ n_p'\text{-}N_a'\text{-}(X'X'X')_k\text{-}N_b'\text{-}Y'Y'Y'\text{-}N_b'\text{-}(Z'Z'Z')_l\text{-}N_a'\text{-}n_q'\ 5'$ (III)

wherein:

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

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

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each

sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

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

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y′; and

wherein the sense strand is conjugated to at least one ligand.

In yet another aspect, the present invention provides RNAi agents, *e.g.*, double-stranded ribonucleic acid (RNAi) agents capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein the double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein the antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein the double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

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

$n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b' differ

from the modification on Y′; and

wherein the sense strand is conjugated to at least one ligand.

In a further aspect, the present invention provides RNAi agents, *e.g.*, double-stranded ribonucleic acid (RNAi agent) capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein the double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein the antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein the double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

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

n_p′ >0 and at least one n_p′ is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a′ independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b′ independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b′ differ from the modification on Y′; and

wherein the sense strand is conjugated to at least one ligand, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

In another aspect, the present invention provides RNAi agents, *e.g.*, double-stranded ribonucleic acid (RNAi) agents capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein the double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein the antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein the double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

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

$n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y′;

wherein the sense strand comprises at least one phosphorothioate linkage; and

wherein the sense strand is conjugated to at least one ligand, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

In yet another aspect, the present invention provides RNAi agents, *e.g.*,double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein the double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein the antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein the double-stranded RNAi agent is represented by formula (III):

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

antisense: 3' n_p'-N_a'- Y′Y′Y′- N_a'- n_q' 5' (IIIa)

wherein:

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

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

$n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-

25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

YYY and Y′Y′Y′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

wherein the sense strand comprises at least one phosphorothioate linkage; and

wherein the sense strand is conjugated to at least one ligand, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

In another aspect, the present invention provides a double-stranded RNAi agent comprising the RNAi agents listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15.

In another aspect, the present invention provides a composition comprising a modified antisense polynucleotide agent, wherein the agent is capable of inhibiting the expression of angiotensinogen (AGT) in a cell, and comprises a sequence complementary to a sense sequence selected from the group of the sequences listed in Tables 3, 4, 7, 8, 11, 13, and 15, wherein the polynucleotide is about 14 to about 30 nucleotides in length.

The present invention also provides cells, vectors, host cells and pharmaceutical compositions comprising the double-stranded RNAi agents of the invention.

In one embodiment, a cell contains the double-stranded RNAi agent.

In some embodiments, the double-stranded RNAi agent or the composition comprising a modified antisense polynucleotide agent is administered using a pharmaceutical composition.

In one embodiment, the pharmaceutical compositions of the invention comprise a lipid formulation, such as XTC or MC3.

In preferred embodiments, the double-stranded RNAi agent is administered in a solution. In some embodiments, the double-stranded RNAi agent is administered in an unbuffered solution. In another embodiment, the unbuffered solution is saline or water. In another embodiment, the double-stranded RNAi agent is administered with a buffer solution. In yet another embodiment, the buffer solution comprises acetate, citrate, prolamine, carbonate, or phosphate or any combination thereof. In some embodiment, the buffer solution is phosphate buffered saline (PBS).

In another aspect, the present invention provides methods of inhibiting angiotensinogen (AGT) expression in a cell. The methods include contacting the cell with the double-stranded RNAi agent, a pharmaceutical composition, a composition comprising a modified antisense polynucleotide agent, or a vector comprising the RNAi agent and maintaining the cell produced for a time sufficient to obtain degradation of the mRNA transcript of a AGT gene, thereby inhibiting expression of the AGT gene in the cell.

In one embodiment, the cell is within a subject. In a further embodiment, the subject is a human. In a further embodiment, the subject suffers from an angiotensinogen-associated disease.

In one embodiment, the AGT expression is inhibited by at least about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 98% or about 100%.

In one embodiment, the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101; 803-843; 834-859; 803-859; 803-875; 834-875; 847-875; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1892-1914; 1894-1914;1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2078-2107; 2078-2011; 2080-2098; 2081-2099; 2081-2104; 2081-2011; 2082-2100; 2084-2102; 2084-2011; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2291-2311; 2291-2318; 2291-2315; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2304-2329; 2306-2324; 2307-2325; 2309-2327; 2309-2329; 2309-2342; 2309-2350; 2309-2358; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1.

In another aspect, the present invention provides methods of treating a subject having a angiotensinogen (AGT)-associated disorder, comprising administering to the subject a therapeutically effective amount of the double-stranded RNAi agent, a composition comprising a modified antisense polynucleotide agent, or a pharmaceutical composition comprising the double-stranded RNAi agent, thereby treating the subject.

In another aspect, the present invention provides methods of treating a subject having a angiotensinogen (AGT)-associated disorder which include subcutaneously administering to the subject a therapeutically effective amount of a double-stranded ribonucleic acid (RNAi agent), wherein the double-stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand comprises at least 15

contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:2, wherein substantially all of the nucleotides of the antisense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoromodification, wherein the antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, wherein substantially all of the nucleotides of the sense strand comprise a modification selected from the group consisting of a 2'-O-methyl modification and a 2'-fluoro modification, wherein the sense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and, wherein the sense strand is conjugated to one or more GalNAc derivatives attached through a branched bivalent or trivalent linker at the 3'-terminus.

In one embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand comprise a modification.

In another aspect, the present invention provides methods of treating a subject having a angiotensinogen (AGT)-associated disorder which include administering to the subject a therapeutically effective amount of a double-stranded ribonucleic acid (RNAi agent), wherein the double-stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101; 803-843; 834-859; 803-859; 803-875; 834-875; 847-875; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1892-1914; 1894-1914;1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2078-2107; 2078-2011; 2080-2098; 2081-2099; 2081-2104; 2081-2011; 2082-2100; 2084-2102; 2084-2011; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2291-2311; 2291-2318; 2291-2315; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2304-2329; 2306-2324; 2307-2325; 2309-2327; 2309-2329; 2309-2342; 2309-2350; 2309-2358; 2314-2332; 2316-2334;

2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2 such that the antisense strand is substantially complementary to the at least 15 contiguous nucleotides in the sense strand. In certain embodiments, substantially all of the nucleotides of the sense strand are modified nucleotides. In other embodiments, substantially all of the nucleotides of the antisense strand are modified nucleotides. In yet other embodiments, substantially all of the nucleotides of both strands are modified nucleotides. In one embodiment, all of the nucleotides of the sense strand and all of the nucleotides of the antisense strand are modified nucleotides. In one embodiment, the sense strand is conjugated to a ligand attached at the 3'-terminus.

In another aspect, the present invention provides methods of treating a subject having a angiotensinogen (AGT)-associated disorder which include administering to the subject a therapeutically effective amount of a double-stranded ribonucleic acid (RNAi agent), wherein the double-stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein the sense strand comprises at least 15 contiguous nucleotides from nucleotides 803-843; 834-859; 803-859; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2080-2098; 2081-2099; 2082-2100; 2084-2102; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2306-2324; 2307-2325; 2309-2327; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2 such that the antisense strand is

substantially complementary to the at least 15 contiguous nucleotides in the sense strand. In certain embodiments, substantially all of the nucleotides of the sense strand are modified nucleotides. In other embodiments, substantially all of the nucleotides of the antisense strand are modified nucleotides. In yet other embodiments, substantially all of the nucleotides of both strands are modified nucleotides. In one embodiment, the sense strand is conjugated to a ligand attached at the 3'-terminus.

In one embodiment, the subject is a human.

In one embodiment, the angiotensinogen-associated disease is selected from the group consisting of hypertension, borderline hypertension, primary hypertension, secondary hypertension, hypertensive emergency, hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension, diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension, Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy, diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure, myocardial infarction, angina, stroke, diabetes mellitus, renal disease, renal failure, systemic sclerosis, intrauterine growth restriction (IUGR) , and fetal growth restriction.

In another embodiment, the angiotensinogen-associated disease is selected from the group consisting of hypertension, hypertensive heart disease, hypertensive nephropathy, pregnancy-associated hypertension, atherosclerosis, arteriosclerosis, chronic kidney disease, glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, primary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure, myocardial infarction, stroke, diabetes mellitus, renal failure, and systemic sclerosis.

In one embodiment, the angiotensinogen-associated disease is pregnancy-associated hypertension (*e.g.,* pregnancy-induced hypertension, preeclampsia, and eclampsia) and administration of an iRNA of the invention to a subject results in a decrease in maternal blood pressure; a decrease in maternal albuminuria; an increase in uteroplacental unit weight; an increase in fetal weight; normalization of the fetal brain:liver ratio; a decrease in AGT mRNA expression in the maternal liver and no significant decrease in hAGT mRNA

expression in the placenta; an increase in overall placenta size; an increase in the size of the villous placenta; no significant change in the size of the trophospongium of the placenta; a reduction in the ratio of sFLT1:PLGF mRNA expression in the maternal kidney; a reduction in the ratio of serum sFLT1:PLGF levels; and/or a decrease in the level of agonistic autoantibodies to AT1.

In one embodiment, the double-stranded RNAi agent is administered at a dose of about 0.01 mg/kg to about 10 mg/kg or about 0.5 mg/kg to about 50 mg/kg. In a preferred embodiment, the double-stranded RNAi agent is administered at a dose of about 10 mg/kg, about 30 mg/kg, or about 3.0 mg/kg. In one embodiment, the double-stranded RNAi agent is administered at a dose of about 10 mg/kg. In one embodiment, the double-stranded RNAi agent is administered at a dose of about 0.5 mg/kg twice per week. In another embodiment, the double-stranded RNAi agent is administered at a dose of about 10 mg/kg every other week. In another embodiment, the double-stranded RNAi agent is administered at a dose of about 0.5-1.0 mg/kg once per week. In another embodiment, the RNAi agent is administered about once per week, once per month, once every other two months, or once a quarter (*i.e.*, once every three months) at a dose of about 0.1 mg/kg to about 5.0 mg/kg.

In one embodiment, the double-stranded RNAi agent is administered subcutaneously or intravenously.

In one embodiment, the RNAi agent is administered in two or more doses.

In one embodiment, the RNAi agent is administered at intervals selected from the group consisting of once every about 12 hours, once every about 24 hours, once every about 48 hours, once every about 72 hours, and once every about 96 hours.

In one embodiment, the RNAi agent is administered twice per week.

In one embodiment, the RNAi agent is administered every other week.

In certain embodiments, the RNAi agent is administered once per month.

In certain embodiments, the RNAi agent is administered once every other month.

In certain embodiments, the RNAi agent is administered once per quarter (*i.e.*, every three months).

In yet another embodiment, the methods further comprise administering to the subject, an additional therapeutic agent. In some embodiments, the additional therapeutic agent is selected from the group consisting of a diuretic, an angiotensin converting enzyme (ACE) inhibitor, an angiotensin II receptor antagonist, a beta-blocker, a vasodialator, a calcium channel blocker, an aldosterone antagonist, an alpha$_2$-agonist, a renin inhibitor, an alpha-blocker, a peripheral acting adrenergic agent, a selective D1 receptor partial agonist, a nonselective alpha-adrenergic antagonist, a synthetic, steroidal antimineralocorticoid agent, or a combination of any of the foregoing, and a hypertension therapeutic agent formulated as a combination of agents.

Brief Description of the Drawings

Figure 1 is a schematic of the renin-angiotensin-aldosterone system (RAAS) including an indication of the various points in the sytem which have been the targets for therapeutic intervention (from Zaman, *et al.* (2002) *Nat Rev Drug Disc* 1:621).

Figure 2A is a graph depicting the reduction in mean arterial blood pressure in pregnant transgenic rats following administration of AD-60771.

Figure 2B is a graph depicting reduction of serum albumin in pregnant transgenic rats following administration of AD-60771.

Figure 3A is a graph depicting increased uteroplacental unit weight following maternal administration of AD-60771 demonstrating the improvement of fetal outcome following maternal administration of AD-60771.

Figure 3B is a graph depicting increased fetal weight following maternal administration of AD-60771demonstrating the improvement of fetal outcome following maternal administration of AD-60771.

Figure 3C is a graph depicting a normalized fetal brain:liver ratio following maternal administration of AD-60771demonstrating the improvement of fetal outcome following maternal administration of AD-60771.

Figure 4A is a graph depicting reduction of hAGT mRNA in the maternal liver following administration of AD-60771 demonstrating that the iRNA does not enter the placental barrier.

Figure 4B is a graph depicting that there is no significant reduction of hAGT mRNA in the placenta demonstrating that the iRNA does not enter the placental barrier.

Figure 5 is a graph depicting the tissue exposure of the maternal liver, placenta and fetal liver to AD-60771.

Figure 6A is a placental section from a pregnant wild-type rat immunohistochemically stained for cytokeratin.

Figure 6B is a placental section from an untreated pregnant PE rat immunohistochemically stained for cytokeratin.

Figure 6C is a placental section from a pregnant PE rat administered AD-60771 immunohistochemically stained for cytokeratin.

Figure 6D is a graph depicting the size of the mesometrial triangle of a pregnant PE rat administered AD-60771 and an untreated pregnant PE rat.

Figure 6E is a graph depicting the size of the trophospongium of a pregnant PE rat administered AD-60771 and an untreated pregnant PE rat.

Figure 6F is a graph depicting the size of the placenta of a pregnant PE rat administered AD-60771 and an untreated pregnant PE rat.

Figure 6G is a graph depicting the size of the labyrinth of a pregnant PE rats administered AD-60771 and an untreated pregnant PE rat.

Figure 7A is a graph depicting a reduction in the amount of mRNA of the anti-angiogenic factor sFLT1 in the maternal kidney following administration of AD-60771.

Figure 7B is a graph depicting a reduction in the amount of mRNA of the angiogenic factor PLGF in the maternal kidney following administration of AD-60771.

Figure 7C is a graph depicting a reduction in the amount of mRNA of the anti-angiogenic factor sFLT1 in the placenta following maternal administration of AD-60771.

Figure 7D is a graph depicting a reduction in the amount of mRNA of the angiogenic factor PLGF in the placenta following maternal administration of AD-60771.

Figure 8 is a graph depicting the reduction in AT1-AA levels in PE rats administered AD-60771 as assessed by the impact of AT1-AA isolated from control PE rats and pregnant PE rats on the spontaneous beating rate of neonatal rat cardiomyocytes.

Figure 9A is a graph depicting the reduction in serum Angiotensin II (Ang 2-10) levels in pregnant PE rats administered AD-60771 as compared to non-pregnant PE rats and as compared to pregnant control Sprague-Dawley rats.

Figure 9B is a graph depicting the reduction in serum human AGT (hAGT) and rat AGT (rAGT) levels in pregnant PE rats administered AD-60771 as compared to non-pregnant PE rats and as compared to pregnant control Sprague-Dawley rats.

Detailed Description of the Invention

The present invention provides iRNA compositions, which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of an angiotensinogen (AGT) gene. The gene may be within a cell, *e.g.*, a cell within a subject, such as a human.

The present invention also provides methods for treating a subject having a disorder that would benefit from inhibiting or reducing the expression of an AGT gene, *e.g.*, an angiotensinogen-associated disease, such as hypertension or pregnancy-associated hypertension, using iRNA compositions which effect the RNA-induced silencing complex (RISC)-mediated cleavage of RNA transcripts of an AGT gene.

The iRNAs of the invention include an RNA strand (the antisense strand) having a region which is about 30 nucleotides or less in length, *e.g.*, 15-30, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24,20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length, which region is substantially complementary to at least part of an mRNA transcript of an AGT gene. In certain embodiments, the iRNAs of the invention

include an RNA strand (the antisense strand) which can include longer lengths, for example up to 66 nucleotides, *e.g.*, 36-66, 26-36, 25-36, 31-60, 22-43, 27-53 nucleotides in length with a region of at least 19 contiguous nucleotides that is substantially complementary to at least a part of an mRNA transcript of an AGT gene. These iRNAs with the longer length antisense strands include a second RNA strand (the sense strand) of 20-60 nucleotides in length wherein the sense and antisense strands form a duplex of 18-30 contiguous nucleotides. The use of these iRNAs enables the targeted degradation of mRNAs of the correponding gene (AGT gene) in mammals. Very low dosages of the iRNAs of the invention, in particular, can specifically and efficiently mediate RNA interference (RNAi), resulting in significant inhibition of expression of the correponding gene (AGT gene). Using *in vitro* and *in vivo* assays, the present inventors have demonstrated that iRNAs targeting an angiotensinogen gene can mediate RNAi, resulting in significant inhibition of expression of AGT, as well as reducing the symptoms associated with an angiotensinogen-associated disease, such as pregnancy-associated hypertension (*e.g.,* pregnancy-induced hypertension, preeclampsia, and eclampsia). Thus, methods and compositions including these iRNAs are useful for treating a subject having an angiotensinogen-associated disease, such as hypertension.

The following detailed description discloses how to make and use compositions containing iRNAs to inhibit the expression of an angiotensinogen gene as well as compositions, uses, and methods for treating subjects having diseases and disorders that would benefit from inhibition and/or reduction of the expression of AGT.

I. Definitions

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

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

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

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

The term “about” is used herein to mean within the typical ranges of tolerances in the art. As used herein, “angiotensinogen,” used interchangeably with the term “AGT” refers to the well-known gene and polypeptide, also known in the art as Serpin Peptidase Inhibitor,

Clade A, Member 8; Alpha-1 Antiproteinase; Antitrypsin; SERPINA8; Angiotensin I; Serpin A8; Angiotensin II; Alpha-1 Antiproteinase angiotensinogen; antitrypsin; pre-angiotensinogen2; ANHU; Serine Proteinase Inhibitor; and Cysteine Proteinase Inhibitor.

The term "AGT" includes human AGT, the amino acid and complete coding sequence of which may be found in for example, GenBank Accession No. GI:188595658 (NM_000029.3; SEQ ID NO:1); *Macaca fascicularis* AGT, the amino acid and complete coding sequence of which may be found in for example, GenBank Accession No. GI: 90075391 (AB170313.1: SEQ ID NO:3); mouse (*Mus musculus*) AGT, the amino acid and complete coding sequence of which may be found in for example, GenBank Accession No. GI: 113461997 (NM_007428.3; SEQ ID NO:5); and rat AGT (*Rattus norvegicus*) AGT the amino acid and complete coding sequence of which may be found in for example, for example GenBank Accession No. GI:51036672 (NM_134432; SEQ ID NO:7).

Additional examples of AGT mRNA sequences are readily available using publicly available databases, *e.g.*, GenBank, UniProt, OMIM, and the *Macaca* genome project web site.

The term"AGT," as used herein, also refers to naturally occurring DNA sequence variations of the AGT gene, such as a single nucleotide polymorphism (SNP) in the AGT gene. Exemplary SNPs may be found in the dbSNP database available at www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?geneId=183. Non-limiting examples of sequence variations within the AGT gene include, for example, those described in U.S. Patent No. 5,589,584, the entire contents of which are incorporated herein by reference. For example, sequence variations within the AGT gene may include as a C→T at position -532 (relative to the transcription start site); a G→A at position -386; a G→A at position -218; a C→T at position -18; a G→A and a A→C at position -6 and -10; a C→T at position +10 (untanslated); a C→T at position +521 (T174M); a T→C at position +597 (P199P); a T→C at position +704 (M235T; also see, *e.g.,* Reference SNP (refSNP) Cluster Report: rs699, available at www.ncbi.nlm.nih.gov/SNP); a A→G at position +743 (Y248C); a C→T at position +813 (N271N); a G→A at position +1017 (L339L); a C→A at position +1075 (L359M); and/or a G→A at position +1162 (V388M).

As used herein, "target sequence" refers to a contiguous portion of the nucleotide sequence of an mRNA molecule formed during the transcription of an AGT gene, including mRNA that is a product of RNA processing of a primary transcription product. In one embodiment, the target portion of the sequence will be at least long enough to serve as a substrate for iRNA-directed cleavage at or near that portion of the nucleotide sequence of an mRNA molecule formed during the transcription of an AGT gene.

The target sequence may be from about 9-36 nucleotides in length, *e.g.*, about 15-30 nucleotides in length. For example, the target sequence can be from about 15-30 nucleotides,

15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24,20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the invention.

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

"G," "C," "A," "T" and "U" each generally stand for a nucleotide that contains guanine, cytosine, adenine, thymidine and uracil as a base, respectively. However, it will be understood that the term "ribonucleotide" or "nucleotide" can also refer to a modified nucleotide, as further detailed below, or a surrogate replacement moiety (see, *e.g.,* Table 2). The skilled person is well aware that guanine, cytosine, adenine, and uracil can be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base can base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine can be replaced in the nucleotide sequences of dsRNA featured in the invention by a nucleotide containing, for example, inosine. In another example, adenine and cytosine anywhere in the oligonucleotide can be replaced with guanine and uracil, respectively to form G-U Wobble base pairing with the target mRNA. Sequences containing such replacement moieties are suitable for the compositions and methods featured in the invention.

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

In one embodiment, an RNAi agent of the invention includes a single stranded RNA that interacts with a target RNA sequence, *e.g.,* an AGT target mRNA sequence, to direct the cleavage of the target RNA. Without wishing to be bound by theory it is believed that long double-stranded RNA introduced into cells is broken down into siRNA by a Type III endonuclease known as Dicer (Sharp *et al.* (2001) *Genes Dev.* 15:485). Dicer, a ribonuclease-III-like enzyme, processes the dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs (Bernstein, *et al.*, (2001) *Nature* 409:363). The siRNAs

are then incorporated into an RNA-induced silencing complex (RISC) where one or more helicases unwind the siRNA duplex, enabling the complementary antisense strand to guide target recognition (Nykanen, *et al.*, (2001) *Cell* 107:309). Upon binding to the appropriate target mRNA, one or more endonucleases within the RISC cleave the target to induce silencing (Elbashir, *et al.*, (2001) *Genes Dev.* 15:188). Thus, in one aspect the invention relates to a single stranded RNA (siRNA) generated within a cell and which promotes the formation of a RISC complex to effect silencing of the target gene, *i.e.,* an AGT gene. Accordingly, the term "siRNA" is also used herein to refer to an RNAi as described above.

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

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

In general, the majority of nucleotides of each strand of a dsRNA molecule are ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, *e.g.*, a deoxyribonucleotide and/or a modified nucleotide. In addition, as used in this specification, an "RNAi agent" may include ribonucleotides with chemical modifications; an RNAi agent may include substantial modifications at multiple nucleotides. As used herein, the term "modified nucleotide" refers to a nucleotide having, independently, a modified sugar moiety, a modified internucleotide linkage, and/or a modified nucleobase. Thus, the term modified nucleotide encompasses substitutions, additions or removal of, *e.g.,* a functional group or atom, to internucleoside linkages, sugar moieties, or nucleobases. The modifications suitable for use in the agents of the invention include all types of modifications disclosed herein or known in the art. Any such

modifications, as used in a siRNA type molecule, are encompassed by "RNAi agent" for the purposes of this specification and claims.

The majority of nucleotides of each strand of a dsRNA molecule may be ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, *e.g.*, a deoxyribonucleotide and/or a modified nucleotide. In addition, as used in this specification, an "RNAi agent" may include ribonucleotides with chemical modifications; an RNAi agent may include substantial modifications at multiple nucleotides. As used herein, the term "modified nucleotide" refers to a nucleotide having, independently, a modified sugar moiety, a modified internucleotide linkage, and/or modified nucleobase. Thus, the term modified nucleotide encompasses substitutions, additions or removal of, *e.g.,* a functional group or atom, to internucleoside linkages, sugar moieties, or nucleobases. The modifications suitable for use in the agents of the invention include all types of modifications disclosed herein or known in the art. Any such modifications, as used in a siRNA type molecule, are encompassed by "RNAi agent" for the purposes of this specification and claims.

The duplex region may be of any length that permits specific degradation of a desired target RNA through a RISC pathway, and may range from about 9 to 36 base pairs in length, *e.g.*, about 15-30 base pairs in length, for example, about 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 base pairs in length, such as about 15-30, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24,20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the invention.

The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting RNA chain is referred to as a "hairpin loop." A hairpin loop can comprise at least one unpaired nucleotide. In some embodiments, the hairpin loop can comprise at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 20, at least 23 or more unpaired nucleotides.

Where the two substantially complementary strands of a dsRNA are comprised by separate RNA molecules, those molecules need not, but can be covalently connected. Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand

forming the duplex structure, the connecting structure is referred to as a "linker." The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the dsRNA minus any overhangs that are present in the duplex. In addition to the duplex structure, an RNAi may comprise one or more nucleotide overhangs.

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

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

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

or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5'-end, 3'-end or both ends of either an antisense or sense strand of a dsRNA.

In one embodiment, the antisense strand of a dsRNA has a 1-10 nucleotide, *e.g.,* a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end and/or the 5'-end. In one embodiment, the sense strand of a dsRNA has a 1-10 nucleotide, *e.g.,* a 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotide, overhang at the 3'-end and/or the 5'-end. In certain embodiments, the overhang on the sense strand or the antisense strand, or both, can include extended lengths longer than 10 nucleotides, *e.g.*, 1-30 nucleotides, 2-30 nucleotides, 10-30 nucleotides, or 10-15 nucleotides in length. In certain embodiments, an extended overhang is on the sense strand of the duplex. In certain embodiments, an extended overhang is present on the 3'end of the sense strand of the duplex. In certain embodiments, an extended overhang is present on the 5'end of the sense strand of the duplex. In certain embodiments, an extended overhang is on the antisense strand of the duplex. In certain embodiments, an extended overhang is present on the 3'end of the antisense strand of the duplex. In certain embodiments, an extended overhang is present on the 5'end of the antisense strand of the duplex. In certain embodiments, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

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

The term "antisense strand" or "guide strand" refers to the strand of an iRNA, *e.g.*, a dsRNA, which includes a region that is substantially complementary to a target sequence, *e.g.,* a AGT mRNA. As used herein, the term "region of complementarity" refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, *e.g.,* an AGT nucleotide sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches can be in the internal or terminal regions of the molecule. Generally, the most tolerated mismatches are in the terminal regions, *e.g.*, within 5, 4, 3, or 2 nucleotides of the 5'- and/or 3'-terminus of the iRNA.

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

As used herein, the term "cleavage region" refers to a region that is located immediately adjacent to the cleavage site. The cleavage site is the site on the target at which

cleavage occurs. In some embodiments, the cleavage region comprises three bases on either end of, and immediately adjacent to, the cleavage site. In some embodiments, the cleavage region comprises two bases on either end of, and immediately adjacent to, the cleavage site. In some embodiments, the cleavage site specifically occurs at the site bound by nucleotides 10 and 11 of the antisense strand, and the cleavage region comprises nucleotides 11, 12, and 13.

As used herein, and unless otherwise indicated, the term "complementary," when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Such conditions can, for example, be stringent conditions, where stringent conditions can include: 400 mM NaCl, 40 mM PIPES pH 6.4, 1 mM EDTA, 50°C or 70°C for 12-16 hours followed by washing (see, *e.g.,* "Molecular Cloning: A Laboratory Manual, Sambrook, *et al.* (1989) Cold Spring Harbor Laboratory Press). Other conditions, such as physiologically relevant conditions as can be encountered inside an organism, can apply. The skilled person will be able to determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

Complementary sequences within an iRNA, *e.g.*, within a dsRNA as described herein, include base-pairing of the oligonucleotide or polynucleotide comprising a first nucleotide sequence to an oligonucleotide or polynucleotide comprising a second nucleotide sequence over the entire length of one or both nucleotide sequences. Such sequences can be referred to as "fully complementary" with respect to each other herein. However, where a first sequence is referred to as "substantially complementary" with respect to a second sequence herein, the two sequences can be fully complementary, or they can form one or more, but generally not more than 5, 4, 3 or 2 mismatched base pairs upon hybridization for a duplex up to 30 base pairs, while retaining the ability to hybridize under the conditions most relevant to their ultimate application, *e.g.*, inhibition of gene expression via a RISC pathway. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide 21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, can yet be referred to as "fully complementary" for the purposes described herein.

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

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

As used herein, a polynucleotide that is "substantially complementary to at least part of" a messenger RNA (mRNA) refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest (*e.g.*, an mRNA encoding AGT). For example, a polynucleotide is complementary to at least a part of an AGT mRNA if the sequence is substantially complementary to a non-interrupted portion of an mRNA encoding AGT.

Accordingly, in some embodiments, the antisense strand polynucleotides disclosed herein are fully complementary to the target AGT sequence. In other embodiments, the antisense strand polynucleotides disclosed herein are substantially complementary to the target AGT sequence and comprise a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NO:1, or a fragment of SEQ ID NO:1, such as about 85%, about 90%, or about 95% complementary.

In one embodiment, an RNAi agent of the invention includes a sense strand that is substantially complementary to an antisense polynucleotide which, in turn, is complementary to a target AGT sequence, and wherein the sense strand polynucleotide comprises a contiguous nucleotide sequence which is at least about 80% complementary over its entire length to the equivalent region of the nucleotide sequence of SEQ ID NO:2, or a fragment of any one of SEQ ID NO:2, such as about 85%, about 90%, or about 95% complementary.

In general, the majority of nucleotides of each strand are ribonucleotides, but as described in detail herein, each or both strands can also include one or more non-ribonucleotides, *e.g.*, a deoxyribonucleotide and/or a modified nucleotide. In addition, an "iRNA" may include ribonucleotides with chemical modifications. Such modifications may include all types of modifications disclosed herein or known in the art. Any such modifications, as used in an iRNA molecule, are encompassed by "iRNA" for the purposes of this specification and claims.

In one aspect of the invention, an agent for use in the methods and compositions of the invention is a single-stranded antisense RNA molecule that inhibits a target mRNA *via* an

antisense inhibition mechanism. The single-stranded antisense RNA molecule is complementary to a sequence within the target mRNA. The single-stranded antisense oligonucleotides can inhibit translation in a stoichiometric manner by base pairing to the mRNA and physically obstructing the translation machinery, see Dias, N. *et al.*, (2002) *Mol Cancer Ther* 1:347-355. The single-stranded antisense RNA molecule may be about 15 to about 30 nucleotides in length and have a sequence that is complementary to a target sequence. For example, the single-stranded antisense RNA molecule may comprise a sequence that is at least about 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from any one of the antisense sequences described herein.

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

The phrase "inhibiting expression of an AGT," as used herein, includes inhibition of expression of any AGT gene (such as, *e.g.*, a mouse AGT gene, a rat AGT gene, a monkey AGT gene, or a human AGT gene) as well as variants or mutants of an AGT gene that encode an AGT protein.

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

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

In one embodiment, at least partial suppression of the expression of an AGT gene, is assessed by a reduction of the amount of AGT mRNA which can be isolated from or detected in a first cell or group of cells in which an AGT gene is transcribed and which has or have been treated such that the expression of an AGT gene is inhibited, as compared to a second cell or group of cells substantially identical to the first cell or group of cells but which has or

have not been so treated (control cells). The degree of inhibition may be expressed in terms of:

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

The phrase "contacting a cell with an RNAi agent," such as a dsRNA, as used herein, includes contacting a cell by any possible means. Contacting a cell with an RNAi agent includes contacting a cell *in vitro* with the iRNA or contacting a cell *in vivo* with the iRNA. The contacting may be done directly or indirectly. Thus, for example, the RNAi agent may be put into physical contact with the cell by the individual performing the method, or alternatively, the RNAi agent may be put into a situation that will permit or cause it to subsequently come into contact with the cell.

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

In one embodiment, contacting a cell with an iRNA includes "introducing" or "delivering the iRNA into the cell" by facilitating or effecting uptake or absorption into the cell. Absorption or uptake of an iRNA can occur through unaided diffusive or active cellular processes, or by auxiliary agents or devices. Introducing an iRNA into a cell may be *in vitro* and/or *in vivo*. For example, for *in vivo* introduction, iRNA can be injected into a tissue site or administered systemically. *In vivo* delivery can also be done by a beta-glucan delivery system, such as those described in U.S. Patent Nos. 5,032,401 and 5,607,677, and U.S. Publication No. 2005/0281781, the entire contents of which are hereby incorporated herein by reference. *In vitro* introduction into a cell includes methods known in the art such as electroporation and lipofection. Further approaches are described herein below and/or are known in the art.

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

As used herein, a "subject" is an animal, such as a mammal, including a primate (such as a human, a non-human primate, *e.g.*, a monkey, and a chimpanzee), a non-primate (such as

a cow, a pig, a camel, a llama, a horse, a goat, a rabbit, a sheep, a hamster, a guinea pig, a cat, a dog, a rat, a mouse, a horse, and a whale), or a bird (*e.g.*, a duck or a goose). In an embodiment, the subject is a human, such as a human being treated or assessed for a disease, disorder or condition that would benefit from reduction in AGT expression; a human at risk for a disease, disorder or condition that would benefit from reduction in AGT expression; a human having a disease, disorder or condition that would benefit from reduction in AGT expression; and/or human being treated for a disease, disorder or condition that would benefit from reduction in AGT expression as described herein.

As used herein, the terms "treating" or "treatment" refer to a beneficial or desired result including, but not limited to, alleviation or amelioration of one or more symptoms associated with unwanted AGT expression, *e.g.,* angiotensin II type 1 receptor activation (AT_1R) (*e.g.,* hypertension, chronic kidney disease, stroke, myocardial infarction, heart failure, aneurysms, peripheral artery disease, heart disease, increased oxidative stress, *e.g.,* increased superoxide formation, inflammation, vasoconstriction, sodium and water retention, potassium and magnesium loss, renin suppression, myocyte and smooth muscle hypertrophy, increased collagen sysnthesis, stimulation of vascular, myocardial and renal fibrosis, increased rate and force of cardiac contractions, altered heart rate, *e.g.,* increased arrhythmia, stimulation of plasminogen activator inhibitor 1 (PAI1), activation of the sympathetic nervous system, and increased endothelin secretion), symptoms of pregnancy-associated hypertension (*e.g.,* preeclampsia, and eclampsia), including, but not limited to intrauterine growth restriction (IUGR) or fetal growth restriction, symptoms associated with malignant hypertension, symptoms associated with hyperaldosteronism; diminishing the extent of unwanted AT_1R activation; stabilization (*i.e.*, not worsening) of the state of chronic AT_1R activation; amelioration or palliation of unwanted AT_1R activation (*e.g.,* hypertension, chronic kidney disease, stroke, myocardial infarction, heart failure, aneurysms, peripheral artery disease, heart disease, increased oxidative stress, *e.g.,* increased superoxide formation, inflammation, vasoconstriction, sodium and water retention, potassium and magnesium loss, renin suppression, myocyte and smooth muscle hypertrophy, increased collagen sysnthesis, stimulation of vascular, myocardial and renal fibrosis, increased rate and force of cardiac contractions, altered heart rate, *e.g.,* increased arrhythmia, stimulation of plasminogen activator inhibitor 1 (PAI1), activation of the sympathetic nervous system, and increased endothelin secretion) whether detectable or undetectable. "Treatment" can also mean prolonging survival as compared to expected survival in the absence of treatment.

The term "lower" in the context of the level of AGT in a subject or a disease marker or symptom refers to a statistically significant decrease in such level. The decrease can be, for example, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%,

at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or more and is preferably down to a level accepted as within the range of normal for an individual without such disorder.

As used herein, "prevention" or "preventing," when used in reference to a disease, disorder or condition thereof, that would benefit from a reduction in expression of an AGT gene, refers to a reduction in the likelihood that a subject will develop a symptom associated with such a disease, disorder, or condition, *e.g.,* a symptom of unwanted AT_1R activation, such as a hypertension, chronic kidney disease, stroke, myocardial infarction, heart failure, aneurysms, peripheral artery disease, heart disease, increased oxidative stress, *e.g.,* increased superoxide formation, inflammation, vasoconstriction, sodium and water retention, potassium and magnesium loss, renin suppression, myocyte and smooth muscle hypertrophy, increased collagen sysnthesis, stimulation of vascular, myocardial and renal fibrosis, increased rate and force of cardiac contractions, altered heart rate, *e.g.,* increased arrhythmia, stimulation of plasminogen activator inhibitor 1 (PAI1), activation of the sympathetic nervous system, and increased endothelin secretion. The likelihood of developing, *e.g.,* hypertension, is reduced, for example, when an individual having one or more risk factors for a hypertension either fails to develop hypertension or develops hypertension with less severity relative to a population having the same risk factors and not receiving treatment as described herein. The failure to develop a disease, disorder or condition, or the reduction in the development of a symptom associated with such a disease, disorder or condition (*e.g.*, by at least about 10% on a clinically accepted scale for that disease or disorder), or the exhibition of delayed symptoms delayed (*e.g.*, by days, weeks, months or years) is considered effective prevention.

As used herein, the term "angiotensinogen-associated disease" or "AGT-associated disease," is a disease or disorder that is caused by, or associated with renin-angiotensin-aldosterone system (RAAS) activation, or a disease or disorder the symptoms of which or progression of which responds to RAAS inactivation. The term "angiotensinogen-associated disease" includes a disease, disorder or condition that would benefit from reduction in AGT expression. Such diseases are typically associated with high blood pressure. Non-limiting examples of angiotensinogen-associated diseases include hypertension, *e.g.,* borderline hypertension (also known as prehypertension), primary hypertension (also known as essential hypertension or idiopathic hypertension), secondary hypertension (also known as inessential hypertension), hypertensive emergency (also known as malignant hypertension), hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension (*e.g.,* preeclampsia, eclampsia, and post-partum preelampsia), diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension (also known as renal hypertension), Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic

hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy (including peripheral vascular disease), diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure (*e.g.,* left ventricular systolic dysfunction), myocardial infarction, angina, stroke, diabetes mellitus (*e.g.,* diabetic nephropathy), renal disease *e.g.*, chronic kidney disease or diabetic nephropathy optionally in the context of pregnancy, renal failure, *e.g.,* chronic renal failure, cognitive dysfunction (such as Alzheimer's), and systemic sclerosis (*e.g.,* scleroderma renal crisis). In certain embodiments, AGT- associated disease includes intrauterine growth restriction (IUGR) or fetal growth restriction.

Based on the average of seated blood pressure readings that are properly measured during two or more office visits, a subject having a normal blood pressure is one having a systolic pressure of about 90–119 mmHg (about 12–15.9 kPa (kN/m^2)) and a diastolic pressure of about 60–79 mmHg (about 8.0–10.5 kPa (kN/m^2)); a subject having prehypertension is one having a systolic pressure of about 120–139 mmHg (about 16.1–18.5 kPa (kN/m^2)) and a diastolic pressure of about 60–79 mmHg (about 8.0–10.5 kPa (kN/m^2)); a subject having hypertension (*e.g.,* Stage I hypertension) is one having a systolic pressure of about 140–159 mmHg (about 18.7–21.2 kPa (kN/m^2)) and a diastolic pressure of about 90–99 mmHg (about 12.0–13.2 kPa (kN/m^2)); and a subject having hypertension (*e.g.,* Stage II hypertension) is one having a systolic pressure of about ≥160 mmHg (about ≥21.3 kPa (kN/m^2)) and a diastolic pressure of about ≥100 mmHg (about ≥13.3 kPa (kN/m^2)). Subjects with blood pressures over 130/80 mmHg along with Type 1 or Type 2 diabetes, or kidney disease are considered as having hypertension.

In one embodiment, an angiotensinogen-associated disease is primary hypertension. "Primary hypertension" is a result of environmental or genetic causes (*e.g.,* a result of no obvious underlying medical cause).

In one embodiment, an angiotensinogen-associated disease is secondary hypertension. "Secondary hypertension" has an identifiable underlying disorder which can be of multiple etiologies, including renal, vascular, and endocrine causes, *e.g.,* renal parenchymal disease (*e.g.,* polycystic kidneys, glomerular or interstitial disease), renal vascular disease (*e.g.,* renal artery stenosis, fibromuscular dysplasia), endocrine disorders (*e.g.,* adrenocorticosteroid or mineralocorticoid excess, pheochromocytoma, hyperthyroidism or hypothyroidism, growth hormone excess, hyperparathyroidism), coarctation of the aorta, or oral contraceptive use.

In one embodiment, an angiotensinogen-associated disease is a hypertensive emergency, *e.g.,* malignant hypertension and accelerated hypertension. "Accelerated hypertension" is severely elevated blood pressure (*i.e.,* equal to or greater than a systolic 180 mmHg or diastolic of 110 mmHg) with direct damage to one or more end organs. Blood pressure must be reduced immediately to prevent further organ damage. "Malignant hypertension" is severely elevated blood pressure (*i.e.,* equal to or greater than a systolic 180 mmHg or diastolic of 110 mmHg) with direct damage to one or more end organs and papilledema. Blood pressure must be reduced immediately to prevent further organ damage. Neurologic end-organ damage due to uncontrolled blood pressure may include hypertensive encephalopathy, cerebral vascular accident/cerebral infarction; subarachnoid hemorrhage, and/or intracranial hemorrhage. Cardiovascular end-organ damage may include myocardial ischemia/infarction, acute left ventricular dysfunction, acute pulmonary edema, and/or aortic dissection. Other organ systems may also be affected by uncontrolled hypertension, which may lead to acute renal failure/insufficiency, retinopathy, eclampsia, or microangiopathic hemolytic anemia.

In one embodiment, an angiotensinogen-associated disease is a hypertensive urgency. "Hypertensive urgency" is severely elevated blood pressure (*i.e.,* equal to or greater than a systolic 180 mmHg or diastolic of 110 mmHg) with no direct damage to one or more organs. Blood pressure can be brought down safely within a few hours.

In one embodiment, an angiotensinogen-associated disease is pregnancy-associated hypertension, *e.g.,* chronic hypertension of pregnancy, gestational hypertension, preeclampsia, eclampsia, preeclampsia superimposed on chronic hypertension, HELLP syndrome, and gestational hypertension (also known as transient hypertension of pregnancy, chronic hypertension identified in the latter half of pregnancy, and pregnancy-induced hypertension (PIH)). A subject having "chronic hypertension of pregnancy" is one having a blood pressure exceeding 140/90 mm Hg before pregnancy or before 20 weeks' gestation. "Gestational hypertension" or "pregnancy-induced hypertension" refers to hypertension with onset in the latter part of pregnancy (>20 weeks' gestation) without any other features of preeclampsia, and followed by normalization of the blood pressure postpartum. "Mild preeclampsia" is defined as the presence of hypertension (blood pressure ≥140/90 mm Hg) on two occasions, at least six hours apart, but without evidence of end-organ damage, in a woman who was normotensive before 20 weeks' gestation. In a subject with preexisting essential hypertension, preeclampsia is diagnosed if systolic blood pressure has increased by 30 mm Hg or if diastolic blood pressure has increased by 15 mm Hg. "Severe preeclampsia" is defined as the presence of 1 of the following symptoms or signs in the presence of preeclampsia; asystolic blood pressure of 160 mm Hg or higher or diastolic blood pressure of 110 mm Hg or higher on two occasions at least six hours apart; proteinuria of more than 5g in

a 24-hour collection or more than 3+ on two random urine samples collected at least four hours apart, pulmonary edema or cyanosis, oliguria (< 400 mL in 24 hours), persistent headaches, epigastric pain and/or impaired liver function, thrombocytopenia, oligohydramnios, decreased fetal growth, or placental abruption. “Eclampsia” is defined as seizures that cannot be attributable to other causes in a woman with preeclampsia. “HELLP syndrome” (also known as edema-proteinuria-hypertension gestosis type B) is Hemolysis, Elevated Liver enzyme levels, and Low Platelet levels in a pregnant subject.

In one embodiment, an angiotensinogen-associated disease is resistant hypertension. “Resistant hypertension” is blood pressure that remains above goal (*e.g.,* 140/90 mmHg) in spite of concurrent use of three antihypertensive agents of different classes, one of which is a thiazide diuretic diuretic. Subjects whose blood pressure is controlled with four or more medications are also considered to have resistant hypertension.

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

“Prophylactically effective amount,” as used herein, is intended to include the amount of an iRNA that, when administered to a subject having an angiotensinogen-associated disease, is sufficient to prevent or ameliorate the disease or one or more symptoms of the disease in a subject susceptible to the disease, i.e., more likely to suffer from the disease than those in the general population due to one or more factors, e.g., age, weight, pregnancy. Ameliorating the disease includes slowing the course of the disease or reducing the severity of later-developing disease. The "prophylactically effective amount" may vary depending on the iRNA, how the agent is administered, the degree of risk of disease, and the history, age, weight, family history, genetic makeup, the types of preceding or concomitant treatments, if any, and other individual characteristics of the patient to be treated.

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

The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of

sound medical judgment, suitable for use in contact with the tissues of human subjects and animal subjects without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

The phrase "pharmaceutically-acceptable carrier" as used herein means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, manufacturing aid (*e.g.*, lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the subject compound from one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the subject being treated. Some examples of materials which can serve as pharmaceutically-acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) lubricating agents, such as magnesium state, sodium lauryl sulfate and talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates and/or polyanhydrides; (22) bulking agents, such as polypeptides and amino acids (23) serum component, such as serum albumin, HDL and LDL; and (22) other non-toxic compatible substances employed in pharmaceutical formulations.

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

II. iRNAs of the Invention

The present invention provides iRNAs which inhibit the expression of an AGT gene. In one embodiment, the iRNA agent includes double-stranded ribonucleic acid (dsRNA)

molecules for inhibiting the expression of an AGT gene in a cell, such as a cell within a subject, *e.g.,* a mammal, such as a human having an angiotensinogen-associated disease, *e.g.,* hypertension. The dsRNA includes an antisense strand having a region of complementarity which is complementary to at least a part of an mRNA formed in the expression of an AGT gene. The region of complementarity is about 30 nucleotides or less in length (*e.g.,* about 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, or 18 nucleotides or less in length). Upon contact with a cell expressing the AGT gene, the iRNA inhibits the expression of the AGT gene (*e.g.,* a human, a primate, a non-primate, or a bird AGT gene) by at least about 10% as assayed by, for example, a PCR or branched DNA (bDNA)-based method, or by a protein-based method, such as by immunofluorescence analysis, using, for example, western blotting or flowcytometric techniques.

A dsRNA includes two RNA strands that are complementary and hybridize to form a duplex structure under conditions in which the dsRNA will be used. One strand of a dsRNA (the antisense strand) includes a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence. The target sequence can be derived from the sequence of an mRNA formed during the expression of an AGT gene. The other strand (the sense strand) includes a region that is complementary to the antisense strand, such that the two strands hybridize and form a duplex structure when combined under suitable conditions. As described elsewhere herein and as known in the art, the complementary sequences of a dsRNA can also be contained as self-complementary regions of a single nucleic acid molecule, as opposed to being on separate oligonucleotides.

Generally, the duplex structure is between 15 and 30 base pairs in length, *e.g.,* between, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24,20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the invention.

Similarly, the region of complementarity to the target sequence is between 15 and 30 nucleotides in length, *e.g.,* between 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24,20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 nucleotides in length. Ranges and lengths intermediate to the above recited ranges and lengths are also contemplated to be part of the invention.

In some embodiments, the dsRNA is about 15 to about 20 nucleotides in length, about 25 to about 30 nucleotides in length, or about 15 to about 23 nucleotides in length. In general, the dsRNA is long enough to serve as a substrate for the Dicer enzyme. For example, it is well-known in the art that dsRNAs longer than about 21-23 nucleotides in length may serve as substrates for Dicer. As the ordinarily skilled person will also recognize, the region of an RNA targeted for cleavage will most often be part of a larger RNA molecule, often an mRNA molecule. Where relevant, a "part" of an mRNA target is a contiguous sequence of an mRNA target of sufficient length to allow it to be a substrate for RNAi-directed cleavage (*i.e.*, cleavage through a RISC pathway).

One of skill in the art will also recognize that the duplex region is a primary functional portion of a dsRNA, *e.g.*, a duplex region of about 9 to 36 base pairs, *e.g.*, about 10-36, 11-36, 12-36, 13-36, 14-36, 15-36, 9-35, 10-35, 11-35, 12-35, 13-35, 14-35, 15-35, 9-34, 10-34, 11-34, 12-34, 13-34, 14-34, 15-34, 9-33, 10-33, 11-33, 12-33, 13-33, 14-33, 15-33, 9-32, 10-32, 11-32, 12-32, 13-32, 14-32, 15-32, 9-31, 10-31, 11-31, 12-31, 13-32, 14-31, 15-31, 15-30, 15-29, 15-28, 15-27, 15-26, 15-25, 15-24, 15-23, 15-22, 15-21, 15-20, 15-19, 15-18, 15-17, 18-30, 18-29, 18-28, 18-27, 18-26, 18-25, 18-24, 18-23, 18-22, 18-21, 18-20, 19-30, 19-29, 19-28, 19-27, 19-26, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-30, 20-29, 20-28, 20-27, 20-26, 20-25, 20-24,20-23, 20-22, 20-21, 21-30, 21-29, 21-28, 21-27, 21-26, 21-25, 21-24, 21-23, or 21-22 base pairs. Thus, in one embodiment, to the extent that it becomes processed to a functional duplex, of *e.g.*, 15-30 base pairs, that targets a desired RNA for cleavage, an RNA molecule or complex of RNA molecules having a duplex region greater than 30 base pairs is a dsRNA. Thus, an ordinarily skilled artisan will recognize that in one embodiment, a miRNA is a dsRNA. In another embodiment, a dsRNA is not a naturally occurring miRNA. In another embodiment, an iRNA agent useful to target AGT expression is not generated in the target cell by cleavage of a larger dsRNA.

A dsRNA as described herein can further include one or more single-stranded nucleotide overhangs *e.g.,* 1, 2, 3, or 4 nucleotides. dsRNAs having at least one nucleotide overhang can have unexpectedly superior inhibitory properties relative to their blunt-ended counterparts. A nucleotide overhang can comprise or consist of a nucleotide/nucleoside analog, including a deoxynucleotide/nucleoside. The overhang(s) can be on the sense strand, the antisense strand or any combination thereof. Furthermore, the nucleotide(s) of an overhang can be present on the 5'-end, 3'-end or both ends of either an antisense or sense strand of a dsRNA. As discussed herein, extended overhang of up to 30 nucleotides in length are also contemplated in various embodiments of the invention.

A dsRNA can be synthesized by standard methods known in the art as further discussed below, *e.g.*, by use of an automated DNA synthesizer, such as are commercially available from, for example, Biosearch, Applied Biosystems®, Inc.

iRNA compounds of the invention may be prepared using a two-step procedure. First, the individual strands of the double-stranded RNA molecule are prepared separately. Then, the component strands are annealed. The individual strands of the siRNA compound can be prepared using solution-phase or solid-phase organic synthesis or both. Organic synthesis offers the advantage that the oligonucleotide strands comprising unnatural or modified nucleotides can be easily prepared. Single-stranded oligonucleotides of the invention can be prepared using solution-phase or solid-phase organic synthesis or both.

In one aspect, a dsRNA of the invention includes at least two nucleotide sequences, a sense sequence and an anti-sense sequence. The sense strand is selected from the group of sequences provided in any one of Tables 3, 4, 7, 8, 11, 13, and 15, and the corresponding antisense strand of the sense strand is selected from the group of sequences of any one of Tables 3, 4, 7, 8, 11, 13, and 15. In this aspect, one of the two sequences is complementary to the other of the two sequences, with one of the sequences being substantially complementary to a sequence of an mRNA generated in the expression of an AGT gene. As such, in this aspect, a dsRNA will include two oligonucleotides, where one oligonucleotide is described as the sense strand in any one of Tables 3, 4, 7, 8, 11, 13, and 15, and the second oligonucleotide is described as the corresponding antisense strand of the sense strand in any one of Tables 3, 4, 7, 8, 11, 13, and 15. In one embodiment, the substantially complementary sequences of the dsRNA are contained on separate oligonucleotides. In another embodiment, the substantially complementary sequences of the dsRNA are contained on a single oligonucleotide.

It will be understood that, although some of the sequences in Tables 3, 4, 7, 8, 11, 13, and 15 are described as modified and/or conjugated sequences, the RNA of the iRNA of the invention *e.g.*, a dsRNA of the invention, may comprise any one of the sequences set forth in Tables 3, 4, 7, 8, 11, 13, and 15 that is un-modified, un-conjugated, and/or modified and/or conjugated differently than described therein.

In another aspect, a double-stranded ribonucleic acid (dsRNA) of the invention for inhibiting expression of angiotensinogen comprises, consists essentially of, or consists of a sense strand and an antisense strand, wherein the sense strand comprises the nucleotide sequence of a sense strand in Table 3, 4, 7, 8, 11, 13, and 15 and the antisense strand comprises the nucleotide sequence of the corresponding antisense strand in Tables 3, 4, 7, 8, 11, 13, and 15.

The skilled person is well aware that dsRNAs having a duplex structure of about 20 to 23 base pairs, *e.g.,* 21, base pairs have been hailed as particularly effective in inducing RNA interference (Elbashir *et al.*, *EMBO* 2001, 20:6877-6888). However, others have found that shorter or longer RNA duplex structures can also be effective (Chu and Rana (2007) *RNA* 14:1714-1719; Kim *et al.* (2005) *Nat Biotech* 23:222-226). In the embodiments described above, by virtue of the nature of the oligonucleotide sequences provided in any one of Tables

3, 4, 7, 8, 11, 13, and 15 , dsRNAs described herein can include at least one strand of a length of minimally 21 nucleotides. It can be reasonably expected that shorter duplexes having one of the sequences of any one of Tables 3, 4, 7, 8, 11, 13, and 15 minus only a few nucleotides on one or both ends can be similarly effective as compared to the dsRNAs described above. Hence, dsRNAs having a sequence of at least 15, 16, 17, 18, 19, 20, or more contiguous nucleotides derived from one of the sequences of any one of Tables 3, 4, 7, 8, 11, 13, and 15, and differing in their ability to inhibit the expression of a AGT gene by not more than about 5, 10, 15, 20, 25, or 30 % inhibition from a dsRNA comprising the full sequence, are contemplated to be within the scope of the present invention.

In addition, the RNAs provided in any one of Tables 3, 4, 7, 8, 11, 13, and 15 identify a site(s) in a AGT transcript that is susceptible to RISC-mediated cleavage. As such, the present invention further features iRNAs that target within one of these sites. As used herein, an iRNA is said to target within a particular site of an RNA transcript if the iRNA promotes cleavage of the transcript anywhere within that particular site. Such an iRNA will generally include at least about 15 contiguous nucleotides from one of the sequences provided in any one of Tables 3, 4, 7, 8, 11, 13, and 15 coupled to additional nucleotide sequences taken from the region contiguous to the selected sequence in a AGT gene.

While a target sequence is generally about 15-30 nucleotides in length, there is wide variation in the suitability of particular sequences in this range for directing cleavage of any given target RNA. Various software packages and the guidelines set out herein provide guidance for the identification of optimal target sequences for any given gene target, but an empirical approach can also be taken in which a "window" or "mask" of a given size (as a non-limiting example, 21 nucleotides) is literally or figuratively (including, *e.g.*, in silico) placed on the target RNA sequence to identify sequences in the size range that can serve as target sequences. By moving the sequence "window" progressively one nucleotide upstream or downstream of an initial target sequence location, the next potential target sequence can be identified, until the complete set of possible sequences is identified for any given target size selected. This process, coupled with systematic synthesis and testing of the identified sequences (using assays as described herein or as known in the art) to identify those sequences that perform optimally can identify those RNA sequences that, when targeted with an iRNA agent, mediate the best inhibition of target gene expression. Thus, while the sequences identified, for example, in any one of Tables 3, 4, 7, 8, 11, 13, and 15 represent effective target sequences, it is contemplated that further optimization of inhibition efficiency can be achieved by progressively "walking the window" one nucleotide upstream or downstream of the given sequences to identify sequences with equal or better inhibition characteristics.

Further, it is contemplated that for any sequence identified, *e.g.*, in any one of Tables 3, 4, 7, 8, 11, 13, and 15, further optimization could be achieved by systematically either adding or removing nucleotides to generate longer or shorter sequences and testing those sequences generated by walking a window of the longer or shorter size up or down the target RNA from that point. Again, coupling this approach to generating new candidate targets with testing for effectiveness of iRNAs based on those target sequences in an inhibition assay as known in the art and/or as described herein can lead to further improvements in the efficiency of inhibition. Further still, such optimized sequences can be adjusted by, *e.g.*, the introduction of modified nucleotides as described herein or as known in the art, addition or changes in overhang, or other modifications as known in the art and/or discussed herein to further optimize the molecule (*e.g.*, increasing serum stability or circulating half-life, increasing thermal stability, enhancing transmembrane delivery, targeting to a particular location or cell type, increasing interaction with silencing pathway enzymes, increasing release from endosomes) as an expression inhibitor.

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

III. Modified iRNAs of the Invention

In one embodiment, the RNA of the iRNA of the invention *e.g.*, a dsRNA, is un-modified, and does not comprise, *e.g.,* chemical modifications and/or conjugations known in the art and described herein. In another embodiment, the RNA of an iRNA of the invention, *e.g.*, a dsRNA, is chemically modified to enhance stability or other beneficial characteristics. In certain embodiments of the invention, substantially all of the nucleotides of an iRNA of the invention are modified. In other embodiments of the invention, all of the nucleotides of an iRNA of the invention are modified iRNAs of the invention in which "substantially all of the

nucleotides are modified" are largely but not wholly modified and can include not more than 5, 4, 3, 2, or 1 unmodified nucleotides.

The nucleic acids featured in the invention can be synthesized and/or modified by methods well established in the art, such as those described in "Current protocols in nucleic acid chemistry," Beaucage, S.L. *et al.* (Edrs.), John Wiley & Sons, Inc., New York, NY, USA, which is hereby incorporated herein by reference. Modifications include, for example, end modifications, *e.g.*, 5'-end modifications (phosphorylation, conjugation, inverted linkages) or 3'-end modifications (conjugation, DNA nucleotides, inverted linkages, *etc.*); base modifications, *e.g.*, replacement with stabilizing bases, destabilizing bases, or bases that base pair with an expanded repertoire of partners, removal of bases (abasic nucleotides), or conjugated bases; sugar modifications (*e.g.*, at the 2'-position or 4'-position) or replacement of the sugar; and/or backbone modifications, including modification or replacement of the phosphodiester linkages. Specific examples of iRNA compounds useful in the embodiments described herein include, but are not limited to RNAs containing modified backbones or no natural internucleoside linkages. RNAs having modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In some embodiments, a modified iRNA will have a phosphorus atom in its internucleoside backbone.

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

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

7,015,315; 7,041,816; 7,273,933; 7,321,029; and US Pat RE39464, the entire contents of each of which are hereby incorporated herein by reference.

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

Representative U.S. patents that teach the preparation of the above oligonucleosides include, but are not limited to, U.S. Patent Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,64,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and, 5,677,439, the entire contents of each of which are hereby incorporated herein by reference.

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

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

referenced U.S. Patent No. 5,602,240. In some embodiments, the RNAs featured herein have morpholino backbone structures of the above-referenced U.S. Patent No. 5,034,506.

Modified RNAs can also contain one or more substituted sugar moieties. The iRNAs, *e.g.*, dsRNAs, featured herein can include one of the following at the 2'-position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl can be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Exemplary suitable modifications include $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. In other embodiments, dsRNAs include one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an iRNA, or a group for improving the pharmacodynamic properties of an iRNA, and other substituents having similar properties. In some embodiments, the modification includes a 2'-methoxyethoxy (2'-O--$CH_2CH_2OCH_3$, also known as 2'-O-(2-methoxyethyl) or 2'-MOE) (Martin *et al.*, *Helv. Chim. Acta*, 1995, 78:486-504) *i.e.*, an alkoxy-alkoxy group. Another exemplary modification is 2'-dimethylaminooxyethoxy, *i.e.*, a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, 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--$N(CH_2)_2$. Further exemplary modifications include : 5'-Me-2'-F nucleotides, 5'-Me-2'-OMe nucleotides, 5'-Me-2'-deoxynucleotides, (both R and S isomers in these three families); 2'-alkoxyalkyl; and 2'-NMA (N-methylacetamide).

Other modifications include 2'-methoxy (2'-OCH_3), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications can also be made at other positions on the RNA of an iRNA, particularly the 3' position of the sugar on the 3' terminal nucleotide or in 2'-5' linked dsRNAs and the 5' position of 5' terminal nucleotide. iRNAs can also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative U.S. patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. Pat. Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; and 5,700,920, certain of which are commonly owned with the instant application,. The entire contents of each of the foregoing are hereby incorporated herein by reference.

An iRNA can also include nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include

the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as deoxy-thymine (dT), 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl anal other 8-substituted adenines and guanines, 5-halo, particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-daazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in Modified Nucleosides in Biochemistry, Biotechnology and Medicine, Herdewijn, P. ed. Wiley-VCH, 2008; those disclosed in The Concise Encyclopedia Of Polymer Science And Engineering, pages 858-859, Kroschwitz, J. L, ed. John Wiley & Sons, 1990, these disclosed by Englisch *et al.*, Angewandte Chemie, International Edition, 1991, 30, 613, and those disclosed by Sanghvi, Y S., Chapter 15, dsRNA Research and Applications, pages 289-302, Crooke, S. T. and Lebleu, B., Ed., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds featured in the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2°C (Sanghvi, Y. S., Crooke, S. T. and Lebleu, B., Eds., dsRNA Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are exemplary base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications.

Representative U.S. patents that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include, but are not limited to, the above noted U.S. Patent Nos. 3,687,808, 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,681,941; 5,750,692; 6,015,886; 6,147,200; 6,166,197; 6,222,025; 6,235,887; 6,380,368; 6,528,640; 6,639,062; 6,617,438; 7,045,610; 7,427,672; and 7,495,088, the entire contents of each of which are hereby incorporated herein by reference.

The RNA of an iRNA can also be modified to include one or more locked nucleic acids (LNA). A locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting the 2' and 4' carbons. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked

nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. *et al.*, (2005) *Nucleic Acids Research* 33(1):439-447; Mook, OR. *et al.*, (2007) *Mol Canc Ther* 6(3):833-843; Grunweller, A. *et al.*, (2003) *Nucleic Acids Research* 31(12):3185-3193).

In some embodiments, the oligonucleotide of the invention comprises one or more monomers that are UNA (unlocked nucleic acid) nucleotides. UNA is unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked "sugar" residue. In one example, UNA also encompasses monomer with bonds between C1'-C4' have been removed (i.e. the covalent carbon-oxygen-carbon bond between the C1' and C4' carbons). In another example, the C2'-C3' bond (i.e. the covalent carbon-carbon bond between the C2' and C3' carbons) of the sugar has been removed (see *Nuc. Acids Symp. Series,* 52, 133-134 (2008) and Fluiter et al., *Mol. Biosyst.,* 2009, 10, 1039 hereby incorporated by reference).

The RNA of an iRNA can also be modified to include one or more bicyclic sugar moities. A "bicyclic sugar" is a furanosyl ring modified by the bridging of two atoms. A"bicyclic nucleoside" ("BNA") is a nucleoside having a sugar moiety comprising a bridge connecting two carbon atoms of the sugar ring, thereby forming a bicyclic ring system. In certain embodiments, the bridge connects the 4′-carbon and the 2′-carbon of the sugar ring. Thus, in some embodiments an agent of the invention may include one or more locked nucleic acids (LNA). A locked nucleic acid is a nucleotide having a modified ribose moiety in which the ribose moiety comprises an extra bridge connecting the 2' and 4' carbons. In other words, an LNA is a nucleotide comprising a bicyclic sugar moiety comprising a 4'-CH2-O-2' bridge. This structure effectively "locks" the ribose in the 3'-endo structural conformation. The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. *et al.*, (2005) *Nucleic Acids Research* 33(1):439-447; Mook, OR. *et al.*, (2007) *Mol Canc Ther* 6(3):833-843; Grunweller, A. *et al.*, (2003) *Nucleic Acids Research* 31(12):3185-3193). Examples of bicyclic nucleosides for use in the polynucleotides of the invention include without limitation nucleosides comprising a bridge between the 4′ and the 2′ ribosyl ring atoms. In certain embodiments, the antisense polynucleotide agents of the invention include one or more bicyclic nucleosides comprising a 4′ to 2′ bridge. Examples of such 4′ to 2′ bridged bicyclic nucleosides, include but are not limited to 4′-(CH_2)—O-2′ (LNA); 4′-(CH2)—S-2′; 4′-(CH_2)$_2$—O-2′ (ENA); 4′-CH(CH_3)—O-2′ (also referred to as "constrained ethyl" or "cEt") and 4′-CH(CH_2OCH_3)—O-2′ (and analogs thereof; see, *e.g.*, U.S. Pat. No. 7,399,845); 4′-C(CH3)(CH3)—O-2′ (and analogs thereof; see *e.g.*, US Patent No. 8,278,283); 4′-CH_2—N(OCH_3)-2′ (and analogs thereof; see *e.g.*, US Patent No. 8,278,425); 4′-CH_2—O—N(CH_3)-2′ (see, e.g.,U.S. Patent Publication No. 2004/0171570); 4′-CH_2—N(R)—O-2′, wherein R is

H, C1-C12 alkyl, or a protecting group (see, *e.g.*, U.S. Pat. No. 7,427,672); 4′-CH_2—C(H)(CH_3)-2′ (see, *e.g.*, Chattopadhyaya *et al., J. Org. Chem.*, 2009, 74, 118-134); and 4′-CH_2—C(=CH_2)-2′ (and analogs thereof; see, *e.g.*, US Patent No. 8,278,426). The entire contents of each of the foregoing are hereby incorporated herein by reference.

Additional representative U.S. Patents and US Patent Publications that teach the preparation of locked nucleic acid nucleotides include, but are not limited to, the following: U.S. Patent Nos. 6,268,490; 6,525,191; 6,670,461; 6,770,748; 6,794,499; 6,998,484; 7,053,207; 7,034,133;7,084,125; 7,399,845; 7,427,672; 7,569,686; 7,741,457; 8,022,193; 8,030,467; 8,278,425; 8,278,426; 8,278,283; US 2008/0039618; and US 2009/0012281, the entire contents of each of which are hereby incorporated herein by reference.

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

The RNA of an iRNA can also be modified to include one or more constrained ethyl nucleotides. As used herein, a "constrained ethyl nucleotide" or "cEt" is a locked nucleic acid comprising a bicyclic sugar moiety comprising a 4'-CH(CH_3)-O-2' bridge. In one embodiment, a constrained ethyl nucleotide is in the S conformation referred to herein as "S-cEt."

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

Representative publications that teach the preparation of certain of the above noted CRN include, but are not limited to, US Patent Publication No. 2013/0190383; and PCT publication WO 2013/036868, the entire contents of each of which are hereby incorporated herein by reference.

One or more of the nucleotides of an iRNA of the invention may also include a hydroxymethyl substituted nucleotide. A "hydroxymethyl substituted nucleotide" is an acyclic 2'-3'-seco-nucleotide, also referred to as an "unlocked nucleic acid" ("UNA") modification

Representative U.S. publications that teach the preparation of UNA include, but are not limited to, US Patent No. 8,314,227; and US Patent Publication Nos. 2013/0096289; 2013/0011922; and 2011/0313020, the entire contents of each of which are hereby incorporated herein by reference.

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

Other modifications of the nucleotides of an iRNA of the invention include a 5' phosphate or 5' phosphate mimic, *e.g.,* a 5'-terminal phosphate or phosphate mimic on the antisense strand of an RNAi agent. Suitable phosphate mimics are disclosed in, for example US Patent Publication No. 2012/0157511, the entire contents of which are incorporated herein by reference.

A. Modified iRNAs Comprising Motifs of the Invention

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

As shown herein and in Provisional Application No. 61/561,710 or PCT Application No. PCT/US2012/065691, a superior result may be obtained by introducing one or more motifs of three identical modifications on three consecutive nucleotides into a sense strand and/or antisense strand of an RNAi agent, particularly at or near the cleavage site. In some embodiments, the sense strand and antisense strand of the RNAi agent may otherwise be completely modified. The introduction of these motifs interrupts the modification pattern, if present, of the sense and/or antisense strand. The RNAi agent may be optionally conjugated with a GalNAc derivative ligand, for instance on the sense strand. The resulting RNAi agents present superior gene silencing activity.

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

Accordingly, the invention provides double-stranded RNAi agents capable of inhibiting the expression of a target gene (*i.e.*, angiotensinogen (AGT) gene) *in vivo*. The RNAi agent comprises a sense strand and an antisense strand. Each strand of the RNAi agent may range from 12-30 nucleotides in length. For example, each strand may be between 14-30 nucleotides in length, 17-30 nucleotides in length, 25-30 nucleotides in length, 27-30

nucleotides in length, 17-23 nucleotides in length, 17-21 nucleotides in length, 17-19 nucleotides in length, 19-25 nucleotides in length, 19-23 nucleotides in length, 19-21 nucleotides in length, 21-25 nucleotides in length, or 21-23 nucleotides in length.

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

In one embodiment, the RNAi agent may contain one or more overhang regions and/or capping groups at the 3'-end, 5'-end, or both ends of one or both strands. The overhang can be 1-6 nucleotides in length, for instance 2-6 nucleotides in length, 1-5 nucleotides in length, 2-5 nucleotides in length, 1-4 nucleotides in length, 2-4 nucleotides in length, 1-3 nucleotides in length, 2-3 nucleotides in length, or 1-2 nucleotides in length. The overhangs can be the result of one strand being longer than the other, or the result of two strands of the same length being staggered. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence. As discussed herein, extended overhang of up to 30 nucleotides in length are also contemplated in various embodiments of the invention. The first and second strands can also be joined, *e.g.*, by additional bases to form a hairpin, or by other non-base linkers.

In one embodiment, the nucleotides in the overhang region of the RNAi agent can each independently be a modified or unmodified nucleotide including, but no limited to 2'-sugar modified, such as, 2-F, 2'-Omethyl, thymidine (T), 2`-O-methoxyethyl-5-methyluridine (Teo), 2`-O-methoxyethyladenosine (Aeo), 2`-O-methoxyethyl-5-methylcytidine (m5Ceo), and any combinations thereof. For example, TT can be an overhang sequence for either end on either strand. The overhang can form a mismatch with the target mRNA or it can be complementary to the gene sequences being targeted or can be another sequence.

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

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

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

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

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

In one embodiment, the RNAi agent comprises a 21 nucleotide sense strand and a 23 nucleotide antisense strand, wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides at positions 9, 10, 11 from the 5'end; the antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at positions 11, 12, 13 from the 5'end, wherein one end of the RNAi agent is blunt, while the other end comprises a 2 nucleotide overhang. Preferably, the 2 nucleotide overhang is at the 3'-end of the antisense strand.

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

one embodiment, every nucleotide in the sense strand and the antisense strand of the RNAi agent, including the nucleotides that are part of the motifs are modified nucleotides. In one embodiment each residue is independently modified with a 2'-O-methyl or 3'-fluoro, *e.g.,* in an alternating motif. Optionally, the RNAi agent further comprises a ligand (preferably $GalNAc_3$).

In one embodiment, the RNAi agent comprises a sense and an antisense strand, wherein the sense strand is 25-30 nucleotide residues in length, wherein starting from the 5' terminal nucleotide (position 1) positions 1 to 23 of the first strand comprise at least 8 ribonucleotides; the antisense strand is 36-66 nucleotide residues in length and, starting from the 3' terminal nucleotide, comprises at least 8 ribonucleotides in the positions paired with positions 1- 23 of sense strand to form a duplex; wherein at least the 3 ' terminal nucleotide of antisense strand is unpaired with sense strand, and up to 6 consecutive 3' terminal nucleotides are unpaired with sense strand, thereby forming a 3' single stranded overhang of 1-6 nucleotides; wherein the 5' terminus of antisense strand comprises from 10-30 consecutive nucleotides which are unpaired with sense strand, thereby forming a 10-30 nucleotide single stranded 5' overhang; wherein at least the sense strand 5' terminal and 3' terminal nucleotides are base paired with nucleotides of antisense strand when sense and antisense strands are aligned for maximum complementarity, thereby forming a substantially duplexed region between sense and antisense strands; and antisense strand is sufficiently complementary to a target RNA along at least 19 ribonucleotides of antisense strand length to reduce target gene expression when the double-stranded nucleic acid is introduced into a mammalian cell; and wherein the sense strand contains at least one motif of three 2'-F modifications on three consecutive nucleotides, where at least one of the motifs occurs at or near the cleavage site. The antisense strand contains at least one motif of three 2'-O-methyl modifications on three consecutive nucleotides at or near the cleavage site.

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

reducing expression of the target gene in the mammal. Optionally, the RNAi agent further comprises a ligand.

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

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

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

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

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

wing modification may occur at one end relative to the first motif which is at or near cleavage site or on either side of the lead motif.

Like the sense strand, the antisense strand of the RNAi agent may contain more than one motifs of three identical modifications on three consecutive nucleotides, with at least one of the motifs occurring at or near the cleavage site of the strand. This antisense strand may also contain one or more wing modifications in an alignment similar to the wing modifications that may be present on the sense strand.

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

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

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

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

In one embodiment, every nucleotide in the sense strand and antisense strand of the RNAi agent, including the nucleotides that are part of the motifs, may be modified. Each nucleotide may be modified with the same or different modification which can include one or more alteration of one or both of the non-linking phosphate oxygens and/or of one or more of the linking phosphate oxygens; alteration of a constituent of the ribose sugar, *e.g.*, of the 2′ hydroxyl on the ribose sugar; wholesale replacement of the phosphate moiety with "dephospho" linkers; modification or replacement of a naturally occurring base; and replacement or modification of the ribose-phosphate backbone.

As nucleic acids are polymers of subunits, many of the modifications occur at a position which is repeated within a nucleic acid, *e.g.*, a modification of a base, or a phosphate moiety, or a non-linking O of a phosphate moiety. In some cases the modification will occur at all of the subject positions in the nucleic acid but in many cases it will not. By way of example, a modification may only occur at a 3' or 5' terminal position, may only occur in a terminal region, *e.g.,* at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10

nucleotides of a strand. A modification may occur in a double strand region, a single strand region, or in both. A modification may occur only in the double strand region of a RNA or may only occur in a single strand region of a RNA. For example, a phosphorothioate modification at a non-linking O position may only occur at one or both termini, may only occur in a terminal region, *e.g.*, at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10 nucleotides of a strand, or may occur in double strand and single strand regions, particularly at termini. The 5' end or ends can be phosphorylated.

It may be possible, *e.g.*, to enhance stability, to include particular bases in overhangs, or to include modified nucleotides or nucleotide surrogates, in single strand overhangs, *e.g.*, in a 5' or 3' overhang, or in both. For example, it can be desirable to include purine nucleotides in overhangs. In some embodiments all or some of the bases in a 3' or 5' overhang may be modified, *e.g.*, with a modification described herein. Modifications can include, *e.g.*, the use of modifications at the 2' position of the ribose sugar with modifications that are known in the art, *e.g.*, the use of deoxyribonucleotides, , 2'-deoxy-2'-fluoro (2'-F) or 2'-O-methyl modified instead of the ribosugar of the nucleobase , and modifications in the phosphate group, *e.g.*, phosphorothioate modifications. Overhangs need not be homologous with the target sequence.

In one embodiment, each residue of the sense strand and antisense strand is independently modified with LNA, CRN, cET, UNA, HNA, CeNA, 2'-methoxyethyl, 2'- O-methyl, 2'-O-allyl, 2'-C- allyl, 2'-deoxy, 2'-hydroxyl, or 2'-fluoro. The strands can contain more than one modification. In one embodiment, each residue of the sense strand and antisense strand is independently modified with 2'- O-methyl or 2'-fluoro.

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

In one embodiment, the N_a and/or N_b comprise modifications of an alternating pattern. The term "alternating motif" as used herein refers to a motif having one or more modifications, each modification occurring on alternating nucleotides of one strand. The alternating nucleotide may refer to one per every other nucleotide or one per every three nucleotides, or a similar pattern. For example, if A, B and C each represent one type of modification to the nucleotide, the alternating motif can be "ABABABABABAB…," "AABBAABBAABB…," "AABAABAABAAB…," "AAABAAABAAAB…," "AAABBBAAABBB…," or "ABCABCABCABC…," *etc.*

The type of modifications contained in the alternating motif may be the same or different. For example, if A, B, C, D each represent one type of modification on the nucleotide, the alternating pattern, *i.e.*, modifications on every other nucleotide, may be the same, but each of the sense strand or antisense strand can be selected from several

possibilities of modifications within the alternating motif such as "ABABAB…", "ACACAC…" "BDBDBD…" or "CDCDCD…," *etc.*

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

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

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

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

The RNAi agent may further comprise at least one phosphorothioate or methylphosphonate internucleotide linkage. The phosphorothioate or methylphosphonate internucleotide linkage modification may occur on any nucleotide of the sense strand or antisense strand or both strands in any position of the strand. For instance, the internucleotide linkage modification may occur on every nucleotide on the sense strand and/or antisense strand; each internucleotide linkage modification may occur in an alternating pattern on the sense strand and/or antisense strand; or the sense strand or antisense strand may contain both internucleotide linkage modifications in an alternating pattern. The alternating pattern of the internucleotide linkage modification on the sense strand may be the same or different from the antisense strand, and the alternating pattern of the internucleotide linkage modification on the sense strand may have a shift relative to the alternating pattern of the internucleotide linkage modification on the antisense strand. In one embodiment, a double-standed RNAi agent comprises 6-8phosphorothioate internucleotide linkages. In one embodiment, the antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and the sense strand comprises at least two phosphorothioate internucleotide linkages at either the 5'-terminus or the 3'-terminus.

In one embodiment, the RNAi comprises a phosphorothioate or methylphosphonate internucleotide linkage modification in the overhang region. For example, the overhang region may contain two nucleotides having a phosphorothioate or methylphosphonate internucleotide linkage between the two nucleotides. Internucleotide linkage modifications also may be made to link the overhang nucleotides with the terminal paired nucleotides within the duplex region. For example, at least 2, 3, 4, or all the overhang nucleotides may be linked through phosphorothioate or methylphosphonate internucleotide linkage, and optionally, there may be additional phosphorothioate or methylphosphonate internucleotide linkages linking the overhang nucleotide with a paired nucleotide that is next to the overhang nucleotide. For instance, there may be at least two phosphorothioate internucleotide linkages between the terminal three nucleotides, in which two of the three nucleotides are overhang nucleotides, and the third is a paired nucleotide next to the overhang nucleotide. These terminal three nucleotides may be at the 3'-end of the antisense strand, the 3'-end of the sense strand, the 5'-end of the antisense strand, and/or the 5'end of the antisense strand.

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

terminal three nucleotides at both the 5'-end of the sense strand and at the 5'-end of the antisense strand.

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

In one embodiment, the RNAi agent comprises at least one of the first 1, 2, 3, 4, or 5 base pairs within the duplex regions from the 5'- end of the antisense strand independently selected from the group of: A:U, G:U, I:C, and mismatched pairs, *e.g.*, non-canonical or other than canonical pairings or pairings which include a universal base, to promote the dissociation of the antisense strand at the 5'-end of the duplex.

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

In another embodiment, the nucleotide at the 3'-end of the sense strand is deoxy-thymine (dT). In another embodiment, the nucleotide at the 3'-end of the antisense strand is deoxy-thymine (dT). In one embodiment, there is a short sequence of deoxy-thymine nucleotides, for example, two dT nucleotides on the 3'-end of the sense and/or antisense strand.

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

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

wherein:

i and j are each independently 0 or 1;

p and q are each independently 0-6;

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

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

each n_p and n_q independently represent an overhang nucleotide;

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

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

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

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

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

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

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

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

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

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

When the sense strand is represented as formula (Id), each N_b independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-5, 0-4, 0-2 or 0 modified nucleotides. Preferably, N_b is 0, 1, 2, 3, 4, 5 or 6 Each N_a can independently represent an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides.
Each of X, Y and Z may be the same or different from each other.

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

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

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

In one embodiment, the antisense strand sequence of the RNAi may be represented by formula (II):

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

wherein:

k and l are each independently 0 or 1;

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

When the antisense strand is represented as formula (IId), each N_b' independently represents an oligonucleotide sequence comprising 0-10, 0-7, 0-10, 0-7, 0-5, 0-4, 0-2 or 0

modified nucleotides. Each N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. Preferably, N_b is 0, 1, 2, 3, 4, 5 or 6.

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

5' $n_{p'}$-$N_{a'}$-Y'Y'Y'- $N_{a'}$-$n_{q'}$ 3' (Ia).

When the antisense strand is represented as formula (IIa), each N_a' independently represents an oligonucleotide sequence comprising 2-20, 2-15, or 2-10 modified nucleotides. Each of X′, Y′ and Z′ may be the same or different from each other.

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

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

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

The sense strand represented by any one of the above formulas (Ia), (Ib), (Ic), and (Id) forms a duplex with a antisense strand being represented by any one of formulas (IIa), (IIb), (IIc), and (IId), respectively.

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

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

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

(III)

wherein:

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

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

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

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

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

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

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

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

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

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

(IIIa)

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

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

(IIIb)

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

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

(IIIc)

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

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

(IIId)

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

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

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

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

Each of X, Y and Z in formulas (III), (IIIa), (IIIb), (IIIc), and (IIId) may be the same or different from each other.

When the RNAi agent is represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId), at least one of the Y nucleotides may form a base pair with one of the Y′ nucleotides. Alternatively, at least two of the Y nucleotides form base pairs with the corresponding Y′ nucleotides; or all three of the Y nucleotides all form base pairs with the corresponding Y′ nucleotides.

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

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

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

In one embodiment, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications. In another embodiment, when the RNAi agent is represented by formula (IIId), the N_a modifications are 2′-O-methyl or 2′-fluoro modifications and $n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide a via phosphorothioate linkage. In yet another embodiment, when the RNAi agent is represented

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

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

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

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

In one embodiment, two RNAi agents represented by formula (III), (IIIa), (IIIb), (IIIc), and (IIId) are linked to each other at the 5' end, and one or both of the 3' ends and are optionally conjugated to to a ligand. Each of the agents can target the same gene or two different genes; or each of the agents can target same gene at two different target sites.

Various publications describe multimeric RNAi agents that can be used in the methods of the invention. Such publications include WO2007/091269, US Patent No. 7858769, WO2010/141511, WO2007/117686, WO2009/014887 and WO2011/031520 the entire contents of each of which are hereby incorporated herein by reference.

As described in more detail below, the RNAi agent that contains conjugations of one or more carbohydrate moieties to a RNAi agent can optimize one or more properties of the RNAi agent. In many cases, the carbohydrate moiety will be attached to a modified subunit of the RNAi agent. For example, the ribose sugar of one or more ribonucleotide subunits of a

dsRNA agent can be replaced with another moiety, *e.g.*, a non-carbohydrate (preferably cyclic) carrier to which is attached a carbohydrate ligand. A ribonucleotide subunit in which the ribose sugar of the subunit has been so replaced is referred to herein as a ribose replacement modification subunit (RRMS). A cyclic carrier may be a carbocyclic ring system, *i.e.*, all ring atoms are carbon atoms, or a heterocyclic ring system, *i.e.*, one or more ring atoms may be a heteroatom, *e.g.*, nitrogen, oxygen, sulfur. The cyclic carrier may be a monocyclic ring system, or may contain two or more rings, *e.g.* fused rings. The cyclic carrier may be a fully saturated ring system, or it may contain one or more double bonds.

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

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

In certain specific embodiments, the RNAi agent for use in the methods of the invention is an agent selected from the group of agents listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15. These agents may further comprise a ligand.

IV. iRNAs Conjugated to Ligands

Another modification of the RNA of an iRNA of the invention involves chemically linking to the RNA one or more ligands, moieties or conjugates that enhance the activity, cellular distribution or cellular uptake of the iRNA. Such moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger *et al.*, *Proc. Natl. Acid. Sci. USA*,

1989, 86: 6553-6556), cholic acid (Manoharan *et al.*, *Biorg. Med. Chem. Let.*, 1994, 4:1053-1060), a thioether, *e.g.*, beryl-S-tritylthiol (Manoharan *et al.*, *Ann. N.Y. Acad. Sci.*, 1992, 660:306-309; Manoharan *et al.*, *Biorg. 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 (Saison-Behmoaras *et al.*, *EMBO J*, 1991, 10:1111-1118; Kabanov *et al.*, *FEBS Lett.*, 1990, 259:327-330; Svinarchuk *et al.*, *Biochimie*, 1993, 75:49-54), a phospholipid, *e.g.*, di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-phosphonate (Manoharan *et al.*, *Tetrahedron Lett.*, 1995, 36:3651-3654; Shea *et al.*, *Nucl. Acids Res.*, 1990, 18:3777-3783), a polyamine or a polyethylene glycol chain (Manoharan *et al.*, *Nucleosides & Nucleotides*, 1995, 14:969-973), or adamantane acetic acid (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-carbonyloxycholesterol moiety (Crooke *et al.*, J. *Pharmacol. Exp. Ther.*, 1996, 277:923-937).

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

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

Ligands can also include targeting groups, *e.g.*, a cell or tissue targeting agent, *e.g.*, a lectin, glycoprotein, lipid or protein, *e.g.*, an antibody, that binds to a specified cell type such as a kidney cell. A targeting group can be a thyrotropin, melanotropin, lectin, glycoprotein,

surfactant protein A, Mucin carbohydrate, multivalent lactose, multivalent galactose, N-acetyl-galactosamine, N-acetyl-gulucoseamine multivalent mannose, multivalent fucose, glycosylated polyaminoacids, multivalent galactose, transferrin, bisphosphonate, polyglutamate, polyaspartate, a lipid, cholesterol, a steroid, bile acid, folate, vitamin B12, vitamin A, biotin, or an RGD peptide or RGD peptide mimetic.

Other examples of ligands include dyes, intercalating agents (*e.g.* acridines), cross-linkers (*e.g.* psoralene, mitomycin C), porphyrins (TPPC4, texaphyrin, Sapphyrin), polycyclic aromatic hydrocarbons (*e.g.*, phenazine, dihydrophenazine), artificial endonucleases (*e.g.* EDTA), lipophilic molecules, *e.g.*, cholesterol, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-Bis-O(hexadecyl)glycerol, geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid,O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine)and peptide conjugates (*e.g.*, antennapedia peptide, Tat peptide), alkylating agents, phosphate, amino, mercapto, PEG (*e.g.*, PEG-40K), MPEG, $[MPEG]_2$, polyamino, alkyl, substituted alkyl, radiolabeled markers, enzymes, haptens (*e.g.* biotin), transport/absorption facilitators (*e.g.*, aspirin, vitamin E, folic acid), synthetic ribonucleases (*e.g.*, imidazole, bisimidazole, histamine, imidazole clusters, acridine-imidazole conjugates, Eu3+ complexes of tetraazamacrocycles), dinitrophenyl, HRP, or AP.

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

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

In some embodiments, a ligand attached to an iRNA as described herein acts as a pharmacokinetic modulator (PK modulator). PK modulators include lipophiles, bile acids, steroids, phospholipid analogues, peptides, protein binding agents, PEG, vitamins *etc*. Exemplary PK modulators include, but are not limited to, cholesterol, fatty acids, cholic acid, lithocholic acid, dialkylglycerides, diacylglyceride, phospholipids, sphingolipids, naproxen, ibuprofen, vitamin E, biotin *etc*. Oligonucleotides that comprise a number of phosphorothioate linkages are also known to bind to serum protein, thus short

oligonucleotides, *e.g.*, oligonucleotides of about 5 bases, 10 bases, 15 bases or 20 bases, comprising multiple of phosphorothioate linkages in the backbone are also amenable to the present invention as ligands (*e.g.* as PK modulating ligands). In addition, aptamers that bind serum components (*e.g.* serum proteins) are also suitable for use as PK modulating ligands in the embodiments described herein.

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

The oligonucleotides used in the conjugates of the present 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, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is also known to use similar techniques to prepare other oligonucleotides, such as the phosphorothioates and alkylated derivatives.

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

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

A. Lipid Conjugates

In one embodiment, the ligand or conjugate is a lipid or lipid-based molecule. Such a lipid or lipid-based molecule preferably binds a serum protein, *e.g.*, human serum albumin (HSA). An HSA binding ligand allows for distribution of the conjugate to a target tissue, *e.g.*, a non-kidney target tissue of the body. For example, the target tissue can be the liver,

including parenchymal cells of the liver. Other molecules that can bind HSA can also be used as ligands. For example, naproxen or aspirin can be used. A lipid or lipid-based ligand can (a) increase resistance to degradation of the conjugate, (b) increase targeting or transport into a target cell or cell membrane, and/or (c) can be used to adjust binding to a serum protein, *e.g.*, HSA.

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

In a preferred embodiment, the lipid based ligand binds HSA. Preferably, it binds HSA with a sufficient affinity such that the conjugate will be preferably distributed to a non-kidney tissue. However, it is preferred that the affinity not be so strong that the HSA-ligand binding cannot be reversed.

In another preferred embodiment, the lipid based ligand binds HSA weakly or not at all, such that the conjugate will be preferably distributed to the kidney. Other moieties that target to kidney cells can also be used in place of or in addition to the lipid based ligand.

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

B. Cell Permeation Agents

In another aspect, the ligand is a cell-permeation agent, preferably a helical cell-permeation agent. Preferably, the agent is amphipathic. An exemplary agent is a peptide such as tat or antennopedia. If the agent is a peptide, it can be modified, including a peptidylmimetic, invertomers, non-peptide or pseudo-peptide linkages, and use of D-amino acids. The helical agent is preferably an alpha-helical agent, which preferably has a lipophilic and a lipophobic phase.

The ligand can be a peptide or peptidomimetic. A peptidomimetic (also referred to herein as an oligopeptidomimetic) is a molecule capable of folding into a defined three-dimensional structure similar to a natural peptide. The attachment of peptide and peptidomimetics to iRNA agents can affect pharmacokinetic distribution of the iRNA, such as by enhancing cellular recognition and absorption. The peptide or peptidomimetic moiety

can be about 5-50 amino acids long, *e.g.*, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acids long.

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

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

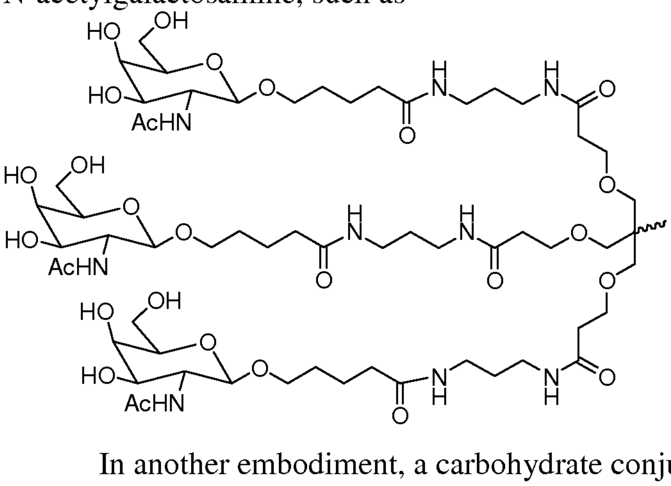
A "cell permeation peptide" is capable of permeating a cell, *e.g.,* a microbial cell, such as a bacterial or fungal cell, or a mammalian cell, such as a human cell. A microbial cell-permeating peptide can be, for example, an α-helical linear peptide (*e.g.*, LL-37 or Ceropin P1), a disulfide bond-containing peptide (*e.g.*, α -defensin, β-defensin or bactenecin), or a peptide containing only one or two dominating amino acids (*e.g.*, PR-39 or indolicidin). A cell permeation peptide can also include a nuclear localization signal (NLS). For example, a cell permeation peptide can be a bipartite amphipathic peptide, such as MPG, which is

derived from the fusion peptide domain of HIV-1 gp41 and the NLS of SV40 large T antigen (Simeoni *et al*., Nucl. Acids Res. 31:2717-2724, 2003).

C. Carbohydrate Conjugates

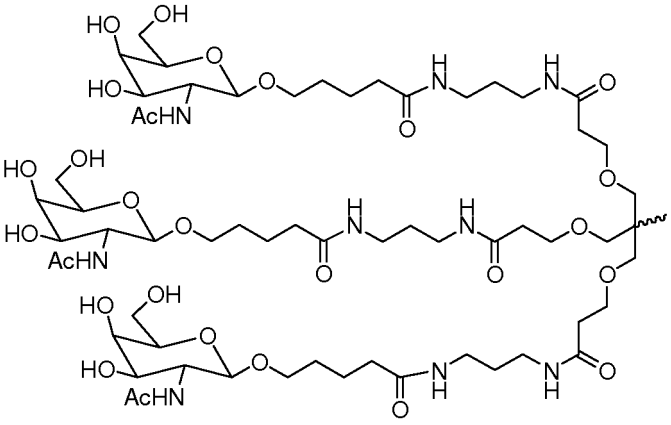
In some embodiments of the compositions and methods of the invention, an iRNA oligonucleotide further comprises a carbohydrate. The carbohydrate conjugated iRNA are advantageous for the *in vivo* delivery of nucleic acids, as well as compositions suitable for *in vivo* therapeutic use, as described herein.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

In one embodiment, a carbohydrate conjugate for use in the compositions and methods of the invention is a monosaccharide. In one embodiment, the monosaccharide is an N-acetylgalactosamine, such as

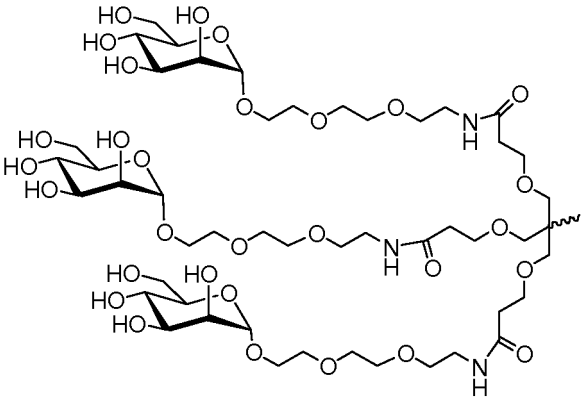


Formula II.

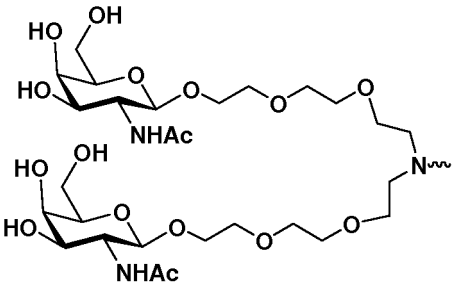
In another embodiment, a carbohydrate conjugate for use in the compositions and methods of the invention is selected from the group consisting of:



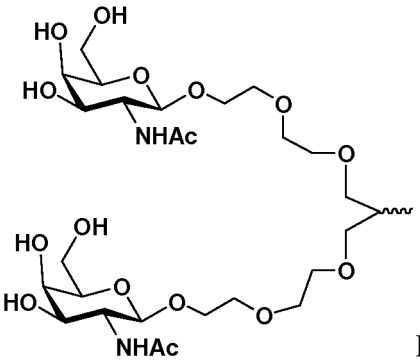
Formula II,



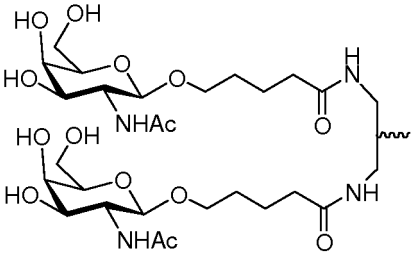
Formula III,



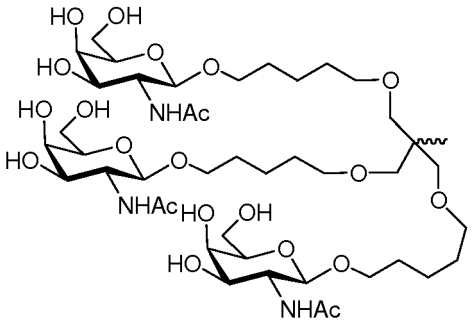
Formula IV,



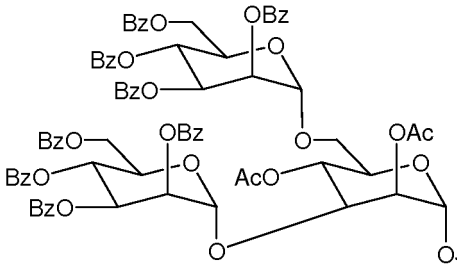
Formula V,



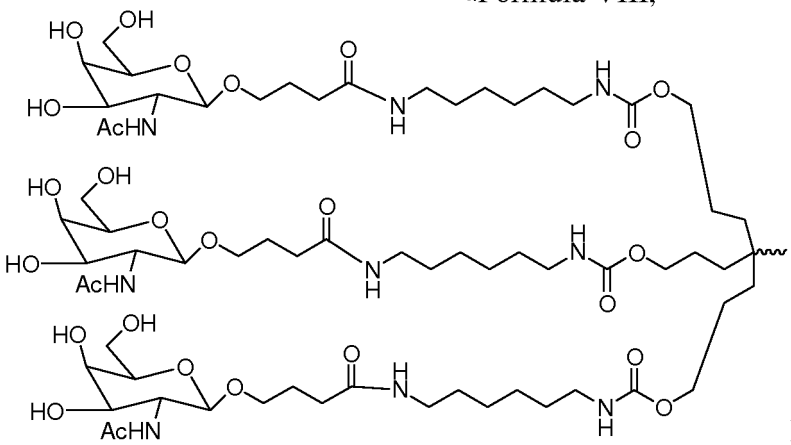
Formula VI,



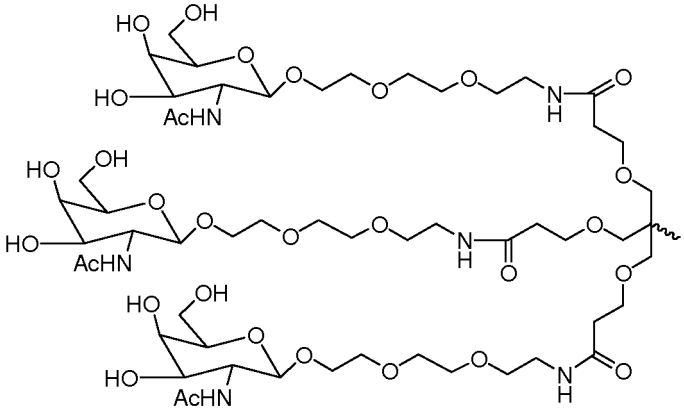
Formula VII,



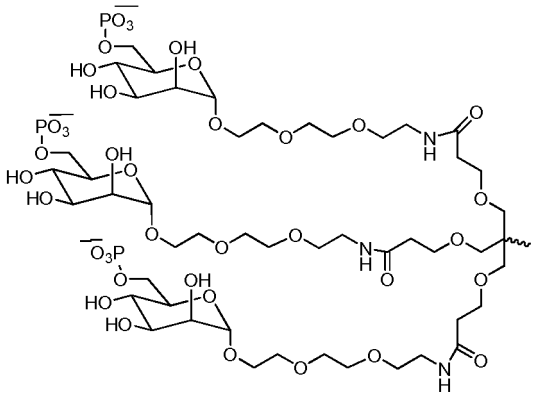
Formula VIII,



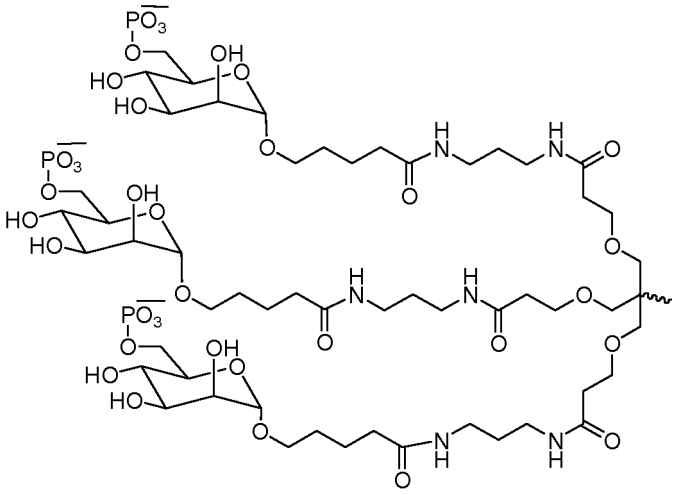
Formula IX,



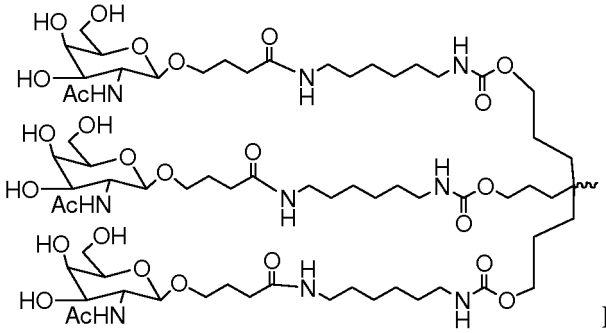
Formula X,



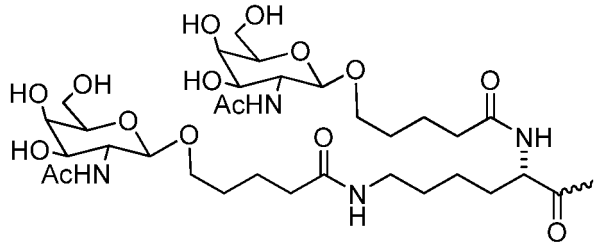
Formula XI,



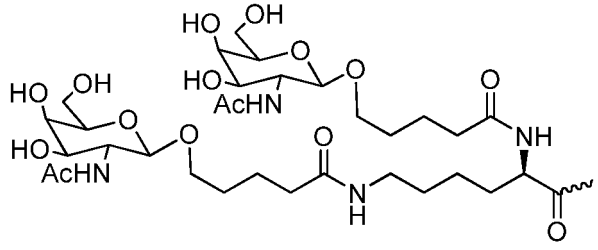
Formula XII,



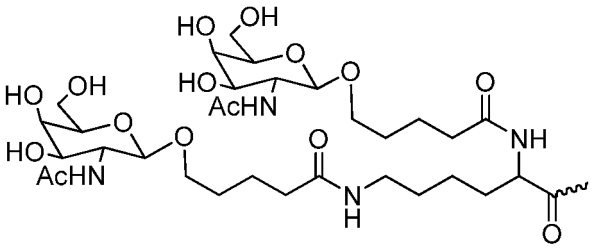
Formula XIII,



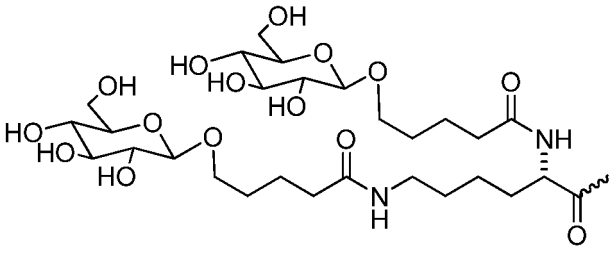
Formula XIV,



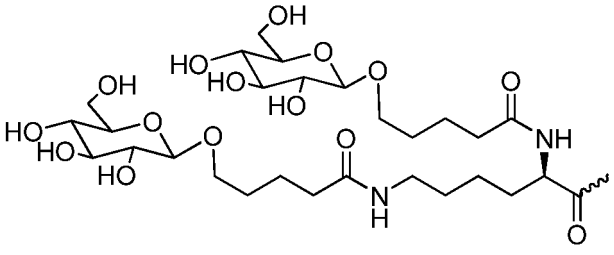
Formula XV,



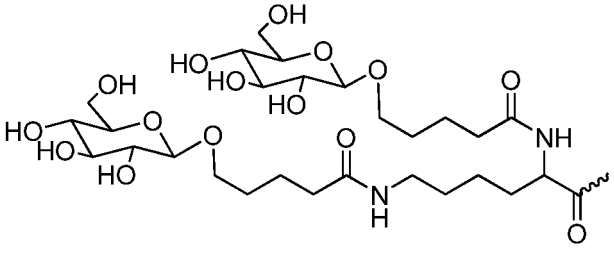
Formula XVI,



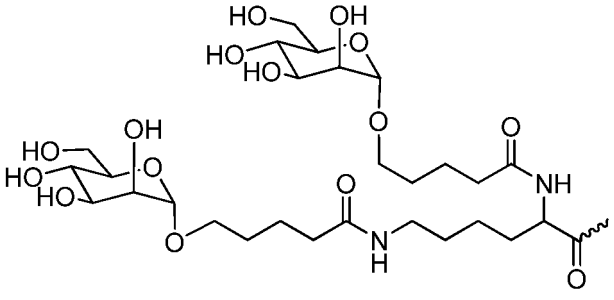
Formula XVII,



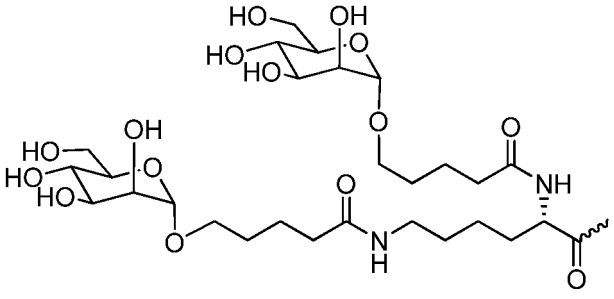
Formula XVIII,



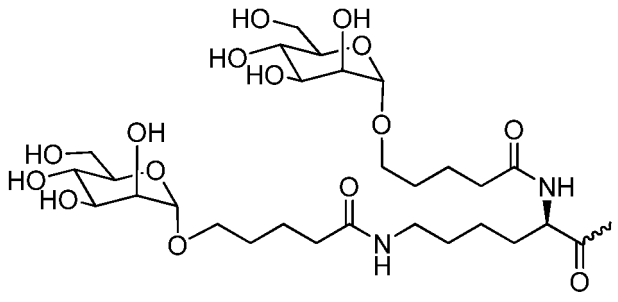
Formula XIX,



Formula XX,

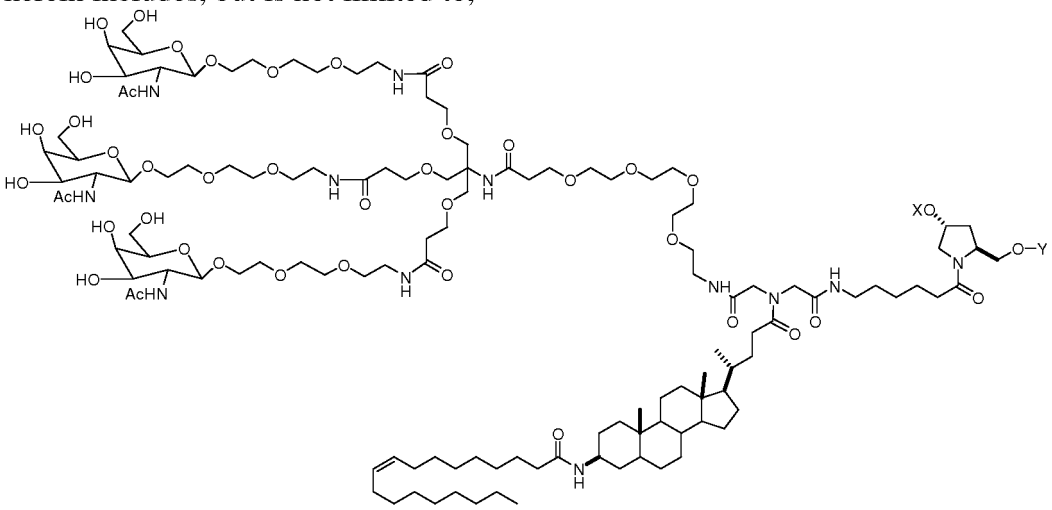


Formula XXI,



Formula XXII.

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



(Formula XXIII), when one of X or Y is an oligonucleotide, the other is a hydrogen.

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

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

D. Linkers

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

The term "linker" or “linking group” means an organic moiety that connects two parts of a compound, *e.g.,* covalently attaches two parts of a compound. Linkers typically comprise a direct bond or an atom such as oxygen or sulfur, a unit such as NR8, C(O), C(O)NH, SO, SO_2, SO_2NH or a chain of atoms, such as, but not limited to, substituted or unsubstituted alkyl, substituted or unsubstituted alkenyl, substituted or unsubstituted alkynyl, arylalkyl, arylalkenyl, arylalkynyl, heteroarylalkyl, heteroarylalkenyl, heteroarylalkynyl, heterocyclylalkyl, heterocyclylalkenyl, heterocyclylalkynyl, aryl, heteroaryl, heterocyclyl, cycloalkyl, cycloalkenyl, alkylarylalkyl, alkylarylalkenyl, alkylarylalkynyl, alkenylarylalkyl,

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

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

Cleavable linking groups are susceptible to cleavage agents, *e.g.*, pH, redox potential or the presence of degradative molecules. Generally, cleavage agents are more prevalent or found at higher levels or activities inside cells than in serum or blood. Examples of such degradative agents include: redox agents which are selected for particular substrates or which have no substrate specificity, including, *e.g.*, oxidative or reductive enzymes or reductive agents such as mercaptans, present in cells, that can degrade a redox cleavable linking group by reduction; esterases; endosomes or agents that can create an acidic environment, *e.g.*, those that result in a pH of five or lower; enzymes that can hydrolyze or degrade an acid cleavable linking group by acting as a general acid, peptidases (which can be substrate specific), and phosphatases.

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

A linker can include a cleavable linking group that is cleavable by a particular enzyme. The type of cleavable linking group incorporated into a linker can depend on the cell to be targeted. For example, a liver-targeting ligand can be linked to a cationic lipid through a linker that includes an ester group. Liver cells are rich in esterases, and therefore the linker will be cleaved more efficiently in liver cells than in cell types that are not esterase-rich. Other cell-types rich in esterases include cells of the lung, renal cortex, and testis.

Linkers that contain peptide bonds can be used when targeting cell types rich in peptidases, such as liver cells and synoviocytes.

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

i. Redox cleavable linking groups

In one embodiment, a cleavable linking group is a redox cleavable linking group that is cleaved upon reduction or oxidation. An example of reductively cleavable linking group is a disulphide linking group (-S-S-). To determine if a candidate cleavable linking group is a suitable "reductively cleavable linking group," or for example is suitable for use with a particular iRNA moiety and particular targeting agent one can look to methods described herein. For example, a candidate can be evaluated by incubation with dithiothreitol (DTT), or other reducing agent using reagents know in the art, which mimic the rate of cleavage which would be observed in a cell, *e.g.*, a target cell. The candidates can also be evaluated under conditions which are selected to mimic blood or serum conditions. In one, candidate compounds are cleaved by at most about 10% in the blood. In other embodiments, useful candidate compounds are degraded at least about 2, 4, 10, 20, 30, 40, 50, 60, 70, 80, 90, or about 100 times faster in the cell (or under *in vitro* conditions selected to mimic intracellular conditions) as compared to blood (or under *in vitro* conditions selected to mimic extracellular conditions). The rate of cleavage of candidate compounds can be determined using standard

enzyme kinetics assays under conditions chosen to mimic intracellular media and compared to conditions chosen to mimic extracellular media.

ii. Phosphate-based cleavable linking groups

In another embodiment, a cleavable linker comprises a phosphate-based cleavable linking group. A phosphate-based cleavable linking group is cleaved by agents that degrade or hydrolyze the phosphate group. An example of an agent that cleaves phosphate groups in cells are enzymes such as phosphatases in cells. Examples of phosphate-based linking groups are -O-P(O)(ORk)-O-, -O-P(S)(ORk)-O-, -O-P(S)(SRk)-O-, -S-P(O)(ORk)-O-, -O-P(O)(ORk)-S-, -S-P(O)(ORk)-S-, -O-P(S)(ORk)-S-, -S-P(S)(ORk)-O-, -O-P(O)(Rk)-O-, -O-P(S)(Rk)-O-, -S-P(O)(Rk)-O-, -S-P(S)(Rk)-O-, -S-P(O)(Rk)-S-, -O-P(S)(Rk)-S-. Preferred embodiments are -O-P(O)(OH)-O-, -O-P(S)(OH)-O-, -O-P(S)(SH)-O-, -S-P(O)(OH)-O-, -O-P(O)(OH)-S-, -S-P(O)(OH)-S-, -O-P(S)(OH)-S-, -S-P(S)(OH)-O-, -O-P(O)(H)-O-, -O-P(S)(H)-O-, -S-P(O)(H)-O, -S-P(S)(H)-O-, -S-P(O)(H)-S-, -O-P(S)(H)-S-. A preferred embodiment is -O-P(O)(OH)-O-. These candidates can be evaluated using methods analogous to those described above.

iii. Acid cleavable linking groups

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

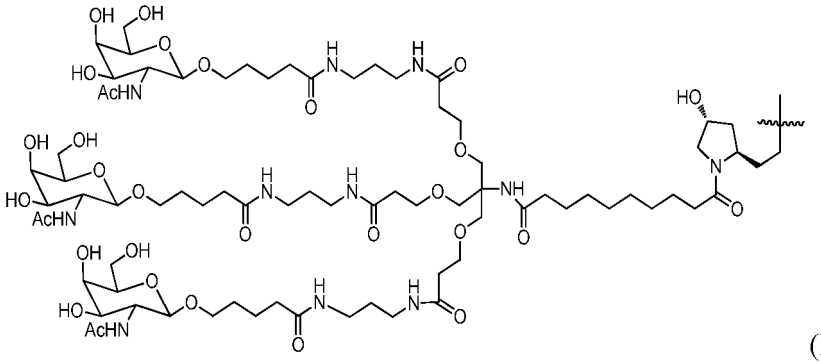
iv. Ester-based linking groups

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

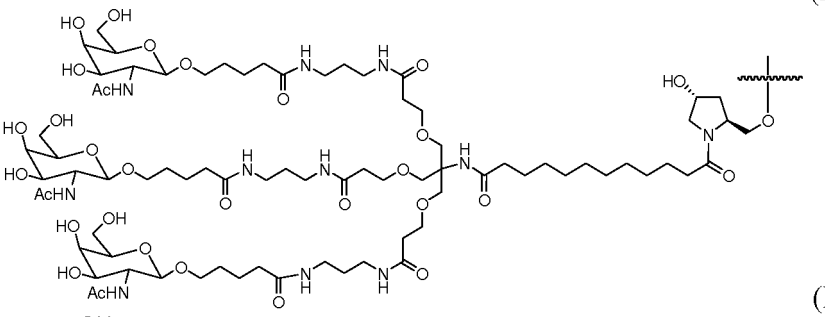
v. Peptide-based cleaving groups

In yet another embodiment, a cleavable linker comprises a peptide-based cleavable linking group. A peptide-based cleavable linking group is cleaved by enzymes such as peptidases and proteases in cells. Peptide-based cleavable linking groups are peptide bonds formed between amino acids to yield oligopeptides (*e.g.*, dipeptides, tripeptides *etc.*) and polypeptides. Peptide-based cleavable groups do not include the amide group (-C(O)NH-). The amide group can be formed between any alkylene, alkenylene or alkynelene. A peptide bond is a special type of amide bond formed between amino acids to yield peptides and proteins. The peptide based cleavage group is generally limited to the peptide bond (*i.e.*, the amide bond) formed between amino acids yielding peptides and proteins and does not include the entire amide functional group. Peptide-based cleavable linking groups have the general formula – NHCHRAC(O)NHCHRBC(O)- , where RA and RB are the R groups of the two adjacent amino acids. These candidates can be evaluated using methods analogous to those described above.

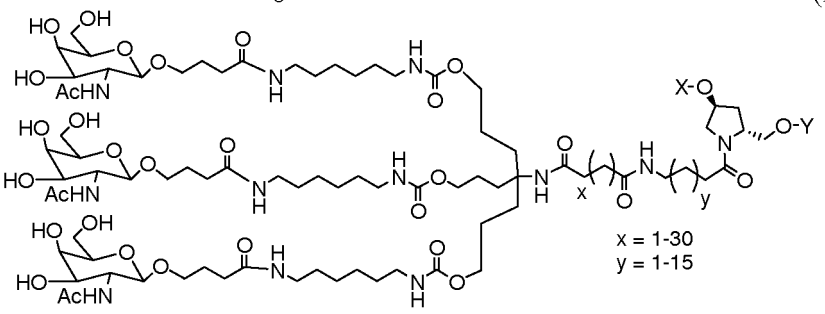
In one embodiment, an iRNA of the invention is conjugated to a carbohydrate through a linker. Non-limiting examples of iRNA carbohydrate conjugates with linkers of the compositions and methods of the invention include, but are not limited to,



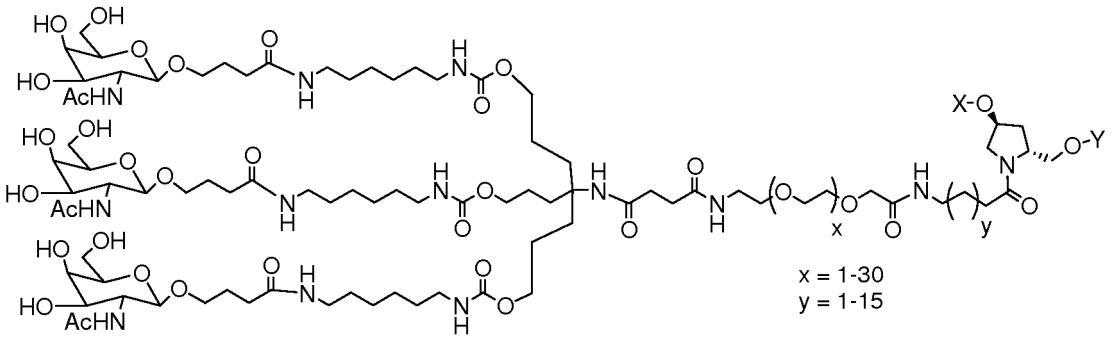
(Formula XXIV),



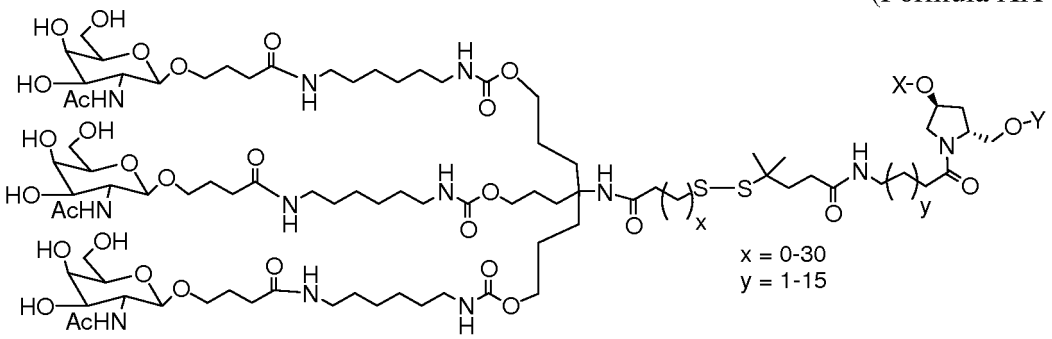
(Formula XXV),



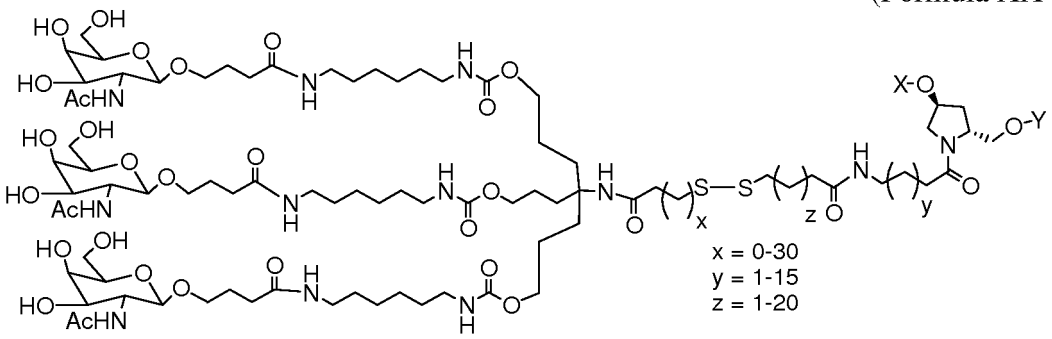
(Formula XXVI),



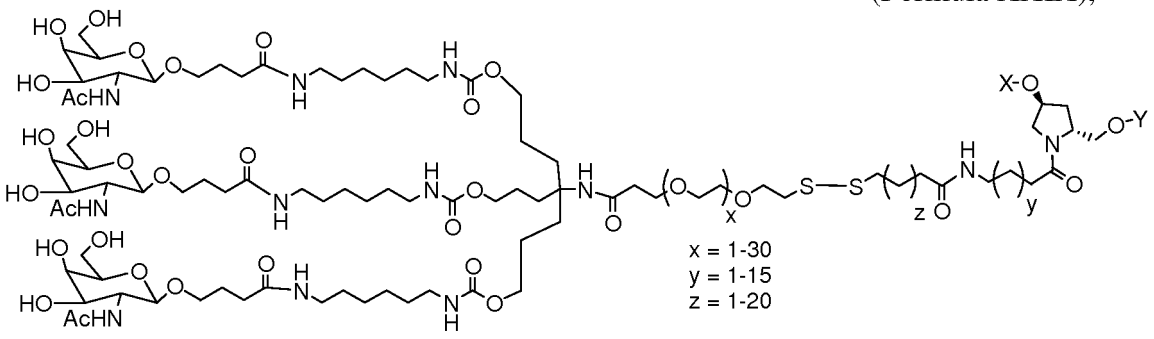
(Formula XXVII),



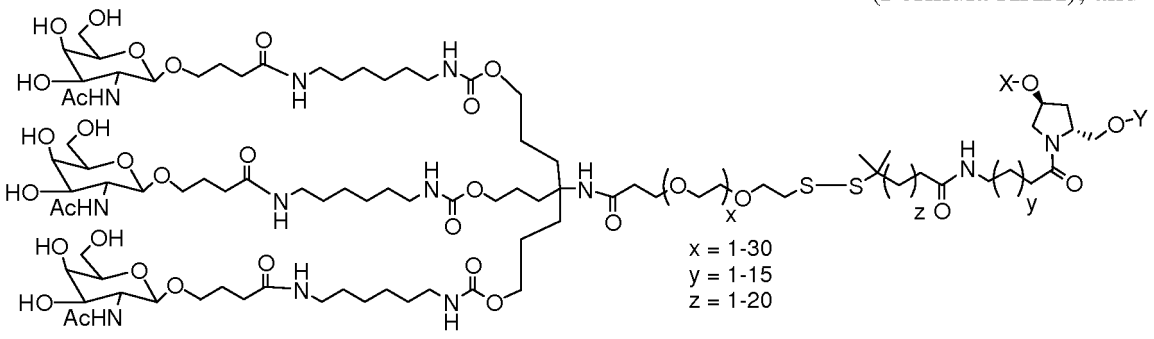
(Formula XXVIII),



(Formula XXIX),



(Formula XXX), and



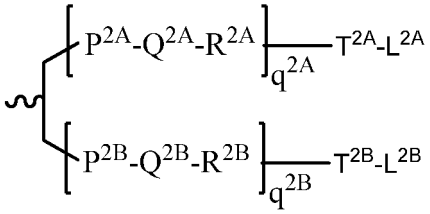
(Formula XXXI),

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

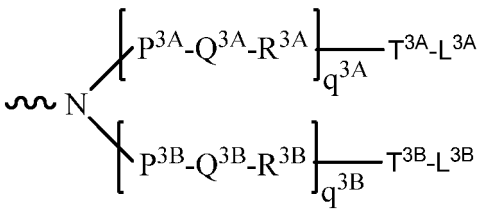
In certain embodiments of the compositions and methods of the invention, a ligand is one or more "GalNAc" (N-acetylgalactosamine) derivatives attached through a bivalent or trivalent branched linker.

In one embodiment, a dsRNA of the invention is conjugated to a bivalent or trivalent branched linker selected from the group of structures shown in any of formula (XXXII) – (XXXV):

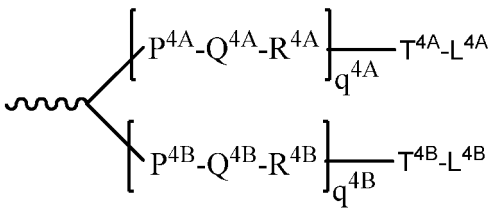
Formula XXXII



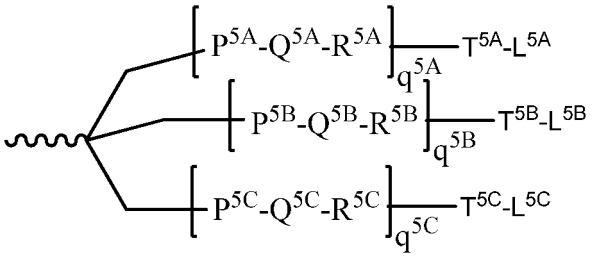
Formula XXXIII



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,



;

Formula XXXIV

Formula XXXV

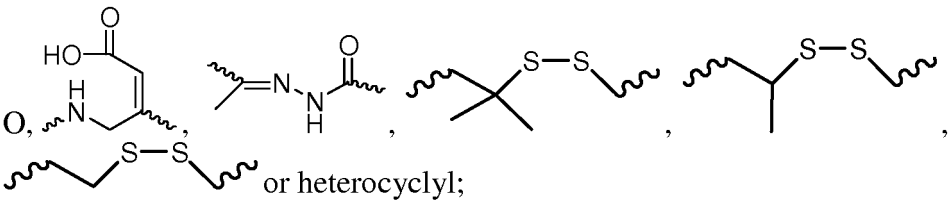
wherein:

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

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

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

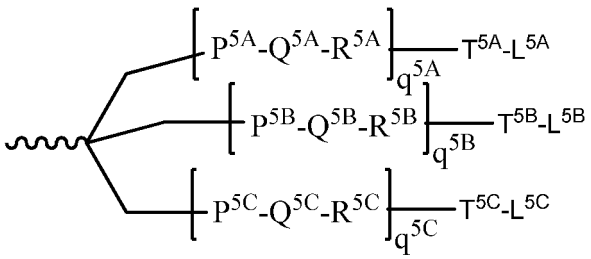
R^{2A}, R^{2B}, R^{3A}, R^{3B}, R^{4A}, R^{4B}, R^{5A}, R^{5B}, R^{5C} are each independently for each occurrence absent, NH, O, S, CH_2, C(O)O, C(O)NH, $NHCH(R^a)C(O)$, -C(O)-$CH(R^a)$-NH-, CO, CH=N-



or heterocyclyl;

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

Formula XXXV



,

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

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

Representative U.S. patents that teach the preparation of RNA 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; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941; 6,294,664; 6,320,017; 6,576,752; 6,783,931; 6,900,297; 7,037,646; 8,106,022, the entire contents of each of which are hereby incorporated herein by reference.

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

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

In certain instances, the RNA of an iRNA can be modified by a non-ligand group. A number of non-ligand molecules have been conjugated to iRNAs in order to enhance the activity, cellular distribution or cellular uptake of the iRNA, and procedures for performing such conjugations are available in the scientific literature. Such non-ligand moieties have included lipid moieties, such as cholesterol (Kubo, T. *et al., Biochem. Biophys. Res. Comm.*, 2007, 365(1):54-61; Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 1989, 86:6553), cholic acid (Manoharan *et al.*, *Bioorg. Med. Chem. Lett.*, 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), a palmityl moiety (Mishra *et al.*, *Biochim. Biophys. Acta*, 1995, 1264:229), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke *et al.*, *J. Pharmacol. Exp. Ther.*, 1996, 277:923). Representative United States patents that teach the preparation of such RNA conjugates have been listed above. Typical conjugation protocols involve the synthesis of an RNAs bearing an aminolinker at one or more positions of the sequence. The amino group is then reacted with the molecule being conjugated using appropriate coupling or activating reagents. The conjugation reaction can be performed either with the RNA still bound to the

solid support or following cleavage of the RNA, in solution phase. Purification of the RNA conjugate by HPLC typically affords the pure conjugate.

V. Delivery of an iRNA of the Invention

The delivery of an iRNA of the invention to a cell *e.g.,* a cell within a subject, such as a human subject (*e.g.,* a subject in need thereof, such as a subject having an antgiotensin associated disease or condition) can be achieved in a number of different ways. For example, delivery may be performed by contacting a cell with an iRNA of the invention either *in vitro* or *in vivo*. *In vivo* delivery may also be performed directly by administering a composition comprising an iRNA, *e.g.,* a dsRNA, to a subject. Alternatively, *in vivo* delivery may be performed indirectly by administering one or more vectors that encode and direct the expression of the iRNA. These alternatives are discussed further below.

In general, any method of delivering a nucleic acid molecule (*in vitro* or *in vivo*) can be adapted for use with an iRNA of the invention (see *e.g.*, Akhtar S. and Julian RL. (1992) *Trends Cell. Biol.* 2(5):139-144 and WO94/02595, which are incorporated herein by reference in their entireties). For *in vivo* delivery, factors to consider in order to deliver an iRNA molecule include, for example, biological stability of the delivered molecule, prevention of non-specific effects, and accumulation of the delivered molecule in the target tissue. The non-specific effects of an iRNA can be minimized by local administration, for example, by direct injection or implantation into a tissue or topically administering the preparation. Local administration to a treatment site maximizes local concentration of the agent, limits the exposure of the agent to systemic tissues that can otherwise be harmed by the agent or that can degrade the agent, and permits a lower total dose of the iRNA molecule to be administered. Several studies have shown successful knockdown of gene products when an iRNA is administered locally. For example, intraocular delivery of a VEGF dsRNA by intravitreal injection in cynomolgus monkeys (Tolentino, MJ., *et al* (2004) *Retina* 24:132-138) and subretinal injections in mice (Reich, SJ., *et al* (2003) *Mol. Vis.* 9:210-216) were both shown to prevent neovascularization in an experimental model of age-related macular degeneration. In addition, direct intratumoral injection of a dsRNA in mice reduces tumor volume (Pille, J., *et al* (2005) *Mol. Ther.*11:267-274) and can prolong survival of tumor-bearing mice (Kim, WJ., *et al* (2006) *Mol. Ther.* 14:343-350; Li, S., *et al* (2007) *Mol. Ther.* 15:515-523). RNA interference has also shown success with local delivery to the CNS by direct injection (Dorn, G., *et al.* (2004) *Nucleic Acids* 32:e49; Tan, PH., *et al* (2005) *Gene Ther.* 12:59-66; Makimura, H., *et al* (2002) *BMC Neurosci.* 3:18; Shishkina, GT., *et al* (2004) *Neuroscience* 129:521-528; Thakker, ER., *et al* (2004) *Proc. Natl. Acad. Sci. U.S.A.* 101:17270-17275; Akaneya,Y., *et al* (2005) *J. Neurophysiol.* 93:594-602) and to the lungs by intranasal administration (Howard, KA., *et al* (2006) *Mol. Ther.* 14:476-484; Zhang, X., *et al*

(2004) *J. Biol. Chem.* 279:10677-10684; Bitko, V., *et al* (2005) *Nat. Med.* 11:50-55). For administering an iRNA systemically for the treatment of a disease, the RNA can be modified or alternatively delivered using a drug delivery system; both methods act to prevent the rapid degradation of the dsRNA by endo- and exo-nucleases *in vivo*. Modification of the RNA or the pharmaceutical carrier can also permit targeting of the iRNA composition to the target tissue and avoid undesirable off-target effects. iRNA molecules can be modified by chemical conjugation to lipophilic groups such as cholesterol to enhance cellular uptake and prevent degradation. For example, an iRNA directed against ApoB conjugated to a lipophilic cholesterol moiety was injected systemically into mice and resulted in knockdown of apoB mRNA in both the liver and jejunum (Soutschek, J., *et al* (2004) *Nature* 432:173-178). Conjugation of an iRNA to an aptamer has been shown to inhibit tumor growth and mediate tumor regression in a mouse model of prostate cancer (McNamara, JO., *et al* (2006) *Nat. Biotechnol.* 24:1005-1015). In an alternative embodiment, the iRNA can be delivered using drug delivery systems such as a nanoparticle, a dendrimer, a polymer, liposomes, or a cationic delivery system. Positively charged cationic delivery systems facilitate binding of an iRNA molecule (negatively charged) and also enhance interactions at the negatively charged cell membrane to permit efficient uptake of an iRNA by the cell. Cationic lipids, dendrimers, or polymers can either be bound to an iRNA, or induced to form a vesicle or micelle (see *e.g.*, Kim SH., *et al* (2008) J*ournal of Controlled Release* 129(2):107-116) that encases an iRNA. The formation of vesicles or micelles further prevents degradation of the iRNA when administered systemically. Methods for making and administering cationic- iRNA complexes are well within the abilities of one skilled in the art (see *e.g.*, Sorensen, DR., *et al* (2003) *J. Mol. Biol* 327:761-766; Verma, UN., *et al* (2003) Clin. *Cancer Res.* 9:1291-1300; Arnold, AS *et al* (2007) *J. Hypertens.* 25:197-205, which are incorporated herein by reference in their entirety). Some non-limiting examples of drug delivery systems useful for systemic delivery of iRNAs include DOTAP (Sorensen, DR., *et al* (2003), supra; Verma, UN., *et al* (2003), *supra*), Oligofectamine, "solid nucleic acid lipid particles" (Zimmermann, TS., *et al* (2006) *Nature* 441:111-114), cardiolipin (Chien, PY., *et al* (2005) *Cancer Gene Ther.* 12:321-328; Pal, A., *et al* (2005) *Int J. Oncol.* 26:1087-1091), polyethyleneimine (Bonnet ME., *et al* (2008) *Pharm. Res.* Aug 16 Epub ahead of print; Aigner, A. (2006) *J. Biomed. Biotechnol.* 71659), Arg-Gly-Asp (RGD) peptides (Liu, S. (2006) *Mol. Pharm.* 3:472-487), and polyamidoamines (Tomalia, DA., *et al* (2007) *Biochem. Soc. Trans.* 35:61-67; Yoo, H., *et al* (1999) *Pharm. Res.* 16:1799-1804). In some embodiments, an iRNA forms a complex with cyclodextrin for systemic administration. Methods for administration and pharmaceutical compositions of iRNAs and cyclodextrins can be found in U.S. Patent No. 7,427,605, which is herein incorporated by reference in its entirety.

A. Vector encoded iRNAs of the Invention

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

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

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

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

Viral vector systems which can be utilized with the methods and compositions described herein include, but are not limited to, (a) adenovirus vectors; (b) retrovirus vectors,

including but not limited to lentiviral vectors, moloney murine leukemia virus, *etc.*; (c) adeno- associated virus vectors; (d) herpes simplex virus vectors; (e) SV 40 vectors; (f) polyoma virus vectors; (g) papilloma virus vectors; (h) picornavirus vectors; (i) pox virus vectors such as an orthopox, *e.g.*, vaccinia virus vectors or avipox, *e.g.* canary pox or fowl pox; and (j) a helper-dependent or gutless adenovirus. Replication-defective viruses can also be advantageous. Different vectors will or will not become incorporated into the cells' genome. The constructs can include viral sequences for transfection, if desired. Alternatively, the construct can be incorporated into vectors capable of episomal replication, *e.g.* EPV and EBV vectors. Constructs for the recombinant expression of an iRNA will generally require regulatory elements, *e.g.*, promoters, enhancers, *etc.*, to ensure the expression of the iRNA in target cells. Other aspects to consider for vectors and constructs are further described below.

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

Expression of the iRNA can be precisely regulated, for example, by using an inducible regulatory sequence that is sensitive to certain physiological regulators, *e.g.*, circulating glucose levels, or hormones (Docherty *et al.*, 1994, *FASEB J.* 8:20-24). Such inducible expression systems, suitable for the control of dsRNA expression in cells or in mammals include, for example, regulation by ecdysone, by estrogen, progesterone, tetracycline, chemical inducers of dimerization, and isopropyl-beta-D1 - thiogalactopyranoside (IPTG). A person skilled in the art would be able to choose the appropriate regulatory/promoter sequence based on the intended use of the iRNA transgene.

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

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

Adeno-associated virus (AAV) vectors may also be used to delivery an iRNA of the invention (Walsh *et al.*, Proc. Soc. Exp. Biol. Med. 204:289-300 (1993); U.S. Pat. No. 5,436,146). In one embodiment, the iRNA can be expressed as two separate, complementary single-stranded RNA molecules from a recombinant AAV vector having, for example, either the U6 or H1 RNA promoters, or the cytomegalovirus (CMV) promoter. Suitable AAV vectors for expressing the dsRNA featured in the invention, methods for constructing the recombinant AV vector, and methods for delivering the vectors into target cells are described in Samulski R *et al.* (1987), *J. Virol.* 61: 3096-3101; Fisher K J *et al.* (1996), *J. Virol*, 70: 520-532; Samulski R *et al.* (1989), *J. Virol.* 63: 3822-3826; U.S. Pat. No. 5,252,479; U.S. Pat. No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641, the entire disclosures of which are herein incorporated by reference.

Another viral vector suitable for delivery of an iRNA of the inevtion is a pox virus such as a vaccinia virus, for example an attenuated vaccinia such as Modified Virus Ankara (MVA) or NYVAC, an avipox such as fowl pox or canary pox.

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

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

VI. Pharmaceutical Compositions of the Invention

The present invention also includes pharmaceutical compositions and formulations which include the iRNAs of the invention. In one embodiment, provided herein are pharmaceutical compositions containing an iRNA, as described herein, and a pharmaceutically acceptable carrier. The pharmaceutical compositions containing the iRNA are useful for treating a disease or disorder associated with the expression or activity of an AGT gene. Such pharmaceutical compositions are formulated based on the mode of delivery. One example is compositions that are formulated for systemic administration *via* parenteral delivery, *e.g.*, by subcutaneous (SC) or intravenous (IV) delivery. Another example is compositions that are formulated for direct delivery into the brain parenchyma, *e.g.*, by infusion into the brain, such as by continuous pump infusion. The pharmaceutical compositions of the invention may be administered in dosages sufficient to inhibit expression of an AGT gene. In general, a suitable dose of an iRNA of the invention will be in the range of about 0.001 to about 200.0 milligrams per kilogram body weight of the recipient per day, generally in the range of about 1 to 50 mg per kilogram body weight per day. For example, the dsRNA can be administered at about 0.01 mg/kg, about 0.05 mg/kg, about 0.5 mg/kg, about 1 mg/kg, about 1.5 mg/kg, about 2 mg/kg, about 3 mg/kg, about 10 mg/kg, about 20 mg/kg, about 30 mg/kg, about 40 mg/kg, or about 50 mg/kg per single dose.

For example, the dsRNA may be administered at a dose of about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, or about 10 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

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

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

For example, the dsRNA may be administered at a dose of about 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, or about 10 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

In another embodiment, the dsRNA is administered at a dose of about 0.5 to about 50 mg/kg, about 0.75 to about 50 mg/kg, about 1 to about 50 mg/kg, about 1.5 to about 50 mg/kg, about 2 to about 50 mg/kg, about 2.5 to about 50 mg/kg, about 3 to about 50 mg/kg, about 3.5 to about 50 mg/kg, about 4 to about 50 mg/kg, about 4.5 to about 50 mg/kg, about 5 to about 50 mg/kg, about 7.5 to about 50 mg/kg, about 10 to about 50 mg/kg, about 15 to about 50 mg/kg, about 20 to about 50 mg/kg, about 20 to about 50 mg/kg, about 25 to about 50 mg/kg, about 25 to about 50 mg/kg, about 30 to about 50 mg/kg, about 35 to about 50 mg/kg, about 40 to about 50 mg/kg, about 45 to about 50 mg/kg, about 0.5 to about 45 mg/kg, about 0.75 to about 45 mg/kg, about 1 to about 45 mg/kg, about 1.5 to about 45 mg/kg, about 2 to about 45 mg/kg, about 2.5 to about 45 mg/kg, about 3 to about 45 mg/kg, about 3.5 to about 45 mg/kg, about 4 to about 45 mg/kg, about 4.5 to about 45 mg/kg, about 5 to about 45 mg/kg, about 7.5 to about 45 mg/kg, about 10 to about 45 mg/kg, about 15 to about 45 mg/kg, about 20 to about 45 mg/kg, about 20 to about 45 mg/kg, about 25 to about 45 mg/kg, about 25 to about 45 mg/kg, about 30 to about 45 mg/kg, about 35 to about 45 mg/kg, about 40 to about 45 mg/kg, about 0.5 to about 40 mg/kg, about 0.75 to about 40 mg/kg, about 1 to about 40 mg/kg, about 1.5 to about 40 mg/kg, about 2 to about 40 mg/kg, about 2.5 to about 40 mg/kg, about 3 to about 40 mg/kg, about 3.5 to about 40 mg/kg, about 4 to about 40 mg/kg, about 4.5 to about 40 mg/kg, about 5 to about 40 mg/kg, about 7.5 to about 40 mg/kg, about 10 to about 40 mg/kg, about 15 to about 40 mg/kg, about 20 to about 40 mg/kg, about 20 to about 40 mg/kg, about 25 to about 40 mg/kg, about 25 to about 40 mg/kg, about 30 to about 40 mg/kg, about 35 to about 40 mg/kg, about 0.5 to about 30 mg/kg, about 0.75 to about 30 mg/kg, about 1 to about 30 mg/kg, about 1.5 to about 30 mg/kg, about 2 to about 30 mg/kg, about 2.5 to about 30 mg/kg, about 3 to about 30 mg/kg, about 3.5 to about 30 mg/kg, about 4 to about 30 mg/kg, about 4.5 to about 30 mg/kg, about 5 to about 30 mg/kg, about 7.5 to about 30 mg/kg, about 10 to about 30 mg/kg, about 15 to about 30 mg/kg, about 20 to about 30 mg/kg, about 20 to about 30 mg/kg, about 25 to about 30 mg/kg, about 0.5 to about 20 mg/kg, about 0.75 to about 20 mg/kg, about 1 to about 20 mg/kg, about 1.5 to about 20 mg/kg, about 2 to about 20 mg/kg, about 2.5 to about 20 mg/kg, about 3 to about 20 mg/kg, about 3.5 to about 20 mg/kg, about 4 to about 20 mg/kg, about 4.5 to about 20 mg/kg, about 5 to about 20 mg/kg, about 7.5 to about 20 mg/kg, about 10 to about 20 mg/kg, or about 15 to about 20 mg/kg. In one embodiment, the dsRNA is administered at a dose of about 10mg/kg to about 30 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

For example, subjects can be administered, *e.g.,* subcutaneously or intravenously, a single therapeutic amount of iRNA, such as about 0.1, 0.125, 0.15, 0.175, 0.2, 0.225, 0.25, 0.275, 0.3, 0.325, 0.35, 0.375, 0.4, 0.425, 0.45, 0.475, 0.5, 0.525, 0.55, 0.575, 0.6, 0.625, 0.65, 0.675, 0.7, 0.725, 0.75, 0.775, 0.8, 0.825, 0.85, 0.875, 0.9, 0.925, 0.95, 0.975, 1, 1.1,

1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.5, 11, 11.5, 12, 12.5, 13, 13.5, 14, 14.5, 15, 15.5, 16, 16.5, 17, 17.5, 18, 18.5, 19, 19.5, 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or about 50 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

In some embodiments, subjects are administered, *e.g.,* subcutaneously or intravenously, multiple doses of a therapeutic amount of iRNA, such as a dose about 0.1, 0.125, 0.15, 0.175, 0.2, 0.225, 0.25, 0.275, 0.3, 0.325, 0.35, 0.375, 0.4, 0.425, 0.45, 0.475, 0.5, 0.525, 0.55, 0.575, 0.6, 0.625, 0.65, 0.675, 0.7, 0.725, 0.75, 0.775, 0.8, 0.825, 0.85, 0.875, 0.9, 0.925, 0.95, 0.975, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.5, 11, 11.5, 12, 12.5, 13, 13.5, 14, 14.5, 15, 15.5, 16, 16.5, 17, 17.5, 18, 18.5, 19, 19.5, 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or about 50 mg/kg. A multi-dose regimine may include administration of a therapeutic amount of iRNA daily, such as for two days, three days, four days, five days, six days, seven days, or longer.

In other embodiments, subjects are administered, *e.g.,* subcutaneously or intravenously, a repeat dose of a therapeutic amount of iRNA, such as a dose about 0.1, 0.125, 0.15, 0.175, 0.2, 0.225, 0.25, 0.275, 0.3, 0.325, 0.35, 0.375, 0.4, 0.425, 0.45, 0.475, 0.5, 0.525, 0.55, 0.575, 0.6, 0.625, 0.65, 0.675, 0.7, 0.725, 0.75, 0.775, 0.8, 0.825, 0.85, 0.875, 0.9, 0.925, 0.95, 0.975, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.5, 11, 11.5, 12, 12.5, 13, 13.5, 14, 14.5, 15, 15.5, 16, 16.5, 17, 17.5, 18, 18.5, 19, 19.5, 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or about 50 mg/kg. A repeat-dose regimine may include administration of a therapeutic amount of iRNA on a regular basis, such as every other day, every third day, every fourth day, twice a week, once a week, every other week, or once a

month. In certain embodiments, the iRNA is administered about once per month to about once per quarter (*i.e.*, about once every three months).

After an initial treatment regimen, the treatments can be administered on a less frequent basis.

In certain embodiments, for example, when a composition of the invention comprises a dsRNA as described herein and a lipid, subjects can be administered a therapeutic amount of iRNA, such as about 0.01 mg/kg to about 5 mg/kg, about 0.01 mg/kg to about 10 mg/kg, about 0.05 mg/kg to about 5 mg/kg, about 0.05 mg/kg to about 10 mg/kg, about 0.1 mg/kg to about 5 mg/kg, about 0.1 mg/kg to about 10 mg/kg, about 0.2 mg/kg to about 5 mg/kg, about 0.2 mg/kg to about 10 mg/kg, about 0.3 mg/kg to about 5 mg/kg, about 0.3 mg/kg to about 10 mg/kg, about 0.4 mg/kg to about 5 mg/kg, about 0.4 mg/kg to about 10 mg/kg, about 0.5 mg/kg to about 5 mg/kg, about 0.5 mg/kg to about 10 mg/kg, about 1 mg/kg to about 5 mg/kg, about 1 mg/kg to about 10 mg/kg, about 1.5 mg/kg to about 5 mg/kg, about 1.5 mg/kg to about 10 mg/kg, about 2 mg/kg to about about 2.5 mg/kg, about 2 mg/kg to about 10 mg/kg, about 3 mg/kg to about 5 mg/kg, about 3 mg/kg to about 10 mg/kg, about 3.5 mg/kg to about 5 mg/kg, about 4 mg/kg to about 5 mg/kg, about 4.5 mg/kg to about 5 mg/kg, about 4 mg/kg to about 10 mg/kg, about 4.5 mg/kg to about 10 mg/kg, about 5 mg/kg to about 10 mg/kg, about 5.5 mg/kg to about 10 mg/kg, about 6 mg/kg to about 10 mg/kg, about 6.5 mg/kg to about 10 mg/kg, about 7 mg/kg to about 10 mg/kg, about 7.5 mg/kg to about 10 mg/kg, about 8 mg/kg to about 10 mg/kg, about 8.5 mg/kg to about 10 mg/kg, about 9 mg/kg to about 10 mg/kg, or about 9.5 mg/kg to about 10 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

For example, the dsRNA may be administered at a dose of about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, or about 10 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

In certain embodiments of the invention, for example, when a double-stranded RNAi agent includes a modification (*e.g.,* one or more motifs of three identical modifications on three consecutive nucleotides), including one such motif at or near the cleavage site of the agent, six phosphorothioate linkages, and a ligand, such an agent is administered at a dose of about 0.01 to about 0.5 mg/kg, about 0.01 to about 0.4 mg/kg, about 0.01 to about 0.3 mg/kg, about 0.01 to about 0.2 mg/kg, about 0.01 to about 0.1 mg/kg, about 0.01 mg/kg to about 0.09 mg/kg, about 0.01 mg/kg to about 0.08 mg/kg, about 0.01 mg/kg to about 0.07 mg/kg, about 0.01 mg/kg to about 0.06 mg/kg, about 0.01 mg/kg to about 0.05 mg/kg, about 0.02 to about

0.5 mg/kg, about 0.02 to about 0.4 mg/kg, about 0.02 to about 0.3 mg/kg, about 0.02 to about 0.2 mg/kg, about 0.02 to about 0.1 mg/kg, about 0.02 mg/kg to about 0.09 mg/kg, about 0.02 mg/kg to about 0.08 mg/kg, about 0.02 mg/kg to about 0.07 mg/kg, about 0.02 mg/kg to about 0.06 mg/kg, about 0.02 mg/kg to about 0.05 mg/kg, about 0.03 to about 0.5 mg/kg, about 0.03 to about 0.4 mg/kg, about 0.03 to about 0.3 mg/kg, about 0.03 to about 0.2 mg/kg, about 0.03 to about 0.1 mg/kg, about 0.03 mg/kg to about 0.09 mg/kg, about 0.03 mg/kg to about 0.08 mg/kg, about 0.03 mg/kg to about 0.07 mg/kg, about 0.03 mg/kg to about 0.06 mg/kg, about 0.03 mg/kg to about 0.05 mg/kg, about 0.04 to about 0.5 mg/kg, about 0.04 to about 0.4 mg/kg, about 0.04 to about 0.3 mg/kg, about 0.04 to about 0.2 mg/kg, about 0.04 to about 0.1 mg/kg, about 0.04 mg/kg to about 0.09 mg/kg, about 0.04 mg/kg to about 0.08 mg/kg, about 0.04 mg/kg to about 0.07 mg/kg, about 0.04 mg/kg to about 0.06 mg/kg, about 0.05 to about 0.5 mg/kg, about 0.05 to about 0.4 mg/kg, about 0.05 to about 0.3 mg/kg, about 0.05 to about 0.2 mg/kg, about 0.05 to about 0.1 mg/kg, about 0.05 mg/kg to about 0.09 mg/kg, about 0.05 mg/kg to about 0.08 mg/kg, or about 0.05 mg/kg to about 0.07 mg/kg. Values and ranges intermediate to the foregoing recited values are also intended to be part of this invention, *e.g.*,, the RNAi agent may be administered to the subject at a dose of about 0.015 mg/kg to about 0.45 mg/kg.

For example, the RNAi agent, *e.g.*, RNAi agent in a pharmaceutical composition, may be administered at a dose of about 0.01 mg/kg, 0.0125 mg/kg, 0.015 mg/kg, 0.0175 mg/kg, 0.02 mg/kg, 0.0225 mg/kg, 0.025 mg/kg, 0.0275 mg/kg, 0.03 mg/kg, 0.0325 mg/kg, 0.035 mg/kg, 0.0375 mg/kg, 0.04 mg/kg, 0.0425 mg/kg, 0.045 mg/kg, 0.0475 mg/kg, 0.05 mg/kg, 0.0525 mg/kg, 0.055 mg/kg, 0.0575 mg/kg, 0.06 mg/kg, 0.0625 mg/kg, 0.065 mg/kg, 0.0675 mg/kg, 0.07 mg/kg, 0.0725 mg/kg, 0.075 mg/kg, 0.0775 mg/kg, 0.08 mg/kg, 0.0825 mg/kg, 0.085 mg/kg, 0.0875 mg/kg, 0.09 mg/kg, 0.0925 mg/kg, 0.095 mg/kg, 0.0975 mg/kg, 0.1 mg/kg, 0.125 mg/kg, 0.15 mg/kg, 0.175 mg/kg, 0.2 mg/kg, 0.225 mg/kg, 0.25 mg/kg, 0.275 mg/kg, 0.3 mg/kg, 0.325 mg/kg, 0.35 mg/kg, 0.375 mg/kg, 0.4 mg/kg, 0.425 mg/kg, 0.45 mg/kg, 0.475 mg/kg, or about 0.5 mg/kg. Values intermediate to the foregoing recited values are also intended to be part of this invention.

The pharmaceutical composition can be administered by intravenous infusion over a period of time, such as over a 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, and 21, 22, 23, 24, or about a 25 minute period. The administration may be repeated, for example, on a regular basis, such as weekly, biweekly (*i.e.*, every two weeks) for one month, two months, three months, four months or longer. After an initial treatment regimen, the treatments can be administered on a less frequent basis. For example, after administration weekly or biweekly for three months, administration can be repeated once per month, for six months or a year or longer.

The pharmaceutical composition can be administered by subcutaneous administration.

The pharmaceutical composition can be administered once daily, or the iRNA can be administered as two, three, or more sub-doses at appropriate intervals throughout the day or even using continuous infusion or delivery through a controlled release formulation. In that case, the iRNA contained in each sub-dose must be correspondingly smaller in order to achieve the total daily dosage. The dosage unit can also be compounded for delivery over several days, *e.g.*, using a conventional sustained release formulation which provides sustained release of the iRNA over a several day period. Sustained release formulations are well known in the art and are particularly useful for delivery of agents at a particular site, such as could be used with the agents of the present invention. In this embodiment, the dosage unit contains a corresponding multiple of the daily dose. A higher dose may be administered initially (*i.e.*, a loading dose), followed by a lower dosage for a sustained period of time.

In other embodiments, a single dose of the pharmaceutical compositions can be long lasting, such that subsequent doses are administered at not more than 3, 4, or 5 day intervals, or at not more than 1, 2, 3, or 4 week intervals. In some embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered once per week. In other embodiments of the invention, a single dose of the pharmaceutical compositions of the invention is administered bi-monthly. In certain embodiments, the iRNA is administered about once per month to about once per quarter (*i.e.*, about once every three months).

The pharmaceutical composition can be administered for an indefinite period of time, *e.g.*, in a subject experiencing elevated blood pressure due to obesity, or during the time at which the cause of an elevated level of AGT is present, *e.g.*, during pregnancy induced high blood pressure.

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

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

administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; subdermal, *e.g.*, via an implanted device; or intracranial, *e.g.*, by intraparenchymal, intrathecal or intraventricular, administration.

The iRNA can be delivered in a manner to target a particular tissue, such as the liver (*e.g.*, the hepatocytes of the liver).

Pharmaceutical compositions and formulations for topical administration can include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like can be necessary or desirable. Coated condoms, gloves and the like can also be useful. Suitable topical formulations include those in which the iRNAs featured in the invention are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Suitable lipids and liposomes include neutral (*e.g.,* dioleoylphosphatidyl DOPE ethanolamine, dimyristoylphosphatidyl choline DMPC, distearolyphosphatidyl choline) negative (*e.g.,* dimyristoylphosphatidyl glycerol DMPG) and cationic (*e.g.,* dioleoyltetramethylaminopropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA). iRNAs featured in the invention can be encapsulated within liposomes or can form complexes thereto, in particular to cationic liposomes. Alternatively, iRNAs can be complexed to lipids, in particular to cationic lipids. Suitable fatty acids and esters include but are not limited to arachidonic acid, oleic acid, eicosanoic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a C_{1-20} alkyl ester (*e.g.,* isopropylmyristate IPM), monoglyceride, diglyceride or pharmaceutically acceptable salt thereof). Topical formulations are described in detail in U.S. Patent No. 6,747,014, which is incorporated herein by reference.

A. iRNA Formulations Comprising Membranous Molecular Assemblies

An iRNA for use in the compositions and methods of the invention can be formulated for delivery in a membranous molecular assembly, *e.g.*, a liposome or a micelle. As used herein, the term "liposome" refers to a vesicle composed of amphiphilic lipids arranged in at least one bilayer, *e.g.*, one bilayer or a plurality of bilayers. Liposomes include unilamellar and multilamellar vesicles that have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the iRNA composition. The lipophilic material isolates the aqueous interior from an aqueous exterior, which typically does not include the iRNA composition, although in some examples, it may. Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a

tissue, the liposomal bilayer fuses with bilayer of the cellular membranes. As the merging of the liposome and cell progresses, the internal aqueous contents that include the iRNA are delivered into the cell where the iRNA can specifically bind to a target RNA and can mediate iRNA. In some cases the liposomes are also specifically targeted, *e.g.*, to direct the iRNA to particular cell types.

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

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

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

Liposomes fall into two broad classes. Cationic liposomes are positively charged liposomes which interact with the negatively charged nucleic acid molecules to form a stable complex. The positively charged nucleic acid/liposome complex binds to the negatively

charged cell surface and is internalized in an endosome. Due to the acidic pH within the endosome, the liposomes are ruptured, releasing their contents into the cell cytoplasm (Wang *et al.*, *Biochem. Biophys. Res. Commun.*, 1987, 147, 980-985).

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

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

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

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

Liposomes also include "sterically stabilized" liposomes, a term which, as used herein, refers to liposomes comprising one or more specialized lipids that, when incorporated into liposomes, result in enhanced circulation lifetimes relative to liposomes lacking such specialized lipids. Examples of sterically stabilized liposomes are those in which part of the vesicle-forming lipid portion of the liposome (A) comprises one or more glycolipids, such as monosialoganglioside G_{M1}, or (B) is derivatized with one or more hydrophilic polymers, such

as a polyethylene glycol (PEG) moiety. While not wishing to be bound by any particular theory, it is thought in the art that, at least for sterically stabilized liposomes containing gangliosides, sphingomyelin, or PEG-derivatized lipids, the enhanced circulation half-life of these sterically stabilized liposomes derives from a reduced uptake into cells of the reticuloendothelial system (RES) (Allen *et al.*, *FEBS Letters*, 1987, 223, 42; Wu *et al.*, *Cancer Research*, 1993, 53, 3765).

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

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

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

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

A DOTMA analogue, 1,2-bis(oleoyloxy)-3-(trimethylammonia)propane (DOTAP) can be used in combination with a phospholipid to form DNA-complexing vesicles. Lipofectin™ Bethesda Research Laboratories, Gaithersburg, Md.) is an effective agent for the delivery of highly anionic nucleic acids into living tissue culture cells that comprise

positively charged DOTMA liposomes which interact spontaneously with negatively charged polynucleotides to form complexes. When enough positively charged liposomes are used, the net charge on the resulting complexes is also positive. Positively charged complexes prepared in this way spontaneously attach to negatively charged cell surfaces, fuse with the plasma membrane, and efficiently deliver functional nucleic acids into, for example, tissue culture cells. Another commercially available cationic lipid, 1,2-bis(oleoyloxy)-3,3-(trimethylammonia)propane ("DOTAP") (Boehringer Mannheim, Indianapolis, Indiana) differs from DOTMA in that the oleoyl moieties are linked by ester, rather than ether linkages.

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

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

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

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

Non-ionic liposomal systems have also been examined to determine their utility in the delivery of drugs to the skin, in particular systems comprising non-ionic surfactant and cholesterol. Non-ionic liposomal formulations comprising Novasome I (glyceryl dilaurate/cholesterol/polyoxyethylene-10-stearyl ether) and Novasome II (glyceryl distearate/ cholesterol/polyoxyethylene-10-stearyl ether) were used to deliver a drug into the dermis of mouse skin. Such formulations with iRNA agent are useful for treating a dermatological disorder.

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

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

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

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

If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are usable over a wide range of pH values. In general their HLB values range from 2 to about 18 depending on their structure. Nonionic surfactants include nonionic esters such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

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

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

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

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

The iRNA for use in the methods of the invention can also be provided as micellar formulations. "Micelles" are defined herein as a particular type of molecular assembly in which amphipathic molecules are arranged in a spherical structure such that all the hydrophobic portions of the molecules are directed inward, leaving the hydrophilic portions

in contact with the surrounding aqueous phase. The converse arrangement exists if the environment is hydrophobic.

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

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

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

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

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

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

B. *Lipid particles*

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

As used herein, the term "LNP" refers to a stable nucleic acid-lipid particle. LNPs typically contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (*e.g.*, a PEG-lipid conjugate). LNPs are extremely useful for systemic applications, as they exhibit extended circulation lifetimes following intravenous (i.v.) injection and accumulate at distal sites (*e.g.*, sites physically separated from the administration site). LNPs include "pSPLP," which include an encapsulated condensing agent-nucleic acid complex as set forth in PCT Publication No. WO 00/03683. The particles of the present invention typically have a mean diameter of about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 nm to about 90 nm, and are substantially nontoxic. In addition, the nucleic acids when present in the nucleic acid- lipid particles of the present invention are resistant in aqueous solution to degradation with a nuclease. Nucleic acid-lipid particles and their method of preparation are disclosed in, *e.g.*, U.S. Patent Nos. 5,976,567; 5,981,501; 6,534,484; 6,586,410; 6,815,432; U.S. Publication No. 2010/0324120 and PCT Publication No. WO 96/40964.

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

The cationic lipid can be, for example, N,N-dioleyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), N-(I -(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(I -(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), N,N-dimethyl-2,3-dioleyloxy)propylamine (DODMA), 1,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA), l,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA), 1,2-Dilinoleylcarbamoyloxy-3-dimethylaminopropane (DLin-C-DAP), 1,2-Dilinoleyoxy-3-(dimethylamino)acetoxypropane (DLin-DAC), 1,2-Dilinoleyoxy-3-morpholinopropane (DLin-MA), 1,2-Dilinoleoyl-3-dimethylaminopropane (DLinDAP), 1,2-Dilinoleylthio-3-

dimethylaminopropane (DLin-S-DMA), 1-Linoleoyl-2-linoleyloxy-3-dimethylaminopropane (DLin-2-DMAP), 1,2-Dilinoleyloxy-3-trimethylaminopropane chloride salt (DLin-TMA.Cl), 1,2-Dilinoleoyl-3-trimethylaminopropane chloride salt (DLin-TAP.Cl), 1,2-Dilinoleyloxy-3-(N-methylpiperazino)propane (DLin-MPZ), or 3-(N,N-Dilinoleylamino)-1,2-propanediol (DLinAP), 3-(N,N-Dioleylamino)-1,2-propanedio (DOAP), 1,2-Dilinoleyloxo-3-(2-N,N-dimethylamino)ethoxypropane (DLin-EG-DMA), 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA), 2,2-Dilinoleyl-4-dimethylaminomethyl-[1,3]-dioxolane (DLin-K-DMA) or analogs thereof, (3aR,5s,6aS)-N,N-dimethyl-2,2-di((9Z,12Z)-octadeca-9,12-dienyl)tetrahydro-3aH-cyclopenta[d][1,3]dioxol-5-amine (ALN100), (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3), 1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (Tech G1), or a mixture thereof. The cationic lipid can comprise from about 20 mol % to about 50 mol % or about 40 mol % of the total lipid present in the particle.

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

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

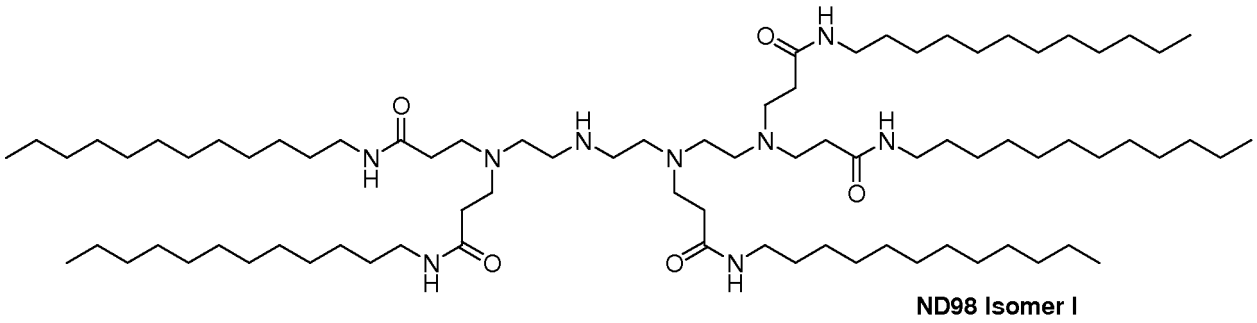
The ionizable/non-cationic lipid can be an anionic lipid or a neutral lipid including, but not limited to, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoylphosphatidylethanolamine (POPE), dioleoyl- phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-l-carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1 -trans PE, 1 -stearoyl-2-oleoyl-phosphatidyethanolamine (SOPE), cholesterol, or a mixture thereof. The non-cationic lipid can be from about 5 mol % to about 90 mol %, about 10 mol %, or about 58 mol % if cholesterol is included, of the total lipid present in the particle.

The conjugated lipid that inhibits aggregation of particles can be, for example, a polyethyleneglycol (PEG)-lipid including, without limitation, a PEG-diacylglycerol (DAG), a PEG-dialkyloxypropyl (DAA), a PEG-phospholipid, a PEG-ceramide (Cer), or a mixture

thereof. The PEG-DAA conjugate can be, for example, a PEG-dilauryloxypropyl (C_{12}), a PEG-dimyristyloxypropyl (C_{14}), a PEG-dipalmityloxypropyl (C_{16}), or a PEG-distearyloxypropyl (C_{18}). The conjugated lipid that prevents aggregation of particles can be from 0 mol % to about 20 mol % or about 2 mol % of the total lipid present in the particle.

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

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



Formula 1

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

Additional exemplary lipid-dsRNA formulations are described in Table 1.

Table 1

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

	Ionizable/Cationic Lipid	**cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio**
LNP12	1,1'-(2-(4-(2-((2-(bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl)amino)ethyl)piperazin-1-yl)ethylazanediyl)didodecan-2-ol (Tech G1)	Tech G1/DSPC/Cholesterol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA 10:1
LNP13	XTC	XTC/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 33:1
LNP14	MC3	MC3/DSPC/Chol/PEG-DMG 40/15/40/5 Lipid:siRNA: 11:1
LNP15	MC3	MC3/DSPC/Chol/PEG-DSG/GalNAc-PEG-DSG 50/10/35/4.5/0.5 Lipid:siRNA: 11:1
LNP16	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 7:1
LNP17	MC3	MC3/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP18	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/38.5/1.5 Lipid:siRNA: 12:1
LNP19	MC3	MC3/DSPC/Chol/PEG-DMG 50/10/35/5 Lipid:siRNA: 8:1
LNP20	MC3	MC3/DSPC/Chol/PEG-DPG 50/10/38.5/1.5 Lipid:siRNA: 10:1
LNP21	C12-200	C12-200/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 7:1

	Ionizable/Cationic Lipid	cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio
LNP22	XTC	XTC/DSPC/Chol/PEG-DSG 50/10/38.5/1.5 Lipid:siRNA: 10:1

DSPC: distearoylphosphatidylcholine
DPPC: dipalmitoylphosphatidylcholine
PEG-DMG: PEG-didimyristoyl glycerol (C14-PEG, or PEG-C14) (PEG with avg mol wt of 2000)
PEG-DSG: PEG-distyryl glycerol (C18-PEG, or PEG-C18) (PEG with avg mol wt of 2000)
PEG-cDMA: PEG-carbamoyl-1,2-dimyristyloxypropylamine (PEG with avg mol wt of 2000)
SNALP (l,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA)) comprising formulations are described in International Publication No. WO2009/127060, filed April 15, 2009, which is hereby incorporated by reference.

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

MC3 comprising formulations are described, *e.g.*, in U.S. Publication No. 2010/0324120, filed June 10, 2010, the entire contents of which are hereby incorporated by reference.

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

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

Synthesis of ionizable/cationic lipids

Any of the compounds, *e.g.*, cationic lipids and the like, used in the nucleic acid-lipid particles of the invention can be prepared by known organic synthesis techniques, including

the methods described in more detail in the Examples. All substituents are as defined below unless indicated otherwise.

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

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

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

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

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

The terms "optionally substituted alkyl", "optionally substituted alkenyl", "optionally substituted alkynyl", "optionally substituted acyl", and "optionally substituted heterocycle" means that, when substituted, at least one hydrogen atom is replaced with a substituent. In the case of an oxo substituent (=O) two hydrogen atoms are replaced. In this regard, substituents include oxo, halogen, heterocycle, -CN, -

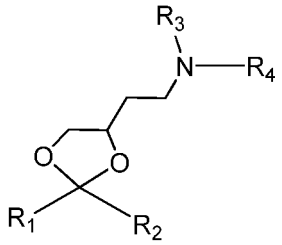
ORx, -NRxRy, -NRxC(=O)Ry, -NRxSO2Ry, -C(=O)Rx, -C(=O)ORx, -C(=O)NRxRy, –SOnRx and -SOnNRxRy, wherein n is 0, 1 or 2, Rx and Ry are the same or different and independently hydrogen, alkyl or heterocycle, and each of said alkyl and heterocycle substituents can be further substituted with one or more of oxo, halogen, -OH, -CN, alkyl, -ORx,
heterocycle, -NRxRy, -NRxC(=O)Ry, -NRxSO2Ry, -C(=O)Rx, -C(=O)ORx, -C(=O)NRxRy, -SOnRx and -SOnNRxRy.

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

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

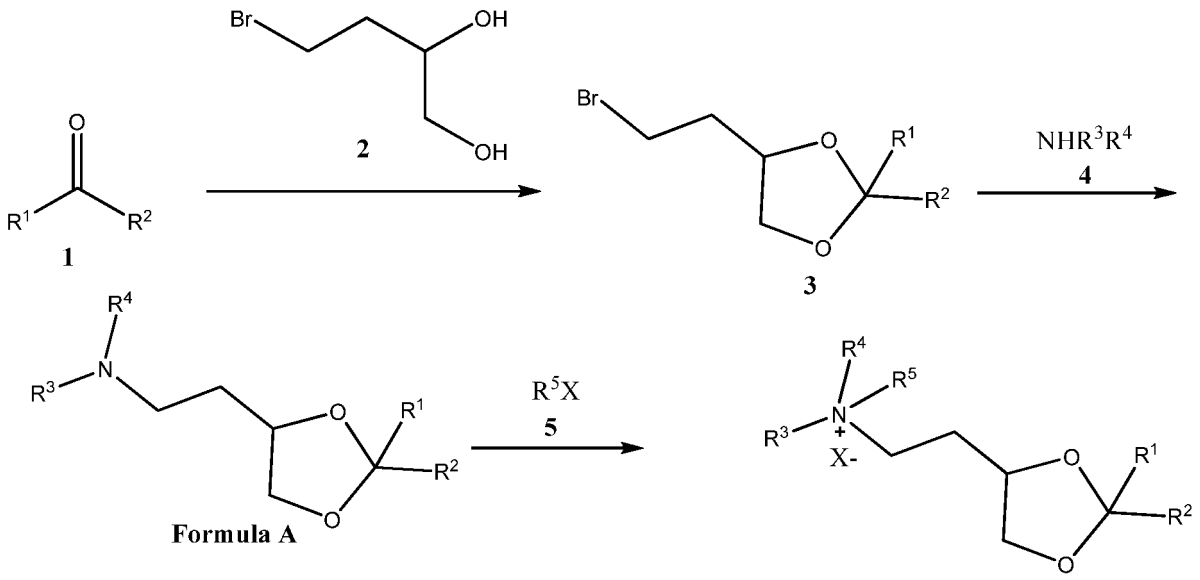
Synthesis of Formula A

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



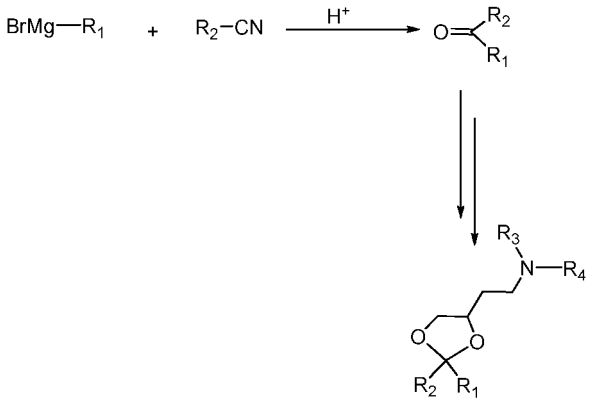
where R1 and R2 are independently alkyl, alkenyl or alkynyl, each can be optionally substituted, and R3 and R4 are independently lower alkyl or R3 and R4 can be taken together to form an optionally substituted heterocyclic ring. In some embodiments, the cationic lipid is XTC (2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane).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

Scheme 1



Lipid A, where R1 and R2 are independently alkyl, alkenyl or alkynyl, each can be optionally substituted, and R3 and R4 are independently lower alkyl or R3 and R4 can be taken together to form an optionally substituted heterocyclic ring, can be prepared according to Scheme 1. Ketone 1 and bromide 2 can be purchased or prepared according to methods known to those of ordinary skill in the art. Reaction of 1 and 2 yields ketal 3. Treatment of ketal 3 with amine 4 yields lipids of formula A. The lipids of formula A can be converted to the corresponding ammonium salt with an organic salt of formula 5, where X is anion counter ion selected from halogen, hydroxide, phosphate, sulfate, or the like.

Scheme 2



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

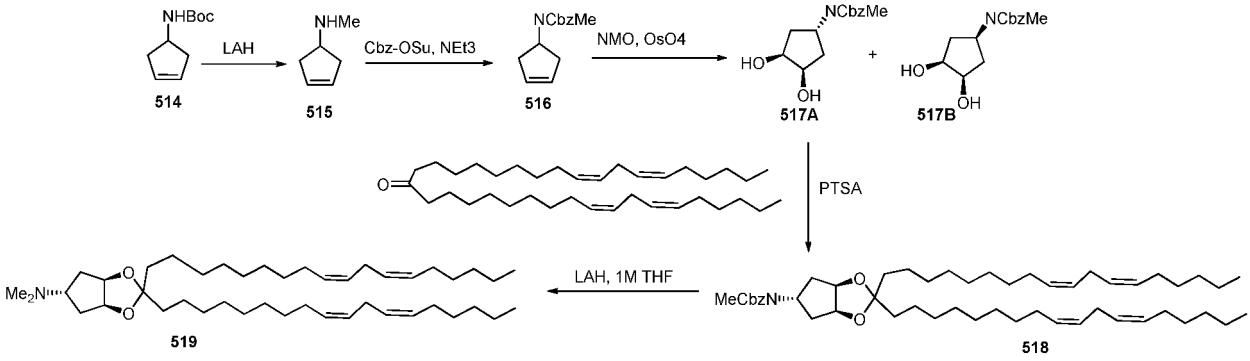
Synthesis of MC3

Preparation of DLin-M-C3-DMA (*i.e.*, (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate) was as follows. A solution of (6Z,9Z,28Z,31Z)-

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

Synthesis of ALNY-100

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



Synthesis of 515

To a stirred suspension of LiAlH4 (3.74 g, 0.09852 mol) in 200 ml anhydrous THF in a two neck RBF (1L), was added a solution of 514 (10g, 0.04926mol) in 70 mL of THF slowly at 0 0C under nitrogen atmosphere. After complete addition, reaction mixture was warmed to room temperature and then heated to reflux for 4 h. Progress of the reaction was monitored by TLC. After completion of reaction (by TLC) the mixture was cooled to 0 0C and quenched with careful addition of saturated Na2SO4 solution. Reaction mixture was stirred for 4 h at room temperature and filtered off. Residue was washed well with THF. The filtrate and washings were mixed and diluted with 400 mL dioxane and 26 mL conc. HCl and stirred for 20 minutes at room temperature. The volatilities were stripped off under vacuum to furnish the hydrochloride salt of 515 as a white solid. Yield: 7.12 g 1H-NMR (DMSO, 400MHz): δ= 9.34 (broad, 2H), 5.68 (s, 2H), 3.74 (m, 1H), 2.66-2.60 (m, 2H), 2.50-2.45 (m, 5H).

Synthesis of 516

To a stirred solution of compound 515 in 100 mL dry DCM in a 250 mL two neck RBF, was added NEt3 (37.2 mL, 0.2669 mol) and cooled to 0 0C under nitrogen atmosphere.

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

Synthesis of 517A and 517B

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

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

Synthesis of 518

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

General Procedure for the Synthesis of Compound 519

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

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

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

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders can be desirable. In some embodiments, oral formulations are those in which dsRNAs featured in the invention are administered in conjunction with one or more penetration enhancer surfactants and chelators. Suitable surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Suitable bile acids/salts include chenodeoxycholic acid (CDCA) and ursodeoxychenodeoxycholic acid (UDCA), cholic acid, dehydrocholic acid, deoxycholic acid, glucholic acid, glycholic acid, glycodeoxycholic acid, taurocholic acid, taurodeoxycholic acid, sodium tauro-24,25-dihydro-fusidate and sodium glycodihydrofusidate. Suitable fatty acids include arachidonic acid, undecanoic acid, oleic

acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a monoglyceride, a diglyceride or a pharmaceutically acceptable salt thereof (*e.g.,* sodium). In some embodiments, combinations of penetration enhancers are used, for example, fatty acids/salts in combination with bile acids/salts. One exemplary combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. DsRNAs featured in the invention can be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. DsRNA complexing agents include poly-amino acids; polyimines; polyacrylates; polyalkylacrylates, polyoxethanes, polyalkylcyanoacrylates; cationized gelatins, albumins, starches, acrylates, polyethyleneglycols (PEG) and starches; polyalkylcyanoacrylates; DEAE-derivatized polyimines, pollulans, celluloses and starches. Suitable complexing agents include chitosan, N-trimethylchitosan, poly-L-lysine, polyhistidine, polyornithine, polyspermines, protamine, polyvinylpyridine, polythiodiethylaminomethylethylene P(TDAE), polyaminostyrene (*e.g.,* p-amino), poly(methylcyanoacrylate), poly(ethylcyanoacrylate), poly(butylcyanoacrylate), poly(isobutylcyanoacrylate), poly(isohexylcynaoacrylate), DEAE-methacrylate, DEAE-hexylacrylate, DEAE-acrylamide, DEAE-albumin and DEAE-dextran, polymethylacrylate, polyhexylacrylate, poly(D,L-lactic acid), poly(DL-lactic-co-glycolic acid (PLGA), alginate, and polyethyleneglycol (PEG). Oral formulations for dsRNAs and their preparation are described in detail in U.S. Patent 6,887,906, US Publn. No. 20030027780, and U.S. Patent No. 6,747,014, each of which is incorporated herein by reference.

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

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions can be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids. Particularly preferred are formulations that target the liver when treating hepatic disorders such as hepatic carcinoma.

The pharmaceutical formulations of the present invention, which can conveniently be presented in unit dosage form, can be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In

general, the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

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

C. Additional Formulations

i. Emulsions

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

Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion can be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that can be incorporated into either phase of the emulsion. Emulsifiers can broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199).

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

Naturally occurring emulsifiers used in emulsion formulations include lanolin, beeswax, phosphatides, lecithin and acacia. Absorption bases possess hydrophilic properties such that they can soak up water to form w/o emulsions yet retain their semisolid consistencies, such as anhydrous lanolin and hydrophilic petrolatum. Finely divided solids have also been used as good emulsifiers especially in combination with surfactants and in viscous preparations. These include polar inorganic solids, such as heavy metal hydroxides,

nonswelling clays such as bentonite, attapulgite, hectorite, kaolin, montmorillonite, colloidal aluminum silicate and colloidal magnesium aluminum silicate, pigments and nonpolar solids such as carbon or glyceryl tristearate.

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

Hydrophilic colloids or hydrocolloids include naturally occurring gums and synthetic polymers such as polysaccharides (for example, acacia, agar, alginic acid, carrageenan, guar gum, karaya gum, and tragacanth), cellulose derivatives (for example, carboxymethylcellulose and carboxypropylcellulose), and synthetic polymers (for example, carbomers, cellulose ethers, and carboxyvinyl polymers). These disperse or swell in water to form colloidal solutions that stabilize emulsions by forming strong interfacial films around the dispersed-phase droplets and by increasing the viscosity of the external phase.

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

The application of emulsion formulations via dermatological, oral and parenteral routes and methods for their manufacture have been reviewed in the literature (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Emulsion formulations for oral delivery have been very widely used because of ease of formulation, as well as efficacy from an absorption and bioavailability standpoint (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume

1, p. 245; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Mineral-oil base laxatives, oil-soluble vitamins and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

ii. Microemulsions

In one embodiment of the present invention, the compositions of iRNAs and nucleic acids are formulated as microemulsions. A microemulsion can be defined as a system of water, oil and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (see e.g., Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems, Allen, LV., Popovich NG., and Ansel HC., 2004, Lippincott Williams & Wilkins (8th ed.), New York, NY; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245). Typically microemulsions are systems that are prepared by first dispersing an oil in an aqueous surfactant solution and then adding a sufficient amount of a fourth component, generally an intermediate chain-length alcohol to form a transparent system. Therefore, microemulsions have also been described as thermodynamically stable, isotropically clear dispersions of two immiscible liquids that are stabilized by interfacial films of surface-active molecules (Leung and Shah, in: Controlled Release of Drugs: Polymers and Aggregate Systems, Rosoff, M., Ed., 1989, VCH Publishers, New York, pages 185-215). Microemulsions commonly are prepared via a combination of three to five components that include oil, water, surfactant, cosurfactant and electrolyte. Whether the microemulsion is of the water-in-oil (w/o) or an oil-in-water (o/w) type is dependent on the properties of the oil and surfactant used and on the structure and geometric packing of the polar heads and hydrocarbon tails of the surfactant molecules (Schott, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 271).

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

Surfactants used in the preparation of microemulsions include, but are not limited to, ionic surfactants, non-ionic surfactants, Brij 96, polyoxyethylene oleyl ethers, polyglycerol

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

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (see e.g., U.S. Patent Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides et al., Pharmaceutical Research, 1994, 11, 1385-1390; Ritschel, Meth. Find. Exp. Clin. Pharmacol., 1993, 13, 205). Microemulsions afford advantages of improved drug solubilization, protection of drug from enzymatic hydrolysis, possible enhancement of drug absorption due to surfactant-induced alterations in membrane fluidity and permeability, ease of preparation, ease of oral administration over solid dosage forms, improved clinical potency, and decreased toxicity (see e.g., U.S. Patent Nos. 6,191,105; 7,063,860; 7,070,802; 7,157,099; Constantinides et al., Pharmaceutical Research, 1994, 11, 1385; Ho et al., J. Pharm. Sci., 1996, 85, 138-143). Often microemulsions can form spontaneously when their components are brought together at ambient temperature. This can be particularly advantageous when formulating thermolabile drugs, peptides or iRNAs. Microemulsions have also been effective in the transdermal delivery of active components in both cosmetic and pharmaceutical applications. It is expected that the microemulsion compositions and formulations of the present invention will facilitate the increased systemic absorption of iRNAs and nucleic acids from the gastrointestinal tract, as well as improve the local cellular uptake of iRNAs and nucleic acids.

Microemulsions of the present invention can also contain additional components and additives such as sorbitan monostearate (Grill 3), Labrasol, and penetration enhancers to improve the properties of the formulation and to enhance the absorption of the iRNAs and

nucleic acids of the present invention. Penetration enhancers used in the microemulsions of the present invention can be classified as belonging to one of five broad categories--surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p. 92). Each of these classes has been discussed above.

iii. Microparticles

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

iv. Penetration Enhancers

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

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

Surfactants (or "surface-active agents") are chemical entities which, when dissolved in an aqueous solution, reduce the surface tension of the solution or the interfacial tension between the aqueous solution and another liquid, with the result that absorption of iRNAs through the mucosa is enhanced. In addition to bile salts and fatty acids, these penetration enhancers include, for example, sodium lauryl sulfate, polyoxyethylene-9-lauryl ether and polyoxyethylene-20-cetyl ether) (see e.g., Malmsten, M. Surfactants and polymers in drug delivery, Informa Health Care, New York, NY, 2002; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p.92); and perfluorochemical emulsions, such as FC-43. Takahashi et al., J. Pharm. Pharmacol., 1988, 40, 252).

Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-

dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C1-20 alkyl esters thereof (e.g., methyl, isopropyl and t-butyl), and mono- and di-glycerides thereof (i.e., oleate, laurate, caprate, myristate, palmitate, stearate, linoleate, etc.) (see e.g., Touitou, E., et al. Enhancement in Drug Delivery, CRC Press, Danvers, MA, 2006; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p.92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; El Hariri et al., J. Pharm. Pharmacol., 1992, 44, 651-654).

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

Chelating agents, as used in connection with the present invention, can be defined as compounds that remove metallic ions from solution by forming complexes therewith, with the result that absorption of iRNAs through the mucosa is enhanced. With regards to their use as penetration enhancers in the present invention, chelating agents have the added advantage of also serving as DNase inhibitors, as most characterized DNA nucleases require a divalent metal ion for catalysis and are thus inhibited by chelating agents (Jarrett, J. Chromatogr., 1993, 618, 315-339). Suitable chelating agents include but are not limited to disodium ethylenediaminetetraacetate (EDTA), citric acid, salicylates (e.g., sodium salicylate, 5-methoxysalicylate and homovanilate), N-acyl derivatives of collagen, laureth-9 and N-amino acyl derivatives of beta-diketones (enamines)(see e.g., Katdare, A. et al., Excipient

development for pharmaceutical, biotechnology, and drug delivery, CRC Press, Danvers, MA, 2006; Lee et al., Critical Reviews in Therapeutic Drug Carrier Systems, 1991, page 92; Muranishi, Critical Reviews in Therapeutic Drug Carrier Systems, 1990, 7, 1-33; Buur et al., J. Control Rel., 1990, 14, 43-51).

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

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

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

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

v. Carriers

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

vi. Excipients

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

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

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

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

vii. Other Components

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

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

In some embodiments, pharmaceutical compositions featured in the invention include (a) one or more iRNA compounds and (b) one or more agents which function by a non-iRNA mechanism and which are useful in treating a hemolytic disorder. Examples of such agents include, but are not lmited to an anti-inflammatory agent, anti-steatosis agent, anti-viral, and/or anti-fibrosis agent. In addition, other substances commonly used to protect the

liver, such as silymarin, can also be used in conjunction with the iRNAs described herein. Other agents useful for treating liver diseases include telbivudine, entecavir, and protease inhibitors such as telaprevir and other disclosed, for example, in Tung et al., U.S. Application Publication Nos. 2005/0148548, 2004/0167116, and 2003/0144217; and in Hale et al., U.S. Application Publication No. 2004/0127488.

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

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

In addition to their administration, as discussed above, the iRNAs featured in the invention can be administered in combination with other known agents effective in treatment of pathological processes mediated by AGT expression. In any event, the administering physician can adjust the amount and timing of iRNA administration on the basis of results observed using standard measures of efficacy known in the art or described herein.

VII. Methods of the Invention

The present invention provides therapeutic and prophylactic methods which include administering to a subject having, or prone to developing, an AGT-associated disease, disorder, and/or condition (*e.g.*, hypertension), pharmaceutical compositions comprising an iRNA agent, or vector comprising an iRNA of the invention.

In one aspect, the present invention provides methods of treating a subject having a disorder that would benefit from reduction in AGT expression, *e.g.,* a AGT-associated

disease, *e.g.* hypertension, *e.g.,* borderline hypertension (also known as prehypertension), primary hypertension (also known as essential hypertension or idiopathic hypertension), secondary hypertension (also known as inessential hypertension), hypertensive emergency (also known as malignant hypertension), hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension (*e.g.,* preeclampsia, eclampsia, and post-partum preelampsia), diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension (also known as renal hypertension), Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy (including peripheral vascular disease), diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure (*e.g.,* left ventricular systolic dysfunction), myocardial infarction, angina, stroke, diabetes mellitus (*e.g.,* diabetic nephropathy), renal disease *e.g.*, chronic kidney disease or diabetic nephropathy optionally in the context of pregnancy, renal failure, *e.g.,* chronic renal failure, cognitive dysfunction (such as Alzheimer's), and systemic sclerosis (*e.g.,* scleroderma renal crisis). In certain embodiments, AGT- associated disease includes intrauterine growth restriction (IUGR) or fetal growth restriction. The treatment methods (and uses) of the invention include administering to the subject, *e.g.,* a human, a therapeutically effective amount of an iRNA agent targeting an AGT gene or a pharmaceutical composition comprising an iRNA agent targeting an AGT gene, thereby treating the subject having a disorder that would benefit from reduction in AGT expression.

In one aspect, the invention provides methods of preventing at least one symptom in a subject having a disorder that would benefit from reduction in AGT expression, *e.g.,* a AGT-associated disease, *e.g.,* hypertension, *e.g.,* borderline hypertension (also known as prehypertension), primary hypertension (also known as essential hypertension or idiopathic hypertension), secondary hypertension (also known as inessential hypertension), hypertensive emergency (also known as malignant hypertension), hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension (*e.g.,* preeclampsia, eclampsia, and post-partum preelampsia), diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension (also known as renal hypertension), Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic

hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy (including peripheral vascular disease), diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure (*e.g.,* left ventricular systolic dysfunction), myocardial infarction, angina, stroke, diabetes mellitus (*e.g.,* diabetic nephropathy), renal disease *e.g.*, chronic kidney disease or diabetic nephropathy optionally in the context of pregnancy, renal failure, *e.g.,* chronic renal failure, cognitive dysfunction (such as Alzheimer's), and systemic sclerosis (*e.g.,* scleroderma renal crisis). In certain embodiments, AGT- associated disease includes intrauterine growth restriction (IUGR) or fetal growth restriction The methods include administering to the subject a therapeutically effective amount of the iRNA agent, *e.g.,* dsRNA, or vector of the invention, thereby preventing at least one symptom in the subject having a disorder that would benefit from reduction in AGT expression.

In another aspect, the present invention provides uses of a therapeutically effective amount of an iRNA agent of the invention for treating a subject, *e.g.*, a subject that would benefit from a reduction and/or inhibition of AGT expression.

In a further aspect, the present invention provides uses of an iRNA agent, *e.g.*, a dsRNA, of the invention targeting an AGT gene or pharmaceutical composition comprising an iRNA agent targeting an AGT gene in the manufacture of a medicament for treating a subject, *e.g.*, a subject that would benefit from a reduction and/or inhibition of AGT expression, such as a subject having a disorder that would benefit from reduction in AGT expression, *e.g.*, a AGT-associated disease, *e.g.*, hypertension, *e.g.,* borderline hypertension (also known as prehypertension), primary hypertension (also known as essential hypertension or idiopathic hypertension), secondary hypertension (also known as inessential hypertension), hypertensive emergency (also known as malignant hypertension), hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension (*e.g.,* preeclampsia, eclampsia, and post-partum preelampsia), diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension (also known as renal hypertension), Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy (including peripheral vascular disease), diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular

fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure (*e.g.,* left ventricular systolic dysfunction), myocardial infarction, angina, stroke, diabetes mellitus (*e.g.,* diabetic nephropathy), renal disease *e.g.*, chronic kidney disease or diabetic nephropathy optionally in the context of pregnancy, renal failure, *e.g.,* chronic renal failure, cognitive dysfunction (such as Alzheimer's), and systemic sclerosis (*e.g.,* scleroderma renal crisis). In certain embodiments, AGT- associated disease includes intrauterine growth restriction (IUGR) or fetal growth restriction.

In another aspect, the invention provides uses of an iRNA, *e.g.,* a dsRNA, of the invention for preventing at least one symptom in a subject suffering from a disorder that would benefit from a reduction and/or inhibition of AGT expression, such as a AGT-associated disease, *e.g.,* hypertension, *e.g.,* borderline hypertension (also known as prehypertension), primary hypertension (also known as essential hypertension or idiopathic hypertension), secondary hypertension (also known as inessential hypertension), hypertensive emergency (also known as malignant hypertension), hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension (*e.g.,* preeclampsia, eclampsia, and post-partum preelampsia), diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension (also known as renal hypertension), Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy (including peripheral vascular disease), diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure (*e.g.,* left ventricular systolic dysfunction), myocardial infarction, angina, stroke, diabetes mellitus (*e.g.,* diabetic nephropathy), renal disease *e.g.*, chronic kidney disease or diabetic nephropathy optionally in the context of pregnancy, renal failure, *e.g.,* chronic renal failure, cognitive dysfunction (such as Alzheimer's), and systemic sclerosis (*e.g.,* scleroderma renal crisis). In certain embodiments, AGT- associated disease includes intrauterine growth restriction (IUGR) or fetal growth restriction.

In a further aspect, the present invention provides uses of an iRNA agent of the invention in the manufacture of a medicament for preventing at least one symptom in a subject suffering from a disorder that would benefit from a reduction and/or inhibition of

AGT expression, such as a AGT-associated disease, *e.g.,* hypertension, *e.g.,* borderline hypertension (also known as prehypertension), primary hypertension (also known as essential hypertension or idiopathic hypertension), secondary hypertension (also known as inessential hypertension), hypertensive emergency (also known as malignant hypertension), hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension (*e.g.,* preeclampsia, eclampsia, and post-partum preelampsia), diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension (also known as renal hypertension), Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy (including peripheral vascular disease), diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure (*e.g.,* left ventricular systolic dysfunction), myocardial infarction, angina, stroke, diabetes mellitus (*e.g.,* diabetic nephropathy), renal disease *e.g.*, chronic kidney disease or diabetic nephropathy optionally in the context of pregnancy, renal failure, *e.g.,* chronic renal failure, cognitive dysfunction (such as Alzheimer's), and systemic sclerosis (*e.g.,* scleroderma renal crisis). In certain embodiments, AGT- associated disease includes intrauterine growth restriction (IUGR) or fetal growth restriction.

In one embodiment, an iRNA agent targeting AGT is administered to a subject having a AGT-associated disease such that AGT levels, *e.g.*, in a cell, tissue, blood or other tissue or fluid of the subject are reduced by at least about 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%, 62%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least about 99% or more when the dsRNA agent is administered to the subject. In preferred embodiments, the AGT level is reduced by at least 20%.

The methods and uses of the invention include administering a composition described herein such that expression of the target AGT gene is decreased, such as for about 1, 2, 3, 4 5, 6, 7, 8, 12, 16, 18, 24, 28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72, 76, or about 80 hours. In one embodiment, expression of the target AGT gene is decreased for an extended duration,

e.g., at least about two, three, four, five, six, seven days or more, *e.g.*, about one week, two weeks, three weeks, or about four weeks or longer.

Administration of the dsRNA according to the methods and uses of the invention may result in a reduction of the severity, signs, symptoms, and/or markers of such diseases or disorders in a patient with an AGT-associated disease. By "reduction" in this context is meant a statistically significant decrease in such level. The reduction can be, for example, at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or about 100%. In preferred embodiments, the AGT level is reduced by at least 20%.

Efficacy of treatment or prevention of disease can be assessed, for example by measuring disease progression, disease remission, symptom severity, reduction in pain, quality of life, dose of a medication required to sustain a treatment effect, level of a disease marker or any other measurable parameter appropriate for a given disease being treated or targeted for prevention. It is well within the ability of one skilled in the art to monitor efficacy of treatment or prevention by measuring any one of such parameters, or any combination of parameters. For example, efficacy of treatment of dyslipidemiahypertension may be assessed, for example, by periodic monitoring of blood pressure. Comparison of the later readings with the initial readings provide a physician an indication of whether the treatment is effective. It is well within the ability of one skilled in the art to monitor efficacy of treatment or prevention by measuring any one of such parameters, or any combination of parameters. In connection with the administration of an iRNA targeting AGT or pharmaceutical composition thereof, "effective against" an AGT-associated disease indicates that administration in a clinically appropriate manner results in a beneficial effect for at least a statistically significant fraction of patients, such as improvement of symptoms, a cure, a reduction in disease, extension of life, improvement in quality of life, or other effect generally recognized as positive by medical doctors familiar with treating a AGT-associated disease and the related causes.

A treatment or preventive effect is evident when there is a statistically significant improvement in one or more parameters of disease status, or by a failure to worsen or to develop symptoms where they would otherwise be anticipated. As an example, a favorable change of at least 10% in a measurable parameter of disease, and preferably at least 20%, 30%, 40%, 50% or more can be indicative of effective treatment. Efficacy for a given iRNA drug or formulation of that drug can also be judged using an experimental animal model for the given disease as known in the art. When using an experimental animal model, efficacy of treatment is evidenced when a statistically significant reduction in a marker or symptom is observed. Suitable animal models of an angiotensinogen-associated disease, *e.g.,* hypertension, include, for example, genetic models of hypertension, *e.g.,* BPH/2 mice,

sponateously hypertensive rats (SHRs), Dahl salt-sensitive rates (DS), TGR(mREN2)27 transgenic rats in which endogenous renal renin has been suppressed, and borderline hypertensive rats (BHR), experimentally induced models of hypertension, *e.g.,* experimentally induced models of renal hypertension the Goldblatt model of renal-induced experimental hypertension, subtotal nephrectomy models, and angiotensin II induced hypertension (see, *e.g.,* Dornal and Silva (2011) *J Biosci* 36:731). Suitable animal models of pregnancy-associated hypertension include, for example, genetic models, *e.g.,* borderline hypertensive mice (*e.g.,* BPH/5 mice), rats and/or mice carrying a transgene encoding human renin and a transgene encoding human angiotensinogen, and experimentally induced models, *e.g.,* sFlt-1 infusion models, AT_1-AA-induced models, reduced uteroplacental perfusion pressure (RUPP) models (see, *e.g.,* McCarthy, *et al.* (2011) *Placenta* 32:413-419).

Subjects can be administered a therapeutic amount of iRNA, such as about 0.01 mg/kg, 0.02 mg/kg, 0.03 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.1 mg/kg, 0.15 mg/kg, 0.2 mg/kg, 0.25 mg/kg, 0.3 mg/kg, 0.35 mg/kg, 0.4 mg/kg, 0.45 mg/kg, 0.5 mg/kg, 0.55 mg/kg, 0.6 mg/kg, 0.65 mg/kg, 0.7 mg/kg, 0.75 mg/kg, 0.8 mg/kg, 0.85 mg/kg, 0.9 mg/kg, 0.95 mg/kg, 1.0 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, 1.5 mg/kg, 1.6 mg/kg, 1.7 mg/kg, 1.8 mg/kg, 1.9 mg/kg, 2.0 mg/kg, 2.1 mg/kg, 2.2 mg/kg, 2.3 mg/kg, 2.4 mg/kg, 2.5 mg/kg dsRNA, 2.6 mg/kg dsRNA, 2.7 mg/kg dsRNA, 2.8 mg/kg dsRNA, 2.9 mg/kg dsRNA, 3.0 mg/kg dsRNA, 3.1 mg/kg dsRNA, 3.2 mg/kg dsRNA, 3.3 mg/kg dsRNA, 3.4 mg/kg dsRNA, 3.5 mg/kg dsRNA, 3.6 mg/kg dsRNA, 3.7 mg/kg dsRNA, 3.8 mg/kg dsRNA, 3.9 mg/kg dsRNA, 4.0 mg/kg dsRNA, 4.1 mg/kg dsRNA, 4.2 mg/kg dsRNA, 4.3 mg/kg dsRNA, 4.4 mg/kg dsRNA, 4.5 mg/kg dsRNA, 4.6 mg/kg dsRNA, 4.7 mg/kg dsRNA, 4.8 mg/kg dsRNA, 4.9 mg/kg dsRNA, 5.0 mg/kg dsRNA, 5.1 mg/kg dsRNA, 5.2 mg/kg dsRNA, 5.3 mg/kg dsRNA, 5.4 mg/kg dsRNA, 5.5 mg/kg dsRNA, 5.6 mg/kg dsRNA, 5.7 mg/kg dsRNA, 5.8 mg/kg dsRNA, 5.9 mg/kg dsRNA, 6.0 mg/kg dsRNA, 6.1 mg/kg dsRNA, 6.2 mg/kg dsRNA, 6.3 mg/kg dsRNA, 6.4 mg/kg dsRNA, 6.5 mg/kg dsRNA, 6.6 mg/kg dsRNA, 6.7 mg/kg dsRNA, 6.8 mg/kg dsRNA, 6.9 mg/kg dsRNA, 7.0 mg/kg dsRNA, 7.1 mg/kg dsRNA, 7.2 mg/kg dsRNA, 7.3 mg/kg dsRNA, 7.4 mg/kg dsRNA, 7.5 mg/kg dsRNA, 7.6 mg/kg dsRNA, 7.7 mg/kg dsRNA, 7.8 mg/kg dsRNA, 7.9 mg/kg dsRNA, 8.0 mg/kg dsRNA, 8.1 mg/kg dsRNA, 8.2 mg/kg dsRNA, 8.3 mg/kg dsRNA, 8.4 mg/kg dsRNA, 8.5 mg/kg dsRNA, 8.6 mg/kg dsRNA, 8.7 mg/kg dsRNA, 8.8 mg/kg dsRNA, 8.9 mg/kg dsRNA, 9.0 mg/kg dsRNA, 9.1 mg/kg dsRNA, 9.2 mg/kg dsRNA, 9.3 mg/kg dsRNA, 9.4 mg/kg dsRNA, 9.5 mg/kg dsRNA, 9.6 mg/kg dsRNA, 9.7 mg/kg dsRNA, 9.8 mg/kg dsRNA, 9.9 mg/kg dsRNA, 9.0 mg/kg dsRNA, 10 mg/kg dsRNA, 15 mg/kg dsRNA, 20 mg/kg dsRNA, 25 mg/kg dsRNA, 30 mg/kg dsRNA, 35 mg/kg dsRNA, 40 mg/kg dsRNA, 45 mg/kg dsRNA, or about 50 mg/kg dsRNA. Values and ranges intermediate to the recited values are also intended to be part of this invention.

In certain embodiments, for example, when a composition of the invention comprises a dsRNA as described herein and a lipid, subjects can be administered a therapeutic amount of iRNA, such as about 0.01 mg/kg to about 5 mg/kg, about 0.01 mg/kg to about 10 mg/kg, about 0.05 mg/kg to about 5 mg/kg, about 0.05 mg/kg to about 10 mg/kg, about 0.1 mg/kg to about 5 mg/kg, about 0.1 mg/kg to about 10 mg/kg, about 0.2 mg/kg to about 5 mg/kg, about 0.2 mg/kg to about 10 mg/kg, about 0.3 mg/kg to about 5 mg/kg, about 0.3 mg/kg to about 10 mg/kg, about 0.4 mg/kg to about 5 mg/kg, about 0.4 mg/kg to about 10 mg/kg, about 0.5 mg/kg to about 5 mg/kg, about 0.5 mg/kg to about 10 mg/kg, about 1 mg/kg to about 5 mg/kg, about 1 mg/kg to about 10 mg/kg, about 1.5 mg/kg to about 5 mg/kg, about 1.5 mg/kg to about 10 mg/kg, about 2 mg/kg to about 2.5 mg/kg, about 2 mg/kg to about 10 mg/kg, about 3 mg/kg to about 5 mg/kg, about 3 mg/kg to about 10 mg/kg, about 3.5 mg/kg to about 5 mg/kg, about 4 mg/kg to about 5 mg/kg, about 4.5 mg/kg to about 5 mg/kg, about 4 mg/kg to about 10 mg/kg, about 4.5 mg/kg to about 10 mg/kg, about 5 mg/kg to about 10 mg/kg, about 5.5 mg/kg to about 10 mg/kg, about 6 mg/kg to about 10 mg/kg, about 6.5 mg/kg to about 10 mg/kg, about 7 mg/kg to about 10 mg/kg, about 7.5 mg/kg to about 10 mg/kg, about 8 mg/kg to about 10 mg/kg, about 8.5 mg/kg to about 10 mg/kg, about 9 mg/kg to about 10 mg/kg, or about 9.5 mg/kg to about 10 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

For example, the dsRNA may be administered at a dose of about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, or about 10 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

In other embodiments, for example, when a composition of the invention comprises a dsRNA as described herein and an N-acetylgalactosamine, subjects can be administered a therapeutic amount of iRNA, such as a dose of about 0.1 to about 50 mg/kg, about 0.25 to about 50 mg/kg, about 0.5 to about 50 mg/kg, about 0.75 to about 50 mg/kg, about 1 to about 50 mg/kg, about 1.5 to about 50 mg/kg, about 2 to about 50 mg/kg, about 2.5 to about 50 mg/kg, about 3 to about 50 mg/kg, about 3.5 to about 50 mg/kg, about 4 to about 50 mg/kg, about 4.5 to about 50 mg/kg, about 5 to about 50 mg/kg, about 7.5 to about 50 mg/kg, about 10 to about 50 mg/kg, about 15 to about 50 mg/kg, about 20 to about 50 mg/kg, about 20 to about 50 mg/kg, about 25 to about 50 mg/kg, about 25 to about 50 mg/kg, about 30 to about 50 mg/kg, about 35 to about 50 mg/kg, about 40 to about 50 mg/kg, about 45 to about 50 mg/kg, about 0.1 to about 45 mg/kg, about 0.25 to about 45 mg/kg, about 0.5 to about 45 mg/kg, about 0.75 to about 45 mg/kg, about 1 to about 45 mg/kg, about 1.5 to about 45

mg/kg, about 2 to about 45 mg/kg, about 2.5 to about 45 mg/kg, about 3 to about 45 mg/kg, about 3.5 to about 45 mg/kg, about 4 to about 45 mg/kg, about 4.5 to about 45 mg/kg, about 5 to about 45 mg/kg, about 7.5 to about 45 mg/kg, about 10 to about 45 mg/kg, about 15 to about 45 mg/kg, about 20 to about 45 mg/kg, about 20 to about 45 mg/kg, about 25 to about 45 mg/kg, about 25 to about 45 mg/kg, about 30 to about 45 mg/kg, about 35 to about 45 mg/kg, about 40 to about 45 mg/kg, about 0.1 to about 40 mg/kg, about 0.25 to about 40 mg/kg, about 0.5 to about 40 mg/kg, about 0.75 to about 40 mg/kg, about 1 to about 40 mg/kg, about 1.5 to about 40 mg/kg, about 2 to about 40 mg/kg, about 2.5 to about 40 mg/kg, about 3 to about 40 mg/kg, about 3.5 to about 40 mg/kg, about 4 to about 40 mg/kg, about 4.5 to about 40 mg/kg, about 5 to about 40 mg/kg, about 7.5 to about 40 mg/kg, about 10 to about 40 mg/kg, about 15 to about 40 mg/kg, about 20 to about 40 mg/kg, about 20 to about 40 mg/kg, about 25 to about 40 mg/kg, about 25 to about 40 mg/kg, about 30 to about 40 mg/kg, about 35 to about 40 mg/kg, about 0.1 to about 30 mg/kg, about 0.25 to about 30 mg/kg, about 0.5 to about 30 mg/kg, about 0.75 to about 30 mg/kg, about 1 to about 30 mg/kg, about 1.5 to about 30 mg/kg, about 2 to about 30 mg/kg, about 2.5 to about 30 mg/kg, about 3 to about 30 mg/kg, about 3.5 to about 30 mg/kg, about 4 to about 30 mg/kg, about 4.5 to about 30 mg/kg, about 5 to about 30 mg/kg, about 7.5 to about 30 mg/kg, about 10 to about 30 mg/kg, about 15 to about 30 mg/kg, about 20 to about 30 mg/kg, about 20 to about 30 mg/kg, about 25 to about 30 mg/kg, about 0.1 to about 20 mg/kg, about 0.25 to about 20 mg/kg, about 0.5 to about 20 mg/kg, about 0.75 to about 20 mg/kg, about 1 to about 20 mg/kg, about 1.5 to about 20 mg/kg, about 2 to about 20 mg/kg, about 2.5 to about 20 mg/kg, about 3 to about 20 mg/kg, about 3.5 to about 20 mg/kg, about 4 to about 20 mg/kg, about 4.5 to about 20 mg/kg, about 5 to about 20 mg/kg, about 7.5 to about 20 mg/kg, about 10 to about 20 mg/kg, or about 15 to about 20 mg/kg. In one embodiment, when a composition of the invention comprises a dsRNA as described herein and an N-acetylgalactosamine, subjects can be administered a therapeutic amount of about 10 to about 30 mg/kg of dsRNA. Values and ranges intermediate to the recited values are also intended to be part of this invention.

For example, subjects can be administered a therapeutic amount of iRNA, such as about 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 2, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8, 8.1, 8.2, 8.3, 8.4, 8.5, 8.6, 8.7, 8.8, 8.9, 9, 9.1, 9.2, 9.3, 9.4, 9.5, 9.6, 9.7, 9.8, 9.9, 10, 10.5, 11, 11.5, 12, 12.5, 13, 13.5, 14, 14.5, 15, 15.5, 16, 16.5, 17, 17.5, 18, 18.5, 19, 19.5, 20, 20.5, 21, 21.5, 22, 22.5, 23, 23.5, 24, 24.5, 25, 25.5, 26, 26.5, 27, 27.5, 28, 28.5, 29, 29.5, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or about 50 mg/kg. Values and ranges intermediate to the recited values are also intended to be part of this invention.

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

For example, the RNAi agent, *e.g.*, RNAi agent in a pharmaceutical composition, may be administered at a dose of about 0.01 mg/kg, 0.0125 mg/kg, 0.015 mg/kg, 0.0175 mg/kg, 0.02 mg/kg, 0.0225 mg/kg, 0.025 mg/kg, 0.0275 mg/kg, 0.03 mg/kg, 0.0325 mg/kg, 0.035 mg/kg, 0.0375 mg/kg, 0.04 mg/kg, 0.0425 mg/kg, 0.045 mg/kg, 0.0475 mg/kg, 0.05 mg/kg, 0.0525 mg/kg, 0.055 mg/kg, 0.0575 mg/kg, 0.06 mg/kg, 0.0625 mg/kg, 0.065 mg/kg, 0.0675 mg/kg, 0.07 mg/kg, 0.0725 mg/kg, 0.075 mg/kg, 0.0775 mg/kg, 0.08 mg/kg, 0.0825 mg/kg, 0.085 mg/kg, 0.0875 mg/kg, 0.09 mg/kg, 0.0925 mg/kg, 0.095 mg/kg, 0.0975 mg/kg, 0.1 mg/kg, 0.125 mg/kg, 0.15 mg/kg, 0.175 mg/kg, 0.2 mg/kg, 0.225 mg/kg, 0.25 mg/kg, 0.275 mg/kg, 0.3 mg/kg, 0.325 mg/kg, 0.35 mg/kg, 0.375 mg/kg, 0.4 mg/kg, 0.425 mg/kg, 0.45 mg/kg, 0.475 mg/kg, or about 0.5 mg/kg. Values intermediate to the foregoing recited values are also intended to be part of this invention.

The iRNA can be administered by intravenous infusion over a period of time, such as over a 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or about a 25 minute period. The administration may be repeated, for example, on a regular basis, such as weekly, biweekly (*i.e.*, every two weeks) for one month, two months, three months, four months or longer. After an initial treatment regimen, the treatments can be administered on a less frequent basis. For example, after administration weekly or biweekly for three months, administration can be repeated once per month, for six months or a year or longer.

Administration of the iRNA can reduce AGT levels, *e.g.*, in a cell, tissue, blood, urine or other compartment of the patient by at least about 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%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or at least about 99% or more.

Before administration of a full dose of the iRNA, patients can be administered a smaller dose, such as a 5% infusion, and monitored for adverse effects, such as an allergic reaction. In another example, the patient can be monitored for unwanted immunostimulatory effects, such as increased cytokine (*e.g.*, TNF-alpha or INF-alpha) levels.

Owing to the inhibitory effects on AGT expression, a composition according to the invention or a pharmaceutical composition prepared therefrom can enhance the quality of life.

An iRNA of the invention may be administered in "naked" form, where the modified or unmodified iRNA agent is directly suspended in aqueous or suitable buffer solvent, as a "free iRNA." A free iRNA is administered in the absence of a pharmaceutical composition. The free iRNA may be in a suitable buffer solution. The buffer solution may comprise acetate, citrate, prolamine, carbonate, or phosphate, or any combination thereof. In one embodiment, the buffer solution is phosphate buffered saline (PBS). The pH and osmolarity of the buffer solution containing the iRNA can be adjusted such that it is suitable for administering to a subject.

Alternatively, an iRNA of the invention may be administered as a pharmaceutical composition, such as a dsRNA liposomal formulation.

Subjects that would benefit from a reduction and/or inhibition of AGT gene expression are those having a AGT-associated disease or disorder as described herein.

Treatment of a subject that would benefit from a reduction and/or inhibition of AGT gene expression includes therapeutic and prophylactic treatment.

The invention further provides methods and uses of an iRNA agent or a pharmaceutical composition thereof for treating a subject that would benefit from reduction and/or inhibition of AGT expression, *e.g.,* a subject having a AGT-associated disease, in combination with other pharmaceuticals and/or other therapeutic methods, *e.g.*, with known pharmaceuticals and/or known therapeutic methods, such as, for example, those which are currently employed for treating these disorders. For example, in certain embodiments, an iRNA targeting AGT is administered in combination with, *e.g.*, an agent useful in treating an AGT-associated disease as described elsewhere herein. For example, additional therapeutics and therapeutic methods suitable for treating a subject that would benefit from reduction in AGT expression, *e.g.,* a subject having a AGT-associated disease, include angioplasty, aortorenal bypass, renal denervation, percutaneous transluminal renal angioplasty (PTRA) and stenting, surgical revascularization, catheter-based renal sympathetic denervation, and surgical removal of pheochromocytoma or reninoma, adrenalectomy, treatment with a diuretic, *e.g.,* a thiazide-type diuretic, *e.g.,* chlorothiazide, hydrochlorothiazide, chlorthalidone, metolazone, and indapamide, a potassium-sparring diuretic, such as triamterene and amiloride, a loop diuretic, *e.g.,* furosemide, torsemide, ethacrynic acid, and bumetanide; an angiotensin converting enzyme (ACE) inhibitor, *e.g.,* fosinopril, captopril, ramipril, enalapril, lisinopril, and quinapril; an angiotensin II receptor antagonist (also known as an angiotensin receptor blocker), *e.g.,* losartan, valsartan, olmesartan, eprosartan, and azilsartan; a beta-blocker, such as a beta-1 selective beta-blocker, *e.g.,* atenolol, metoprolol, propranolol, bisoprolol, and timolol, an alpha-1 receptor beta-blocker, *e.g.,* labetalol, esmolol, and carvedilol, an intrinsic sympathomimetic beta-blocker, *e.g.,* acebutolol and pindolol; a vasodialator, *e.g.,* hydralazine, minoxidil, sodium nitroprusside, and nitroglycerin; a calcium channel blocker, *e.g.,* nifedipine, clevidipine, amlodipine, felodipine, diltiazem, nicardipine, and verapamil; an aldosterone antagonist, such as a selective aldosterone antagonist, *e.g.,* eplerenone and spironolactone; an alpha$_2$-agonist, such as a central-acting alpha$_2$-agonist, *e.g.,* methyldopa, clonidine, and guanfacine, a renin inhibitor, *e.g.,* aliskiren; an alpha-blocker, *e.g.,* prazosin, terazosin, and doxazosin; a peripheral acting adrenergic agent, *e.g.,* reserpine; a selective D1 receptor partial agonist, *e.g.,* fenoldopam mesylate; a nonselective alpha-adrenergic antagonist, *e.g.,* phentolamine; a synthetic, steroidal antimineralocorticoid agent, *e.g.,* spironolactone, or a combination of any of the foregoing; and a therapeutic agent formulated as a combination of agents, *e.g.,* a combination of amlodipine/benazepril (Lotrel), amlodipine/olmesartan (Azor), amlodipine/telmisartan (Twynsta), amlodipine/valsartan (Exforge), amlodipine/valsartan/hydrochlorothiazide (Exforge HCT), amlodipine/aliskiren (Tekamlo), amlodipine/aliskiren/hydrochlorothiazide (Amturnide), olmesartan/amlodipine/hydrochlorothiazide (Tribenzor), trandolapril/verapamil (Tarka), benazepril/hydrochlorothiazide (Lotensin HCT), captopril/hydrochlorothiazide

(Capozide), enalapril/hydrochlorothiazide (Vaseretic), fosinopril/hydrochlorothiazide, lisinopril/hydrochlorothiazide (Prinzide, Zestoretic), moexipril/hydrochlorothiazide (Uniretic), quinapril/hydrochlorothiazide (Accuretic), candesartan/hydrochlorothiazide (Atacand HCT), eprosartan/hydrochlorothiazide (Teveten HCT), irbesartan/hydrochlorothiazide (Avalide), losartan/hydrochlorothiazide (Hyzaar), olmesartan/hydrochlorothiazide (Benicar HCT), telmisartan/hydrochlorothiazide (Micardis HCT), valsartan/hydrochlorothiazide (Diovan HCT), atenolol/chlorthalidone (Tenoretic), bisoprolol/hydrochlorothiazide (Ziac), metoprolol/hydrochlorothiazide (Lopressor HCT), nadolol/bendroflumethiazide (Corzide), propranolol/hydrochlorothiazide, aliskiren/hydrochlorothiazide (Tekturna HCT), clonidine/chlorthalidone (Clorpres), spironolactone/hydrochlorothiazide (Aldactazide), triamterene/hydrochlorothiazide (Dyazide, Maxzide), methyldopa/hydrochlorothiazide, and amiloride/hydrochlorothiazide, or other therapeutic agents for treating a AGT-associated disease.

The iRNA agent and an additional therapeutic agent and/or treatment may be administered at the same time and/or in the same combination, *e.g.*, parenterally, or the additional therapeutic agent can be administered as part of a separate composition or at separate times and/or by another method known in the art or described herein.

The present invention also provides methods of using an iRNA agent of the invention and/or a composition containing an iRNA agent of the invention to reduce and/or inhibit AGT expression in a cell. In other aspects, the present invention provides an iRNA of the invention and/or a composition comprising an iRNA of the invention for use in reducing and/or inhibiting AGT expression in a cell. In yet other aspects, use of an iRNA of the invention and/or a composition comprising an iRNA of the invention for the manufacture of a medicament for reducing and/or inhibiting AGT expression in a cell are provided.

The methods and uses include contacting the cell with an iRNA, *e.g.,* a dsRNA, of the invention and maintaining the cell for a time sufficient to obtain degradation of the mRNA transcript of an AGT gene, thereby inhibiting expression of the AGT gene in the cell.

Reduction in gene expression can be assessed by any methods known in the art. For example, a reduction in the expression of AGT may be determined by determining the mRNA expression level of AGT using methods routine to one of ordinary skill in the art, *e.g.,* northern blotting, qRT-PCR, by determining the protein level of AGT using methods routine to one of ordinary skill in the art, such as western blotting, immunological techniques, flow cytometry methods, ELISA, and/or by determining a biological activity of AGT.

In the methods and uses of the invention the cell may be contacted *in vitro* or *in vivo*, *i.e.*, the cell may be within a subject.

A cell suitable for treatment using the methods of the invention may be any cell that expresses an AGT gene. A cell suitable for use in the methods and uses of the invention may

be a mammalian cell, *e.g.,* a primate cell (such as a human cell or a non-human primate cell, *e.g.*, a monkey cell or a chimpanzee cell), a non-primate cell (such as a cow cell, a pig cell, a camel cell, a llama cell, a horse cell, a goat cell, a rabbit cell, a sheep cell, a hamster, a guinea pig cell, a cat cell, a dog cell, a rat cell, a mouse cell, a lion cell, a tiger cell, a bear cell, or a buffalo cell), a bird cell (*e.g.*, a duck cell or a goose cell), or a whale cell. In one embodiment, the cell is a human cell, *e.g.,* a human liver cell.

AGT expression may be inhibited in the cell by at least about 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%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or about 100%. In preferred embodiments, the AGT level is reduced by at least 20%.

The *in vivo* methods and uses of the invention may include administering to a subject a composition containing an iRNA, where the iRNA includes a nucleotide sequence that is complementary to at least a part of an RNA transcript of the AGT gene of the mammal to be treated. When the organism to be treated is a human, the composition can be administered by any means known in the art including, but not limited to subcutaneous, intravenous, oral, intraperitoneal, or parenteral routes, including intracranial (*e.g.*, intraventricular, intraparenchymal and intrathecal), intramuscular, transdermal, airway (aerosol), nasal, rectal, and topical (including buccal and sublingual) administration. In certain embodiments, the compositions are administered by subcutaneous or intravenous infusion or injection.

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

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

A higher dose may be administered initially (*i.e.*, a loading dose), followed by a lower dosage for a sustained period of time.

The mode of administration may be chosen based upon whether local or systemic treatment is desired and based upon the area to be treated. The route and site of administration may be chosen to enhance targeting.

In one aspect, the present invention also provides methods for inhibiting the expression of an AGT gene in a mammal, *e.g.,* a human. The present invention also provides a composition comprising an iRNA, *e.g.,* a dsRNA, that targets an AGT gene in a cell of a mammal for use in inhibiting expression of the AGT gene in the mammal. In another aspect, the present invention provides use of an iRNA, *e.g.,* a dsRNA, that targets an AGT gene in a cell of a mammal in the manufacture of a medicament for inhibiting expression of the AGT gene in the mammal.

The methods and uses include administering to the mammal, *e.g.,* a human, a composition comprising an iRNA, *e.g.,* a dsRNA, that targets an AGT gene in a cell of the mammal and maintaining the mammal for a time sufficient to obtain degradation of the mRNA transcript of the AGT gene, thereby inhibiting expression of the AGT gene in the mammal.

Reduction in gene expression can be assessed in peripheral blood sample of the iRNA-administered subject by any methods known it the art, *e.g.* qRT-PCR, described herein. Reduction in protein production can be assessed by any methods known it the art and by methods, *e.g.*, ELISA or western blotting, described herein. In one embodiment, a puncture liver biopsy sample serves as the tissue material for monitoring the reduction in AGT gene and/or protein expression. In another embodiment, a blood sample serves as the tissue material for monitoring the reduction in AGT gene and/or protein expression.

In one embodiment, verification of RISC medicated cleavage of target *in vivo* following administration of iRNA agent is done by performing 5'-RACE or modifications of the protocol as known in the art (Lasham A *et al.*, (2010) *Nucleic Acid Res.*, 38 (3) p-e19) (Zimmermann *et al.* (2006) *Nature* 441: 111-4).

This invention is further illustrated by the following examples which should not be construed as limiting. The entire contents of all references, patents and published patent applications cited throughout this application, as well as the Figures and the Sequence Listing, are hereby incorporated herein by reference.

EXAMPLES

Example 1. iRNA Synthesis

Source of reagents

Where the source of a reagent is not specifically given herein, such reagent can be obtained from any supplier of reagents for molecular biology at a quality/purity standard for application in molecular biology.

Transcripts

siRNA design was carried out to identify siRNAs targeting human (*Homo sapiens*), cynomolgus monkey (*Macaca fascicularis*; henceforth "cyno"), mouse (*Mus musculus*), and rat (*Rattus norvegicus*) AGT transcripts annotated in the NCBI Gene database (www.ncbi.nlm.nih.gov/gene/). Design used the following transcripts from NCBI: Human - NM_000029.3; Monkey - AB170313.1; Mouse - NM_007428.3. The cynomolgus monkey transcript was extended using sequence obtained from a liver-derived cDNA library. Due to high primate / rodent sequence divergence, siRNA duplexes were designed in separate batches, including but not limited to batches containing duplexes matching human and monkey transcripts only and mouse transcript only. All siRNA duplexes were designed that shared 100% identity to the listed human transcript and other species transcripts considered in each design batch.

siRNA Design, Specificity, and Efficacy Prediction

The predicted specificity of all possible 19mers was predicted from each sequence. Candidate 19mers were then selected that lacked repeats longer than seven nucleotides. These 706 candidate human/monkey and 1815 mouse siRNAs were used in comprehensive searches against the appropriate transcriptomes (defined as the set of NM_ and XM_ records within the human, monkey, or mouse NCBI Refseq sets) using an exhaustive "brute-force" algorithm implemented in the python script 'BruteForce.py'. The script next parsed the transcript-oligo alignments to generate a score based on the position and number of mismatches between the siRNA and any potential "off-target" transcript. The off-target score was weighted to emphasize differences in the "seed region" of siRNAs, in positions 2-9 from the 5' end of the molecule. Each oligo-transcript pair from the brute-force search was given a mismatch score by summing the individual mismatch scores; mismatches in the position 2-9 were counted as 2.8, mismatches in the cleavage site positions 10-11 were counted as 1.2, and mismatches in region 12-19 counted as 1.0. An additional off-target prediction was carried out by comparing the frequency of heptamers and octamers derived from 3 distinct, seed-derived hexamers of each oligo. The hexamers from positions 2-7 relative to the 5' start

is used to create 2 heptamers and one octamer. "Heptamer1" was created by adding a 3' A to the hexamer; "heptamer2" was created by adding a 5' A to the hexamer; the octamer was created by adding an A to both 5' and 3' ends of the hexamer. The frequency of octomers and heptamers in the human, monkey, or mouse 3'UTRome (defined as the subsequence of the transcriptome from NCBI's Refseq database where the end of the coding region, the 'CDS', is clearly defined) was pre-calculated. The octamer frequency was normalized to the heptamer frequency using the median value from the range of octamer frequencies. A "mirSeedScore" was then calculated by calculating the sum of ((3 X normalized octomer count) + (2 X heptamer2 count) + (1 X heptamer1 count)).

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

Candidate GalNAc-conjugated duplexes, 21 and 23 nucleotides long on the sense and antisense strands, respectively, were designed by extending antisense 19mers four additional nucleotides in the 3' direction (preserving perfect complementarity with the target transcript). The sense strand was specified as the reverse complement of the first 21 nucleotides of the antisense 23mer. Duplexes were selected that maintained perfect matches to all selected species transcripts across all 23 nucleotides.

siRNA sequence selection

A total of 117 sense and 117 antisense derived human/monkey and 42 sense and 42 antisense derived mouse siRNA 19mer oligos were synthesized and formed into GalNAc-conjugated duplexes. A total of 38 sense and 38 antisense derived human/monkey 21/23mer oligos and a total of 26 mouse 21/23mer oligos were synthesized and formed into GalNAc-conjugated duplexes.

A detailed list of the unmodified 19mer AGT sense and antisense strand sequences is shown in Table 3.

A detailed list of the modified 19mer AGT sense and antisense strand sequences is shown in Table 4.

A detailed list of the unmodified 21/23mer AGT sense and antisense strand sequences is shown in Table 7.

A detailed list of the modified 21/23mer AGT sense and antisense strand sequences is shown in Table 8.

A detailed list of unmodified 19mer AGT sense and antisense strand sequences is shown in Table 11.

A detailed list of the unmodified 21/23mer AGT sense and antisense strand sequences is shown in Table 13.

A detailed list of the modified 21/23mer AGT sense and antisense strand sequences is shown in Table 15.

siRNA Synthesis

General Small and Medium Scale RNA Synthesis Procedure

RNA oligonucleotides are synthesized at scales between 0.2–500 µmol using commercially available 5'-*O*-(4,4'-dimethoxytrityl)-2'-*O*-t-butyldimethylsilyl-3'-*O*-(2-cyanoethyl-*N,N*-diisopropyl)phosphoramidite monomers of uridine, 4-*N*-acetylcytidine, 6-*N*-benzoyladenosine and 2-*N*-isobutyrylguanosine and the corresponding 2'-*O*-methyl and 2'-fluoro phosphoramidites according to standard solid phase oligonucleotide synthesis protocols. The amidite solutions are prepared at 0.1-0.15 M concentration and 5-ethylthio-1H-tetrazole (0.25-0.6 M in acetonitrile) is used as the activator. Phosphorothioate backbone modifications are introduced during synthesis using 0.2 M phenylacetyl disulfide (PADS) in lutidine:acetonitrile (1:1) (v;v) or 0.1 M 3-(dimethylaminomethylene) amino-3H-1,2,4-dithiazole-5-thione (DDTT) in pyridine for the oxidation step. After completion of synthesis, the sequences are cleaved from the solid support and deprotected using methylamine followed by triethylamine.3HF to remove any 2'-*O*-t-butyldimethylsilyl protecting groups present.

For synthesis scales between 5–500 µmol and fully 2' modified sequences (2'-fluoro and/ or 2'-*O*-methyl or combinations thereof) the oligonucleotides are deprotected using 3:1 (v/v) ethanol and concentrated (28-32%) aqueous ammonia either at 35°C 16 h or 55°C for 5.5 h. Prior to ammonia deprotection the oligonucleotides are treated with 0.5 M piperidine in acetonitrile for 20 min on the solid support. The crude oligonucleotides are analyzed by LC–MS and anion-exchange HPLC (IEX-HPLC). Purification of the oligonucleotides is carried out by IEX HPLC using: 20 mM phosphate, 10%-15% ACN, pH = 8.5 (buffer A) and 20 mM phosphate, 10%-15% ACN, 1 M NaBr, pH = 8.5 (buffer B). Fractions are analyzed for purity by analytical HPLC. The product-containing fractions with suitable purity are pooled and concentrated on a rotary evaporator prior to desalting. The samples are desalted by size exclusion chromatography and lyophilized to dryness. Equal molar amounts of sense and antisense strands are annealed in 1x PBS buffer to prepare the corresponding siRNA duplexes.

For small scales (0.2–1 µmol), synthesis is performed on a MerMade 192 synthesizer in a 96 well format. In case of fully 2'-modified sequences (2'-fluoro and/or 2'-*O*-methyl or

combinations thereof) the oligonucleotides are deprotected using methylamine at room temperature for 30-60 min followed by incubation at 60°C for 30 min or using 3:1 (v/v) ethanol and concentrated (28-32%) aqueous ammonia at room temperature for 30-60 min followed by incubation at 40°C for 1.5 hours. The crude oligonucleotides are then precipitated in a solution of acetonitrile: acetone (9:1) and isolated by centrifugation and decanting the supernatant. The crude oligonucleotide pellet is re-suspended in 20 mM NaOAc buffer and analyzed by LC-MS and anion exchange HPLC. The crude oligonucleotide sequences are desalted in 96 deep well plates on a 5 mL HiTrap Sephadex G25 column (GE Healthcare). In each well about 1.5 mL samples corresponding to an individual sequence is collected. These purified desalted oligonucleotides are analyzed by LC-MS and anion exchange chromatography. Duplexes are prepared by annealing equimolar amounts of sense and antisense sequences on a Tecan robot. Concentration of duplexes is adjusted to 10 μM in 1x PBS buffer.

Synthesis of GalNAc-Conjugated Oligonucleotides for *In Vivo* Analysis

Oligonucleotides conjugated with GalNAc ligand at their 3'-terminus are synthesized at scales between 0.2–500 μmol using a solid support pre-loaded with a Y-shaped linker bearing a 4,4'-dimethoxytrityl (DMT)-protected primary hydroxy group for oligonucleotide synthesis and a GalNAc ligand attached through a tether.

For synthesis of GalNAc conjugates in the scales between 5–500 μmol, the above synthesis protocol for RNA is followed with the following adaptions: For polystyrene-based synthesis supports 5% dichloroacetic acid in toluene is used for DMT-cleavage during synthesis. Cleavage from the support and deprotection is performed as described above. Phosphorothioate-rich sequences (usually > 5 phorphorothioates) are synthesized without removing the final 5'-DMT group ("DMT-on") and, after cleavage and deprotection as described above, purified by reverse phase HPLC using 50 mM ammonium acetate in water (buffer A) and 50 mM ammoniumacetate in 80% acetonitirile (buffer B). Fractions are analyzed for purity by analytical HPLC and/or LC-MS. The product-containing fractions with suitable purity are pooled and concentrated on a rotary evaporator. The DMT-group is removed using 20%-25% acetic acid in water until completion. The samples are desalted by size exclusion chromatography and lyophilized to dryness. Equal molar amounts of sense and antisense strands are annealed in 1x PBS buffer to prepare the corresponding siRNA duplexes.

For small scale synthesis of GalNAc conjugates (0.2–1 μmol), including sequences with multiple phosphorothioate linkages, the protocols described above for synthesis of RNA or fully 2'-F/2'-OMe-containing sequences on MerMade platform are applied. Synthesis is

performed on pre-packed columns containing GalNAc-functionalized controlled pore glass support.

Example 2. *In vitro* screening of siRNA duplexes

Cell culture and 96-well transfections

Hep3B cells (ATCC, Manassas, VA) were grown to near confluence at 37°C in an atmosphere of 5% CO_2 in Eagle's Minimum Essential Medium (ATCC) supplemented with 10% FBS, streptomycin, and glutamine (ATCC) before being released from the plate by trypsinization. Cells were washed and re-suspended at 0.125 x10^6 cells/ml. During transfections, cells were plated onto a 96-well plate with about 20,000 cells per well.

Transfection was carried out by adding 14.8 µl of Opti-MEM plus 0.2 µl of Lipofectamine RNAiMax per well (Invitrogen™, Carlsbad CA. catalog number 13778-150) to 5 µl of each siRNA duplex to an individual well in a 96-well plate. The mixture was then incubated at room temperature for 20 minutes. Eighty µl of complete growth media without antibiotic containing the appropriate cell number was then added to the siRNA mixture. Cells were incubated for 24 hours prior to RNA purification.

Single dose experiments were performed at 10nM and 0.01nM final duplex concentration. Dose response experiments were done at 10, 1.67, 0.28, 0.046, 0.0077, 0.0013, 0.00021, 0.000036 nM final duplex concentration.

Cell culture and 384-well transfections

Hep3B cells (ATCC, Manassas, VA) were grown to near confluence at 37°C in an atmosphere of 5% CO_2 in Eagle's Minimum Essential Medium (ATCC®) supplemented with 10% FBS, streptomycin, and glutamine (ATCC®) before being released from the plate by trypsinization. Cells were washed and re-suspended at 0.125 x10^6 cells/ml. During transfections, cells were plated onto a 384-well plate with about 5,000 cells per well.

Transfection was carried out by adding 4.9 µl of Opti-MEM plus 0.1 µl of Lipofectamine RNAiMax per well (Invitrogen™, Carlsbad CA. catalog number 13778-150) to 5 µl of each siRNA duplex to an individual well in a 96-well plate. The mixture was then incubated at room temperature for 20 minutes. Forty µl of complete growth media without antibiotic containing the appropriate cell number was then added to the siRNA mixture. Cells were incubated for 24 hours prior to RNA purification.

Single dose experiments were performed at 10nM and 0.01nM final duplex concentration. Dose response experiments were done at 10, 1.67, 0.28, 0.046, 0.0077, 0.0013, 0.00021, 0.000036 nM final duplex concentration

Total RNA isolation using DYNABEADS mRNA Isolation Kit (Invitrogen™, part #: 610-12) – 96-Well Isolation

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

cDNA synthesis using ABI High capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA, Cat #4368813)

A master mix of 2 µl 10X Buffer, 0.8 µl 25X dNTPs, 2 µl Random primers, 1 µl Reverse Transcriptase, 1 µl RNase inhibitor and 3.2 µl of H_2O per reaction were added into 10 µl total RNA. cDNA was generated using a Bio-Rad C-1000 or S-1000 thermal cycler (Hercules, CA) through the following steps: 25°C 10 min, 37°C 120 min, 85°C 5 sec, 4°C hold.

Total RNA isolation using DYNABEADS mRNA Isolation Kit (Invitrogen™, part #: 610-12)-384-well extraction

Cells were lysed in 50µl of Lysis/Binding Buffer. Magenetic Dynabeads were washed in Lysis/Binding Buffer and resuspended in the same. 25µl Lysis/Binding Buffer containing 2µl of Dynabeads were then added per well. After shaking plates for 10 minutes at "7" on a Vibratranslator (UnionScientific), an automated plate washing system was utilized (Biotek EL406 with Biostacker, and magnetic capture plate). Plates were then washed in a manner similar to that described for the 96-well process: twice with buffer A (90µl), once with buffer B (90µl), and twice with buffer C (100µl). The last wash was removed from the plate, and cDNA synthesis begun immediately.

cDNA synthesis using ABI High capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA, Cat #4368813) – 384-well synthesis

A master mix of 2 µl 10X Buffer, 0.8 µl 25X dNTPs, 2 µl Random primers, 1 µl Reverse Transcriptase, 1 µl RNase inhibitor and 13.2 µl of H_2O per reaction were added to the wells of a 384-well plate containing only extracted RNA and magnetic beads (20µl total volume) . cDNA was generated by incubation at 25°C for 10 min, 37°C for 120 min, and 85°C for 8 minutes.

Real time PCR:

Two µl of cDNA were added to a master mix containing 0.5µl human GAPDH TaqMan Probe (Applied Biosystems Cat #4326317E) and 0.5µl human AGT TaqMan probe (Applied Biosystems cat # Hs00174854m1), 2µL of nuclease-free water and 5µl Lightcycler 480 probe master mix (Roche Cat #04887301001) per well in a 384 well plates (Roche cat # 04887301001). qPCR was performed in a LightCycler 480 real-time PCR machine (Roche). To calculate relative fold change, data were analyzed using the ΔΔCt method and normalized to assays performed with cells transfected with 10nM AD-1955, or mock transfected cells. IC_{50}s were calculated using a 4 parameter fit model using XLFit and normalized to cells transfected with AD-1955 or mock-transfected.

The sense and antisense sequences of AD-1955 are:

SENSE: cuuAcGcuGAGuAcuucGAdTsdT (SEQ ID NO:13)

ANTISENSE: UCGAAGuACUcAGCGuAAGdTsdT (SEQ ID NO:14).

Table 5 shows the results of a single dose screen in Hep3B cells transfected using the 96-well method with the indicated 19mer AGT iRNAs. Data are expressed as percent of mRNA remaining relative to untreated cells.

Table 6 shows the dose response of Hep3B cells transfected using the 96-well method with the indicated 19mer AGT iRNAs. The indicated IC_{50} values represent the IC_{50} values relative to untreated cells.

Table 9 shows the results of a single dose screen in Hep3B cells transfected using the 384-well method with the indicated 21/23mer conjugate AGT iRNAs. Data are expressed as percent of mRNA remaining relative to untreated cells.

Table 10 shows the dose response of Hep3B cells transfected using the 384-well method with the indicated 21/23mer conjugate AGT iRNAs. The indicated IC_{50} values represent the IC_{50} values relative to untreated cells.

Table 12 shows the results of a single dose screen in Hep3B cells transfected using the 96-well method with the indicated 19mer AGT iRNAs. Data are expressed as percent of mRNA remaining relative to untreated cells.

Table 14 shows the results of a single dose, dose-reponse screen of hAGT knockdown with the indicated 21/23mer conjugate AGT iRNAs in mice infected with an AAV vector expressing hAGT.

Table 16 shows the results of a single dose, dose-reponse screen of hAGT knockdown with the indicated 21/23mer conjugate AGT iRNAs in mice infected with an AAV vector expressing hAGT.

Table 2. Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds.

Abbreviation	Nucleotide(s)
A	Adenosine-3'-phosphate
Af	2'-fluoroadenosine-3'-phosphate
Afs	2'-fluoroadenosine-3'-phosphorothioate
As	adenosine-3'-phosphorothioate
C	cytidine-3'-phosphate
Cf	2'-fluorocytidine-3'-phosphate
Cfs	2'-fluorocytidine-3'-phosphorothioate
Cs	cytidine-3'-phosphorothioate
G	guanosine-3'-phosphate
Gf	2'-fluoroguanosine-3'-phosphate
Gfs	2'-fluoroguanosine-3'-phosphorothioate
Gs	guanosine-3'-phosphorothioate
T	5'-methyluridine-3'-phosphate
Tf	2'-fluoro-5-methyluridine-3'-phosphate
Tfs	2'-fluoro-5-methyluridine-3'-phosphorothioate
Ts	5-methyluridine-3'-phosphorothioate
U	Uridine-3'-phosphate
Uf	2'-fluorouridine-3'-phosphate
Ufs	2'-fluorouridine -3'-phosphorothioate
Us	uridine -3'-phosphorothioate
N	any nucleotide (G, A, C, T or U)
a	2'-O-methyladenosine-3'-phosphate
as	2'-O-methyladenosine-3'- phosphorothioate
c	2'-O-methylcytidine-3'-phosphate
cs	2'-O-methylcytidine-3'- phosphorothioate
g	2'-O-methylguanosine-3'-phosphate

Abbreviation	Nucleotide(s)
gs	2'-O-methylguanosine-3'- phosphorothioate
t	2'-O-methyl-5-methyluridine-3'-phosphate
ts	2'-O-methyl-5-methyluridine-3'-phosphorothioate
u	2'-O-methyluridine-3'-phosphate
us	2'-O-methyluridine-3'-phosphorothioate
s	phosphorothioate linkage
L96	N-[tris(GalNAc-alkyl)-amidodecanoyl)]-4-hydroxyprolinol Hyp-(GalNAc-alkyl)3
(dt) or dT	deoxy-thymine
dC	2`-deoxycytidine-3`-phosphate
Y44	inverted abasic DNA (2-hydroxymethyl-tetrahydrofurane-5-phosphate)
(Tgn)	Thymidine-glycol nucleic acid (GNA) S-Isomer
P	Phosphate
VP	Vinyl-phosphate
(Aam)	2`-O-(N-methylacetamide)adenosine-3`-phosphate
(Aams)	2`-O-(N-methylacetamide)adenosine-3`-phosphorothioate
(Tgn)	Thymidine-glycol nucleic acid (GNA) S-Isomer
(Cgn)	Cytidine-glycol nucleic acid (GNA)

Table 3. Unmodified Sense and Antisense Strand Sequences of AGT dsRNAs (19mers)

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO
UM AD-56041.1	485-503	A-115161.1	UUCUGGGUACUACAGCAGA	15	A-115162.1	485-503	UCUGCUGUAGUACCCAGAA	131
UM AD-52431.1	491-509	A-107992.1	GUACUACAGCAGAAGGGUA	16	A-107993.1	491-509	UACCCUUCUGCUGUAGUAC	132
UM AD-56057.1	606-624	A-115229.1	GUGACCGGGUGUACAUACA	17	A-115230.1	606-624	UGUAUGUACACCCGGUCAC	133
UM AD-56047.1	635-653	A-115163.1	CUCGUCAUCCACAAUGAGA	18	A-115164.1	635-653	UCUCAUUGUGGAUGACGAG	134
UM AD-52437.1	643-661	A-107994.1	CCACAAUGAGAGUACCUGU	19	A-107995.1	643-661	ACAGGUACUCUCAUUGUGG	135
UM AD-56064.1	644-662	A-115247.1	CACAAUGAGAGUACCUGUG	20	A-115248.1	644-662	CACAGGUACUCUCAUUGUG	136
UM AD-56021.1	658-676	A-115123.1	CUGUGAGCAGCUGGCAAAG	21	A-115124.1	658-676	CUUUGCCAGCUGCUCACAG	137
UM AD-56067.1	741-759	A-115201.1	CUGUGGAUGAAAAGGCCCU	22	A-115202.1	741-759	AGGGCCUUUUCAUCCACAG	138
UM AD-56030.1	822-840	A-115173.1	UGGUCGGGAUGCUGGCCAA	23	A-115174.1	822-840	UUGGCCAGCAUCCCGACCA	139
UM AD-56034.1	825-843	A-115237.1	UCGGGAUGCUGGCCAACUU	24	A-115238.1	825-843	AAGUUGGCCAGCAUCCCGA	140
UM AD-52443.1	828-846	A-107996.1	GGAUGCUGGCCAACUUCUU	25	A-107997.1	828-846	AAGAAGUUGGCCAGCAUCC	141
UM AD-56017.1	834-852	A-115153.1	UGGCCAACUUCUUGGGCUU	26	A-115154.1	834-852	AAGCCCAAGAAGUUGGCCA	142
UM AD-52449.1	841-859	A-107998.1	CUUCUUGGGCUUCCGUAUA	27	A-107999.1	841-859	UAUACGGAAGCCCAAGAAG	143
UM AD-52455.1	844-862	A-108000.1	CUUGGGCUUCCGUAUAUAU	28	A-108001.1	844-862	AUAUAUACGGAAGCCCAAG	144
UM AD-52461.1	849-867	A-108002.1	GCUUCCGUAUAUAUGGCAU	29	A-108003.1	849-867	AUGCCAUAUAUACGGAAGC	145
UM AD-56025.1	855-873	A-115187.1	GUAUAUAUGGCAUGCACAG	30	A-115188.1	855-873	CUGUGCAUGCCAUAUAUAC	146
UM AD-52467.1	863-881	A-108004.1	GGCAUGCACAGUGAGCUAU	31	A-108005.1	863-881	AUAGCUCACUGUGCAUGCC	147
UM AD-56061.1	878-896	A-115199.1	CUAUGGGGCGUGGUCCAUG	32	A-115200.1	878-896	CAUGGACCACGCCCCAUAG	148
UM AD-52473.1	910-928	A-108006.1	CUCCCCAACGGCUGUCUUU	33	A-108007.1	910-928	AAAGACAGCCGUUGGGGAG	149
UM AD-56063.1	911-929	A-115231.1	UCCCCAACGGCUGUCUUUG	34	A-115232.1	911-929	CAAAGACAGCCGUUGGGGA	150
UM AD-56046.1	1002-1020	A-115241.1	CUUGGAAGGACAAGAACUG	35	A-115242.1	1002-1020	CAGUUCUUGUCCUUCCAAG	151
UM AD-52432.1	1214-1232	A-108008.1	CCACGCUCUCUGGACUUCA	36	A-108009.1	1214-1232	UGAAGUCCAGAGAGCGUGG	152
UM AD-52438.1	1247-1265	A-108010.1	GCUGCUGAGAAGAUUGACA	37	A-108011.1	1247-1265	UGUCAAUCUUCUCAGCAGC	153

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO
UM AD-56059.1	1248-1266	A-115167.1	CUGCUGAGAAGAUUGACAG	38	A-115168.1	1248-1266	CUGUCAAUCUUCUCAGCAG	154
UM AD-56016.1	1249-1267	A-115137.1	UGCUGAGAAGAUUGACAGG	39	A-115138.1	1249-1267	CCUGUCAAUCUUCUCAGCA	155
UM AD-56068.1	1250-1268	A-115217.1	GCUGAGAAGAUUGACAGGU	40	A-115218.1	1250-1268	ACCUGUCAAUCUUCUCAGC	156
UM AD-55989.1	1251-1269	A-115081.1	CUGAGAAGAUUGACAGGUU	41	A-115082.1	1251-1269	AACCUGUCAAUCUUCUCAG	157
UM AD-56040.1	1260-1278	A-115239.1	UUGACAGGUUCAUGCAGGC	42	A-115240.1	1260-1278	GCCUGCAUGAACCUGUCAA	158
UM AD-56069.1	1277-1295	A-115233.1	GCUGUGACAGGAUGGAAGA	43	A-115234.1	1277-1295	UCUUCCAUCCUGUCACAGC	159
UM AD-52444.1	1403-1421	A-108012.1	GAGUUCUGGGUGGACAACA	44	A-108013.1	1403-1421	UGUUGUCCACCCAGAACUC	160
UM AD-56033.1	1408-1426	A-115221.1	CUGGGUGGACAACAGCACC	45	A-115222.1	1408-1426	GGUGCUGUUGUCCACCCAG	161
UM AD-56058.1	1413-1431	A-115245.1	UGGACAACAGCACCUCAGU	46	A-115246.1	1413-1431	ACUGAGGUGCUGUUGUCCA	162
UM AD-52450.1	1417-1435	A-108014.1	CAACAGCACCUCAGUGUCU	47	A-108015.1	1417-1435	AGACACUGAGGUGCUGUUG	163
UM AD-55981.1	1566-1584	A-115141.1	UGGACAAGGUGGAGGGUCU	48	A-115142.1	1566-1584	AGACCCUCCACCUUGUCCA	164
UM AD-56032.1	1570-1588	A-115205.1	CAAGGUGGAGGGUCUCACU	49	A-115206.1	1570-1588	AGUGAGACCCUCCACCUUG	165
UM AD-56066.1	1572-1590	A-115185.1	AGGUGGAGGGUCUCACUUU	50	A-115186.1	1572-1590	AAAGUGAGACCCUCCACCU	166
UM AD-52456.1	1587-1605	A-108016.1	CUUUCCAGCAAAACUCCCU	51	A-108017.1	1587-1605	AGGGAGUUUUGCUGGAAAG	167
UM AD-56054.1	1591-1609	A-115181.1	CCAGCAAAACUCCCUCAAC	52	A-115182.1	1591-1609	GUUGAGGGAGUUUUGCUGG	168
UM AD-56035.1	1592-1610	A-115159.1	CAGCAAAACUCCCUCAACU	53	A-115160.1	1592-1610	AGUUGAGGGAGUUUUGCUG	169
UM AD-52462.1	1595-1613	A-108018.1	CAAAACUCCCUCAACUGGA	54	A-108019.1	1595-1613	UCCAGUUGAGGGAGUUUUG	170
UM AD-56026.1	1601-1619	A-115203.1	UCCCUCAACUGGAUGAAGA	55	A-115204.1	1601-1619	UCUUCAUCCAGUUGAGGGA	171
UM AD-56022.1	1602-1620	A-115139.1	CCCUCAACUGGAUGAAGAA	56	A-115140.1	1602-1620	UUCUUCAUCCAGUUGAGGG	172
UM AD-55983.1	1605-1623	A-115079.1	UCAACUGGAUGAAGAAACU	57	A-115080.1	1605-1623	AGUUUCUUCAUCCAGUUGA	173
UM AD-56028.1	1728-1746	A-115235.1	CCGAGCUGAACCUGCAAAA	58	A-115236.1	1728-1746	UUUUGCAGGUUCAGCUCGG	174
UM AD-55980.1	1729-1747	A-115125.1	CGAGCUGAACCUGCAAAAA	59	A-115126.1	1729-1747	UUUUUGCAGGUUCAGCUCG	175
UM AD-56036.1	1735-1753	A-115175.1	GAACCUGCAAAAAUUGAGC	60	A-115176.1	1735-1753	GCUCAAUUUUUUGCAGGUUC	176
UM AD-56014.1	1737-1755	A-115105.1	ACCUGCAAAAAUUGAGCAA	61	A-115106.1	1737-1755	UUGCUCAAUUUUUUGCAGGU	177
UM AD-56007.1	1738-1756	A-115087.1	CCUGCAAAAAUUGAGCAAU	62	A-115088.1	1738-1756	AUUGCUCAAUUUUUUGCAGG	178

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO
UM AD-56012.1	1739-1757	A-115073.1	CUGCAAAAAUUGAGCAAUG	63	A-115074.1	1739-1757	CAUUGCUCAAUUUUUGCAG	179
UM AD-56055.1	1740-1758	A-115197.1	UGCAAAAAUUGAGCAAUGA	64	A-115198.1	1740-1758	UCAUUGCUCAAUUUUUGCA	180
UM AD-56029.1	1741-1759	A-115157.1	GCAAAAAUUGAGCAAUGAC	65	A-115158.1	1741-1759	GUCAUUGCUCAAUUUUUGC	181
UM AD-52469.1	1767-1785	A-108036.1	GGGUGGGGGAGGUGCUGAA	66	A-108037.1	1767-1785	UUCAGCACCUCCCCCACCC	182
UM AD-56053.1	1810-1828	A-115165.1	GGAUGAGAGAGAGCCCACA	67	A-115166.1	1810-1828	UGUGGGCUCUCUCUCAUCC	183
UM AD-52468.1	1879-1897	A-108020.1	CCGCCCAUUCCUGUUUUGCU	68	A-108021.1	1879-1897	AGCAAACAGGAAUGGGCGG	184
UM AD-56045.1	1885-1903	A-115225.1	AUUCCUGUUUUGCUGUGUAU	69	A-115226.1	1885-1903	AUACACAGCAAACAGGAAU	185
UM AD-56056.1	1887-1905	A-115213.1	UCCUGUUUUGCUGUGUAUGA	70	A-115214.1	1887-1905	UCAUACACAGCAAACAGGA	186
UM AD-56010.1	1891-1909	A-115135.1	GUUUUGCUGUGUAUGAUCAA	71	A-115136.1	1891-1909	UUGAUCAUACACAGCAAAC	187
UM AD-56015.1	1892-1910	A-115121.1	UUUGCUGUGUAUGAUCAAA	72	A-115122.1	1892-1910	UUUGAUCAUACACAGCAAA	188
UM AD-56039.1	2070-2088	A-115223.1	CCCCCAGUCUCCCACCUUU	73	A-115224.1	2070-2088	AAAGGUGGGAGACUGGGGG	189
UM AD-55991.1	2080-2098	A-115113.1	CCCACCUUUUCUUCUAAUG	74	A-115114.1	2080-2098	CAUUAGAAGAAAAAGGUGGG	190
UM AD-52474.1	2081-2099	A-108022.1	CCACCUUUUCUUCUAAUGA	75	A-108023.1	2081-2099	UCAUUAGAAGAAAAAGGUGG	191
UM AD-56024.1	2082-2100	A-115171.1	CACCUUUUCUUCUAAUGAG	76	A-115172.1	2082-2100	CUCAUUAGAAGAAAAAGGUG	192
UM AD-52433.1	2125-2143	A-108024.1	GUUUCUCCUUGGUCUAAGU	77	A-108025.1	2125-2143	ACUUAGACCAAGGAGAAAC	193
UM AD-56037.1	2199-2217	A-115191.1	UUGCUGGGUUUAUUUUAGA	78	A-115192.1	2199-2217	UCUAAAAUAAACCCAGCAA	194
UM AD-56049.1	2200-2218	A-115195.1	UGCUGGGUUUAUUUUAGAG	79	A-115196.1	2200-2218	CUCUAAAAUAAACCCAGCA	195
UM AD-52439.1	2201-2219	A-108026.1	GCUGGGUUUAUUUUAGAGA	80	A-108027.1	2201-2219	UCUCUAAAAUAAACCCAGC	196
UM AD-55978.1	2202-2220	A-115093.1	CUGGGUUUAUUUUAGAGAA	81	A-115094.1	2202-2220	UUCUCUAAAAUAAACCCAG	197
UM AD-55999.1	2203-2221	A-115147.1	UGGGUUUAUUUUAGAGAAU	82	A-115148.1	2203-2221	AUUCUCUAAAAUAAACCCA	198
UM AD-56050.1	2206-2224	A-115211.1	GUUUAUUUUAGAGAAUGGG	83	A-115212.1	2206-2224	CCCAUUCUCUAAAAUAAAC	199
UM AD-56031.1	2209-2227	A-115189.1	UAUUUUAGAGAAUGGGGGU	84	A-115190.1	2209-2227	ACCCCCAUUCUCUAAAAUA	200
UM AD-56027.1	2227-2245	A-115219.1	UGGGGAGGCAAGAACCAGU	85	A-115220.1	2227-2245	ACUGGUUCUUGCCUCCCCA	201
UM AD-55987.1	2230-2248	A-115143.1	GGAGGCAAGAACCAGUGUU	86	A-115144.1	2230-2248	AACACUGGUUCUUGCCUCC	202
UM AD-56043.1	2266-2284	A-115193.1	UCCAAAAAGAAUUCCAACC	87	A-115194.1	2266-2284	GGUUGGAAUUCUUUUUGGA	203

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO
UM AD-56001.1	2268-2286	A-115085.1	CAAAAAGAAUUCCAACCGA	88	A-115086.1	2268-2286	UCGGUUGGAAUUCUUUUUG	204
UM AD-52445.1	2279-2297	A-108028.1	CCAACCGACCAGCUUGUUU	89	A-108029.1	2279-2297	AAACAAGCUGGUCGGUUGG	205
UM AD-52451.1	2283-2301	A-108030.1	CCGACCAGCUUGUUUGUGA	90	A-108031.1	2283-2301	UCACAAACAAGCUGGUCGG	206
UM AD-52457.1	2284-2302	A-108032.1	CGACCAGCUUGUUUGUGAA	91	A-108033.1	2284-2302	UUCACAAACAAGCUGGUCG	207
UM AD-52463.1	2285-2303	A-108034.1	GACCAGCUUGUUUGUGAAA	92	A-108035.1	2285-2303	UUUCACAAACAAGCUGGUC	208
UM AD-55982.1	2290-2308	A-115063.1	GCUUGUUUGUGAAACAAAA	93	A-115064.1	2290-2308	UUUUGUUUCACAAACAAGC	209
UM AD-56019.1	2291-2309	A-115091.1	CUUGUUUGUGAAACAAAAA	94	A-115092.1	2291-2309	UUUUUGUUUCACAAACAAG	210
UM AD-55988.1	2292-2310	A-115065.1	UUGUUUGUGAAACAAAAAA	95	A-115066.1	2292-2310	UUUUUUGUUUCACAAACAA	211
UM AD-55994.1	2294-2312	A-115067.1	GUUUGUGAAACAAAAAAGU	96	A-115068.1	2294-2312	ACUUUUUUGUUUCACAAAC	212
UM AD-56013.1	2296-2314	A-115089.1	UUGUGAAACAAAAAAGUGU	97	A-115090.1	2296-2314	ACACUUUUUUGUUUCACAA	213
UM AD-56065.1	2299-2317	A-115169.1	UGAAACAAAAAAGUGUUCC	98	A-115170.1	2299-2317	GGAACACUUUUUUGUUUCA	214
UM AD-56008.1	2304-2322	A-115103.1	CAAAAAAGUGUUCCCUUUU	99	A-115104.1	2304-2322	AAAAGGGAACACUUUUUUG	215
UM AD-56048.1	2306-2324	A-115179.1	AAAAAGUGUUCCCUUUUCA	100	A-115180.1	2306-2324	UGAAAAGGGAACACUUUUU	216
UM AD-56003.1	2307-2325	A-115117.1	AAAAGUGUUCCCUUUUCAA	101	A-115118.1	2307-2325	UUGAAAAGGGAACACUUUU	217
UM AD-56051.1	2314-2332	A-115227.1	UUCCCUUUUCAAGUUGAGA	102	A-115228.1	2314-2332	UCUCAACUUGAAAAGGGAA	218
UM AD-56044.1	2317-2335	A-115209.1	CCUUUUCAAGUUGAGAACA	103	A-115210.1	2317-2335	UGUUCUCAACUUGAAAAGG	219
UM AD-55996.1	2320-2338	A-115099.1	UUUCAAGUUGAGAACAAAA	104	A-115100.1	2320-2338	UUUUGUUCUCAACUUGAAA	220
UM AD-56002.1	2321-2339	A-115101.1	UUCAAGUUGAGAACAAAAA	105	A-115102.1	2321-2339	UUUUUGUUCUCAACUUGAA	221
UM AD-55976.1	2323-2341	A-115061.1	CAAGUUGAGAACAAAAAUU	106	A-115062.1	2323-2341	AAUUUUUGUUCUCAACUUG	222
UM AD-56062.1	2325-2343	A-115215.1	AGUUGAGAACAAAAAUUGG	107	A-115216.1	2325-2343	CCAAUUUUUGUUCUCAACU	223
UM AD-56011.1	2326-2344	A-115151.1	GUUGAGAACAAAAAUUGGG	108	A-115152.1	2326-2344	CCCAAUUUUUGUUCUCAAC	224
UM AD-56009.1	2328-2346	A-115119.1	UGAGAACAAAAAUUGGGUU	109	A-115120.1	2328-2346	AACCCAAUUUUUGUUCUCA	225
UM AD-56020.1	2329-2347	A-115107.1	GAGAACAAAAAUUGGGUUU	110	A-115108.1	2329-2347	AAACCCAAUUUUUGUUCUC	226
UM AD-55979.1	2331-2349	A-115109.1	GAACAAAAAUUGGGUUUUA	111	A-115110.1	2331-2349	UAAAACCCAAUUUUUGUUC	227
UM AD-55997.1	2332-2350	A-115115.1	AACAAAAAUUGGGUUUUAA	112	A-115116.1	2332-2350	UUAAAACCCAAUUUUUGUU	228

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO
UM AD-56000.1	2333-2351	A-115069.1	ACAAAAAAUUGGGUUUUAAA	113	A-115070.1	2333-2351	UUUAAAACCCAAUUUUUGU	229
UM AD-56006.1	2334-2352	A-115071.1	CAAAAAAUUGGGUUUUUAAAA	114	A-115072.1	2334-2352	UUUUAAAAACCCAAUUUUUG	230
UM AD-55990.1	2339-2357	A-115097.1	AUUUGGGUUUUUAAAAAUUAAA	115	A-115098.1	2339-2357	UUUAAUUUUUAAAAACCCAAU	231
UM AD-55984.1	2340-2358	A-115095.1	UUGGGUUUUUAAAAAUUAAAG	116	A-115096.1	2340-2358	CUUUAAUUUUUAAAAACCCAA	232
UM AD-55995.1	2341-2359	A-115083.1	UGGGUUUUUAAAAAUUAAAGU	117	A-115084.1	2341-2359	ACUUUAAUUUUUAAAAACCCA	233
UM AD-56004.1	2346-2364	A-115133.1	UUUAAAAAUUAAAGUAUACA	118	A-115134.1	2346-2364	UGUAUACUUUAAUUUUUAAA	234
UM AD-56042.1	2347-2365	A-115177.1	UUAAAAAUUAAAGUAUACAU	119	A-115178.1	2347-2365	AUGUAUACUUUAAUUUUUAA	235
UM AD-55992.1	2384-2402	A-115129.1	UUGUAUUUAGUGUCUUGAA	120	A-115130.1	2384-2402	UUCAAGACACUAAAUACAA	236
UM AD-55977.1	2385-2403	A-115077.1	UGUAUUUAGUGUCUUGAAU	121	A-115078.1	2385-2403	AUUCAAGACACUAAAUACA	237
UM AD-56005.1	2391-2409	A-115149.1	UAGUGUCUUGAAUGUAAGA	122	A-115150.1	2391-2409	UCUUACAUUCAAGACACUA	238
UM AD-56052.1	2397-2415	A-115243.1	CUUGAAUGUAAGAACAUGA	123	A-115244.1	2397-2415	UCAUGUUCUUACAUUCAAG	239
UM AD-55985.1	2398-2416	A-115111.1	UUGAAUGUAAGAACAUGAC	124	A-115112.1	2398-2416	GUCAUGUUCUUACAUUCAA	240
UM AD-56038.1	2439-2457	A-115207.1	CUUAGUUUUUUCCACAGAU	125	A-115208.1	2439-2457	AUCUGUGGAAAAAACUAAG	241
UM AD-56023.1	2450-2468	A-115155.1	CCACAGAUGCUUGUGAUUU	126	A-115156.1	2450-2468	AAAUCACAAGCAUCUGUGG	242
UM AD-56018.1	2452-2470	A-115075.1	ACAGAUGCUUGUGAUUUUU	127	A-115076.1	2452-2470	AAAAAUCACAAGCAUCUGU	243
UM AD-56060.1	2497-2515	A-115183.1	CUGAAUUUCUGUUUGAAUG	128	A-115184.1	2497-2515	CAUUCAAACAGAAAUUCAG	244
UM AD-55993.1	2519-2537	A-115145.1	AACCAUAGCUGGUUAUUUC	129	A-115146.1	2519-2537	GAAAUAACCAGCUAUGGUU	245
UM AD-55986.1	2521-2539	A-115127.1	CCAUAGCUGGUUAUUUCUC	130	A-115128.1	2521-2539	GAGAAAUAACCAGCUAUGG	246

Table 4. Modified Sense and Antisense Strand Sequences of AGT dsRNAs (19mers)

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Antisense Sequence	SEQ ID NO.
AD-56041.1	A-115161.1	uucuGGGuAcuAcAGcAGAdTsdT	247	A-115162.1	UCUGCUGuAGuACCcAGAAdTsdT	363
AD-52431.1	A-107992.1	GuAcuAcAGcAGAAGGGuAdTsdT	248	A-107993.1	uACCCUUCUGCUGuAGuACdTsdT	364
AD-56057.1	A-115229.1	GuGAccGGGuGuAcAuAcAdTsdT	249	A-115230.1	UGuAUGuAcACCCGGUcACdTsdT	365
AD-56047.1	A-115163.1	cucGucAuccAcAAuGAGAdTsdT	250	A-115164.1	UCUcAUUGUGGAUGACGAGdTsdT	366
AD-52437.1	A-107994.1	ccAcAAuGAGAGuAccuGudTsdT	251	A-107995.1	AcAGGuACUCUcAUUGUGGdTsdT	367
AD-56064.1	A-115247.1	cAcAAuGAGAGuAccuGuGdTsdT	252	A-115248.1	cAcAGGuACUCUcAUUGUGdTsdT	368
AD-56021.1	A-115123.1	cuGuGAGcAGcuGGcAAAGdTsdT	253	A-115124.1	CUUUGCcAGCUGCUcAcAGdTsdT	369
AD-56067.1	A-115201.1	cuGuGGAuGAAAAGGcccudTsdT	254	A-115202.1	AGGGCCUUUUcAUCcAcAGdTsdT	370
AD-56030.1	A-115173.1	uGGucGGGAuGcuGGccAAdTsdT	255	A-115174.1	UUGGCcAGcAUCCCGACcAdTsdT	371
AD-56034.1	A-115237.1	ucGGGAuGcuGGccAAcuudTsdT	256	A-115238.1	AAGUUGGCcAGcAUCCCCGAdTsdT	372
AD-52443.1	A-107996.1	GGAuGcuGGccAAcuucuudTsdT	257	A-107997.1	AAGAAGUUGGCcAGcAUCCdTsdT	373
AD-56017.1	A-115153.1	uGGccAAcuucuuGGGcuudTsdT	258	A-115154.1	AAGCCcAAGAAGUUGGCcAdTsdT	374
AD-52449.1	A-107998.1	cuucuuGGGcuuccGuAuAdTsdT	259	A-107999.1	uAuACGGAAGCCcAAGAAGdTsdT	375
AD-52455.1	A-108000.1	cuuGGGcuuccGuAuAuAudTsdT	260	A-108001.1	AuAuAuACGGAAGCCcAAGdTsdT	376

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Antisense Sequence	SEQ ID NO.
AD-52461.1	A-108002.1	GcuuccGuAuAuAuGcAudTsdT	261	A-108003.1	AUGCcAuAuAuACGGAAGCdTsdT	377
AD-56025.1	A-115187.1	GuAuAuAuGcAuGcAcAGdTsdT	262	A-115188.1	CUGUGcAUGCcAuAuAuACdTsdT	378
AD-52467.1	A-108004.1	GGcAuGcAcAGuGAGcuAudTsdT	263	A-108005.1	AuAGCUcACUGUGcAUGCCdTsdT	379
AD-56061.1	A-115199.1	cuAuGGGGcGuGGuccAuGdTsdT	264	A-115200.1	cAUGGACcACGCCCcAuAGdTsdT	380
AD-52473.1	A-108006.1	cuccccAAcGGcuGucuuudTsdT	265	A-108007.1	AAAGAcAGCCGUUGGGGAGdTsdT	381
AD-56063.1	A-115231.1	ucccAAcGGcuGucuuuGdTsdT	266	A-115232.1	cAAAGAcAGCCGUUGGGGAdTsdT	382
AD-56046.1	A-115241.1	cuuGGAAGGAcAAGAAcuGdTsdT	267	A-115242.1	cAGUUCUUGUCCUUCcAAGdTsdT	383
AD-52432.1	A-108008.1	ccAcGcucucuGGAcuucAdTsdT	268	A-108009.1	UGAAGUCcAGAGAGCGUGGdTsdT	384
AD-52438.1	A-108010.1	GcuGcuGAGAAGAuuGAcAdTsdT	269	A-108011.1	UGUcAAUCUUCUCcAGcAGCdTsdT	385
AD-56059.1	A-115167.1	cuGcuGAGAAGAuuGAcAGdTsdT	270	A-115168.1	CUGUcAAUCUUCUCcAGcAGdTsdT	386
AD-56016.1	A-115137.1	uGcuGAGAAGAuuGAcAGGdTsdT	271	A-115138.1	CCUGUcAAUCUUCUCcAGcAdTsdT	387
AD-56068.1	A-115217.1	GcuGAGAAGAuuGAcAGGudTsdT	272	A-115218.1	ACCUGUcAAUCUUCUCcAGCdTsdT	388
AD-55989.1	A-115081.1	cuGAGAAGAuuGAcAGGuudTsdT	273	A-115082.1	AACCUGUcAAUCUUCUCcAGdTsdT	389
AD-56040.1	A-115239.1	uuGAcAGGuucAuGcAGGcdTsdT	274	A-115240.1	GCCUGcAUGAACCUGUcAAdTsdT	390
AD-56069.1	A-115233.1	GcuGuGAcAGGAuGGAAGAdTsdT	275	A-115234.1	UCUUCcAUCCUGUcAcAGCdTsdT	391
AD-52444.1	A-108012.1	GAGuucuGGGuGGAcAAcAdTsdT	276	A-108013.1	UGUUGUCcACCcAGAACUCdTsdT	392
AD-56033.1	A-115221.1	cuGGGuGGAcAAcAGcAccdTsdT	277	A-115222.1	GGUGCUGUUGUCcACCcAGdTsdT	393
AD-56058.1	A-115245.1	uGGAcAAcAGcAccucAGudTsdT	278	A-115246.1	ACUGAGGUGCUGUUGUCcAdTsdT	394
AD-52450.1	A-108014.1	cAAcAGcAccucAGuGucudTsdT	279	A-108015.1	AGAcACUGAGGUGCUGUUGdTsdT	395
AD-55981.1	A-115141.1	uGGAcAAGGuGGAGGGucudTsdT	280	A-115142.1	AGACCCUCCcACCUUGUCcAdTsdT	396
AD-56032.1	A-115205.1	cAAGGuGGAGGGucucAcudTsdT	281	A-115206.1	AGUGAGACCCUCCcACCUUGdTsdT	397
AD-56066.1	A-115185.1	AGGuGGAGGGucucAcuuudTsdT	282	A-115186.1	AAAGUGAGACCCUCCcACCUUdTsdT	398

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Antisense Sequence	SEQ ID NO.
AD-52456.1	A-108016.1	cuuuccAGcAAAAcucccudTsdT	283	A-108017.1	AGGGAGUUUUGCUGGAAAGdTsdT	399
AD-56054.1	A-115181.1	ccAGcAAAAcucccucAAcdTsdT	284	A-115182.1	GUUGAGGGAGUUUUGCUGGdTsdT	400
AD-56035.1	A-115159.1	cAGcAAAAcucccucAAcudTsdT	285	A-115160.1	AGUUGAGGGAGUUUUGCUGdTsdT	401
AD-52462.1	A-108018.1	cAAAAcucccucAAcuGGAdTsdT	286	A-108019.1	UCcAGUUGAGGGAGUUUUGdTsdT	402
AD-56026.1	A-115203.1	ucccucAAcuGGAuGAAGAdTsdT	287	A-115204.1	UCUUcAUCcAGUUGAGGGAdTsdT	403
AD-56022.1	A-115139.1	cccucAAcuGGAuGAAGAAdTsdT	288	A-115140.1	UUCUUcAUCcAGUUGAGGGdTsdT	404
AD-55983.1	A-115079.1	ucAAcuGGAuGAAGAAAcudTsdT	289	A-115080.1	AGUUUCUUcAUCcAGUUGAdTsdT	405
AD-56028.1	A-115235.1	ccGAGcuGAAccuGcAAAAAdTsdT	290	A-115236.1	UUUUGcAGGUUcAGCUCGGdTsdT	406
AD-55980.1	A-115125.1	cGAGcuGAAccuGcAAAAAdTsdT	291	A-115126.1	UUUUUGcAGGUUcAGCUCGdTsdT	407
AD-56036.1	A-115175.1	GAAccuGcAAAAAuuGAGcdTsdT	292	A-115176.1	GCUcAAUUUUUUGcAGGUUCdTsdT	408
AD-56014.1	A-115105.1	AccuGcAAAAAuuGAGcAAdTsdT	293	A-115106.1	UUGCUcAAUUUUUUGcAGGUUdTsdT	409
AD-56007.1	A-115087.1	ccuGcAAAAAuuGAGcAAudTsdT	294	A-115088.1	AUUGCUcAAUUUUUUGcAGGdTsdT	410
AD-56012.1	A-115073.1	cuGcAAAAAuuGAGcAAuGdTsdT	295	A-115074.1	cAUUGCUcAAUUUUUUGcAGdTsdT	411
AD-56055.1	A-115197.1	uGcAAAAAuuGAGcAAuGAdTsdT	296	A-115198.1	UcAUUGCUcAAUUUUUUGcAdTsdT	412
AD-56029.1	A-115157.1	GcAAAAAuuGAGcAAuGAcdTsdT	297	A-115158.1	GUcAUUGCUcAAUUUUUUGCdTsdT	413
AD-52469.1	A-108036.1	GGGuGGGGGAGGuGcuGAAdTsdT	298	A-108037.1	UUcAGcACCUCCCCCcACCCdTsdT	414
AD-56053.1	A-115165.1	GGAuGAGAGAGAGcccAcAdTsdT	299	A-115166.1	UGUGGGCUCUCUCUCcAUCCdTsdT	415
AD-52468.1	A-108020.1	ccGcccAuuccuGuuuGcudTsdT	300	A-108021.1	AGcAAAcAGGAAUGGGCGGdTsdT	416
AD-56045.1	A-115225.1	AuuccuGuuuGcuGuGuAudTsdT	301	A-115226.1	AuAcAcAGcAAAcAGGAAUdTsdT	417
AD-56056.1	A-115213.1	uccuGuuuGcuGuGuAuGAdTsdT	302	A-115214.1	UcAuAcAcAGcAAAcAGGAdTsdT	418
AD-56010.1	A-115135.1	GuuuGcuGuGuAuGAucAAdTsdT	303	A-115136.1	UUGAUcAuAcAcAGcAAACdTsdT	419
AD-56015.1	A-115121.1	uuuGcuGuGuAuGAucAAAdTsdT	304	A-115122.1	UUUGAUcAuAcAcAGcAAAdTsdT	420

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Antisense Sequence	SEQ ID NO.
AD-56039.1	A-115223.1	cccccAGucucccAccuuudTsdT	305	A-115224.1	AAAGGUGGGAGACUGGGGGdTsdT	421
AD-55991.1	A-115113.1	cccAccuuuucuucuAAuGdTsdT	306	A-115114.1	cAUuAGAAGAAAAGGUGGGdTsdT	422
AD-52474.1	A-108022.1	ccAccuuuucuucuAAuGAdTsdT	307	A-108023.1	UcAUuAGAAGAAAAGGUGGdTsdT	423
AD-56024.1	A-115171.1	cAccuuuucuucuAAuGAGdTsdT	308	A-115172.1	CUcAUuAGAAGAAAAGGUGdTsdT	424
AD-52433.1	A-108024.1	GuuucuccuuGGucuAAGudTsdT	309	A-108025.1	ACUuAGACcAAGGAGAAAACdTsdT	425
AD-56037.1	A-115191.1	uuGcuGGGuuuAuuuuAGAdTsdT	310	A-115192.1	UCuAAAAAuAAACCcAGcAAdTsdT	426
AD-56049.1	A-115195.1	uGcuGGGuuuAuuuuAGAGdTsdT	311	A-115196.1	CUCuAAAAAuAAACCcAGcAdTsdT	427
AD-52439.1	A-108026.1	GcuGGGuuuAuuuuAGAGAdTsdT	312	A-108027.1	UCUCuAAAAAuAAACCcAGCdTsdT	428
AD-55978.1	A-115093.1	cuGGGuuuAuuuuAGAGAAdTsdT	313	A-115094.1	UUCUCuAAAAAuAAACCcAGdTsdT	429
AD-55999.1	A-115147.1	uGGGuuuAuuuuAGAGAAudTsdT	314	A-115148.1	AUUCUCuAAAAAuAAACCcAdTsdT	430
AD-56050.1	A-115211.1	GuuuAuuuuAGAGAAuGGdTsdT	315	A-115212.1	CCcAUUCUCuAAAAAuAAACdTsdT	431
AD-56031.1	A-115189.1	uAuuuuAGAGAAuGGGGGudTsdT	316	A-115190.1	ACCCCcAUUCUCuAAAAAuAdTsdT	432
AD-56027.1	A-115219.1	uGGGGAGGcAAGAAccAGudTsdT	317	A-115220.1	ACUGGUUCUUGCCUCCCcAdTsdT	433
AD-55987.1	A-115143.1	GGAGGcAAGAAccAGuGuudTsdT	318	A-115144.1	AAcACUGGUUCUUGCCUCCdTsdT	434
AD-56043.1	A-115193.1	uccAAAAAGAAuuccAAccdTsdT	319	A-115194.1	GGUUGGAAUUCUUUUUGGAdTsdT	435
AD-56001.1	A-115085.1	cAAAAAGAAuuccAAccGAdTsdT	320	A-115086.1	UCGGUUGGAAUUCUUUUUGdTsdT	436
AD-52445.1	A-108028.1	ccAAccGAccAGcuuGuuudTsdT	321	A-108029.1	AAAcAAGCUGGUCGGUUGGdTsdT	437
AD-52451.1	A-108030.1	ccGAccAGcuuGuuuGuGAdTsdT	322	A-108031.1	UcAcAAAcAAGCUGGUCGGdTsdT	438
AD-52457.1	A-108032.1	cGAccAGcuuGuuuGuGAAdTsdT	323	A-108033.1	UUcAcAAAcAAGCUGGUCCGdTsdT	439
AD-52463.1	A-108034.1	GAccAGcuuGuuuGuGAAAdTsdT	324	A-108035.1	UUUcAcAAAcAAGCUGGUCdTsdT	440
AD-55982.1	A-115063.1	GcuuGuuuGuGAAAcAAAAdTsdT	325	A-115064.1	UUUUGUUUcAcAAAcAAGCdTsdT	441
AD-56019.1	A-115091.1	cuuGuuuGuGAAAcAAAAAdTsdT	326	A-115092.1	UUUUUGUUUcAcAAAcAAGdTsdT	442

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Antisense Sequence	SEQ ID NO.
AD-55988.1	A-115065.1	uuGuuuGuGAAAcAAAAAAdTsdT	327	A-115066.1	UUUUUUGUUUcAcAAAcAAdTsdT	443
AD-55994.1	A-115067.1	GuuuGuGAAAcAAAAAAGudTsdT	328	A-115068.1	ACUUUUUUGUUUcAcAAACdTsdT	444
AD-56013.1	A-115089.1	uuGuGAAAcAAAAAAGuGudTsdT	329	A-115090.1	AcACUUUUUUGUUUcAcAAdTsdT	445
AD-56065.1	A-115169.1	uGAAAcAAAAAAGuGuuccdTsdT	330	A-115170.1	GGAAcACUUUUUUGUUUcAdTsdT	446
AD-56008.1	A-115103.1	cAAAAAAGuGuucccuuuudTsdT	331	A-115104.1	AAAAGGGAAcACUUUUUUGdTsdT	447
AD-56048.1	A-115179.1	AAAAAGuGuucccuuuucAdTsdT	332	A-115180.1	UGAAAAGGGAAcACUUUUUUdTsdT	448
AD-56003.1	A-115117.1	AAAAGuGuucccuuuucAAdTsdT	333	A-115118.1	UUGAAAAGGGAAcACUUUUUdTsdT	449
AD-56051.1	A-115227.1	uucccuuuucAAGuuGAGAdTsdT	334	A-115228.1	UCUcAACUUGAAAAGGGAAdTsdT	450
AD-56044.1	A-115209.1	ccuuuucAAGuuGAGAAcAdTsdT	335	A-115210.1	UGUUCUcAACUUGAAAAGGdTsdT	451
AD-55996.1	A-115099.1	uuucAAGuuGAGAAcAAAAAdTsdT	336	A-115100.1	UUUUGUUCUcAACUUGAAAAdTsdT	452
AD-56002.1	A-115101.1	uucAAGuuGAGAAcAAAAAAdTsdT	337	A-115102.1	UUUUUGUUCUcAACUUGAAAdTsdT	453
AD-55976.1	A-115061.1	cAAGuuGAGAAcAAAAAAuudTsdT	338	A-115062.1	AAUUUUUGUUCUcAACUUGdTsdT	454
AD-56062.1	A-115215.1	AGuuGAGAAcAAAAAAuuGGdTsdT	339	A-115216.1	CcAAUUUUUGUUCUcAACUUdTsdT	455
AD-56011.1	A-115151.1	GuuGAGAAcAAAAAAuuGGGdTsdT	340	A-115152.1	CCcAAUUUUUGUUCUcAACdTsdT	456
AD-56009.1	A-115119.1	uGAGAAcAAAAAAuuGGGuudTsdT	341	A-115120.1	AACCcAAUUUUUGUUCUcAdTsdT	457
AD-56020.1	A-115107.1	GAGAAcAAAAAAuuGGGuuudTsdT	342	A-115108.1	AAACCcAAUUUUUGUUCUCdTsdT	458
AD-55979.1	A-115109.1	GAAcAAAAAAuuGGGuuuuAdTsdT	343	A-115110.1	uAAAACCcAAUUUUUGUUCdTsdT	459
AD-55997.1	A-115115.1	AAcAAAAAAuuGGGuuuuAAdTsdT	344	A-115116.1	UuAAAACCcAAUUUUUGUUdTsdT	460
AD-56000.1	A-115069.1	AcAAAAAAuuGGGuuuuAAAdTsdT	345	A-115070.1	UUuAAAACCcAAUUUUUGUdTsdT	461
AD-56006.1	A-115071.1	cAAAAAAuuGGGuuuuAAAAdTsdT	346	A-115072.1	UUUuAAAACCcAAUUUUUGdTsdT	462
AD-55990.1	A-115097.1	AuuGGGuuuuAAAAuuAAAdTsdT	347	A-115098.1	UUuAAUUUUuAAAACCcAAUdTsdT	463
AD-55984.1	A-115095.1	uuGGGuuuuAAAAuuAAAGdTsdT	348	A-115096.1	CUUuAAUUUUuAAAACCcAAdTsdT	464

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Antisense Sequence	SEQ ID NO.
AD-55995.1	A-115083.1	uGGGuuuuAAAAuuAAAGudTsdT	349	A-115084.1	ACUUuAAUUUUuAAAACCcAdTsdT	465
AD-56004.1	A-115133.1	uuuAAAAuuAAAGuAuAcAdTsdT	350	A-115134.1	UGuAuACUUuAAUUUuAAAAdTsdT	466
AD-56042.1	A-115177.1	uuAAAAuuAAAGuAuAcAudTsdT	351	A-115178.1	AUGuAuACUUuAAUUUuAAAdTsdT	467
AD-55992.1	A-115129.1	uuGuAuuuAGuGucuuGAAdTsdT	352	A-115130.1	UUcAAGAcACuAAAAuAcAAdTsdT	468
AD-55977.1	A-115077.1	uGuAuuuAGuGucuuGAAudTsdT	353	A-115078.1	AUUcAAGAcACuAAAAuAcAdTsdT	469
AD-56005.1	A-115149.1	uAGuGucuuGAAuGuAAGAdTsdT	354	A-115150.1	UCUuAcAUUcAAGAcACuAdTsdT	470
AD-56052.1	A-115243.1	cuuGAAuGuAAGAAcAuGAdTsdT	355	A-115244.1	UcAUGUUCUuAcAUUcAAGdTsdT	471
AD-55985.1	A-115111.1	uuGAAuGuAAGAAcAuGAcdTsdT	356	A-115112.1	GUcAUGUUCUuAcAUUcAAdTsdT	472
AD-56038.1	A-115207.1	cuuAGuuuuuuccAcAGAudTsdT	357	A-115208.1	AUCUGUGGAAAAAAACuAAGdTsdT	473
AD-56023.1	A-115155.1	ccAcAGAuGcuuGuGAuuudTsdT	358	A-115156.1	AAAUcAcAAGcAUCUGUGGdTsdT	474
AD-56018.1	A-115075.1	AcAGAuGcuuGuGAuuuuudTsdT	359	A-115076.1	AAAAAUcAcAAGcAUCUGUdTsdT	475
AD-56060.1	A-115183.1	cuGAAuuucuGuuuGAAuGdTsdT	360	A-115184.1	cAUUcAAAcAGAAAUUcAGdTsdT	476
AD-55993.1	A-115145.1	AAccAuAGcuGGuuAuuucdTsdT	361	A-115146.1	GAAAuAACcAGCuAUGGUUdTsdT	477
AD-55986.1	A-115127.1	ccAuAGcuGGuuAuuucucdTsdT	362	A-115128.1	GAGAAAuAACcAGCuAUGGdTsdT	478

Table 5. AGT single dose screen in Hep3B cells

	10nM Avg	10nM SD	0.1nM Avg	0.1nM SD	0.01nM Avg	0.01nM SD	Start relative to NM_000029.3
AD-52457.1	9.4	0.6	13.3	1.3	15.1	2.3	2284
AD-52438.1	3.4	0.1	12.2	1.8	17.7	1.7	1247
AD-52463.1	9.8	0.9	16.9	2.9	19.3	2.1	2285
AD-52433.1	7.4	1.5	14.4	1.0	24.8	1.3	2125
AD-52439.1	15.1	1.1	23.9	0.2	29.9	1.4	2201
AD-52449.1	5.7	0.6	22.7	1.2	42.4	5.3	841
AD-52451.1	10.4	0.5	29.0	1.1	47.4	1.1	2283
AD-52474.1	5.0	0.3	30.6	2.2	49.1	1.9	2081
AD-52462.1	6.1	0.1	23.7	2.7	50.8	1.6	1595
AD-52445.1	11.0	0.3	24.2	1.4	55.1	0.4	2279
AD-52456.1	11.9	0.3	38.7	0.5	71.7	1.4	1587
AD-52469.1	15.9	0.6	40.6	3.1	84.1	0.8	1767
AD-52461.1	62.8	1.1	78.5	0.3	85.0	0.6	849
AD-52443.1	16.9	0.0	49.4	2.0	88.4	3.0	828
AD-52468.1	27.6	1.5	85.1	3.7	91.6	1.4	1879
AD-52431.1	24.6	3.7	75.2	1.8	92.3	3.1	491
AD-52444.1	67.0	2.8	74.4	0.3	94.1	0.2	1403
AD-52455.1	57.0	0.5	89.5	4.1	94.4	1.6	844
AD-52432.1	70.6	2.3	93.6	8.2	95.7	3.7	1214
AD-52473.1	46.4	0.2	75.6	0.2	95.8	0.1	910
AD-52450.1	20.3	1.7	53.0	2.5	96.3	4.8	1417
AD-52437.1	36.3	4.1	86.6	0.6	96.6	0.9	643
AD-52467.1	59.5	0.8	94.5	1.7	102.9	5.1	863
AD-55976.1			3.6	5.8			2323
AD-55977.1			77.2	70.0			2385
AD-55978.1			8.3	11.8			2202
AD-55979.1			7.7	9.1			2331
AD-55980.1			14.1	17.4			1729
AD-55981.1			21.2	29.4			1566
AD-56023.1			74.1	77.1			2450
AD-56024.1			17.6	27.8			2082
AD-56025.1			66.5	75.0			855
AD-56026.1			13.7	20.2			1601
AD-56027.1			16.9	22.2			2227
AD-56028.1			63.8	74.0			1728
AD-55982.1			22.9	26.1			2290
AD-55983.1			6.2	8.7			1605
AD-55984.1			52.0	59.9			2340
AD-55985.1			70.1	65.1			2398
AD-55986.1			80.5	79.3			2521
AD-55987.1			12.5	15.5			2230

	10nM Avg	10nM SD	0.1nM Avg	0.1nM SD	0.01nM Avg	0.01nM SD	Start relative to NM_000029.3
AD-56029.1			51.3	62.2			1741
AD-56030.1			53.3	58.0			822
AD-56031.1			38.1	43.7			2204
AD-56032.1			12.6	15.3			1570
AD-56033.1			99.8	100.7			1408
AD-56034.1			87.8	93.0			825
AD-55988.1			46.4	49.5			2292
AD-55989.1			5.8	9.7			1251
AD-55990.1			6.5	5.0			2339
AD-55991.1			50.4	38.2			2080
AD-55992.1			76.4	60.5			2384
AD-55993.1			66.5	62.9			2519
AD-56035.1			17.9	17.6			1592
AD-56036.1			47.7	59.9			1735
AD-56037.1			80.8	83.5			2199
AD-56038.1			84.8	90.4			2439
AD-56039.1			47.9	66.7			2070
AD-56040.1			95.0	98.3			1260
AD-55994.1			3.6	5.5			2294
AD-55995.1			31.4	47.8			2341
AD-55996.1			5.1	5.0			2320
AD-55997.1			83.3	76.6			2332
AD-55999.1			74.6	75.0			2203
AD-56041.1			21.9	21.4			485
AD-56042.1			73.3	73.5			2347
AD-56043.1			53.1	57.8			2266
AD-56044.1			12.0	13.9			2317
AD-56045.1			41.7	48.8			1885
AD-56046.1			83.0	90.1			1002
AD-56000.1			13.3	20.3			2333
AD-56001.1			4.7	5.7			2268
AD-56002.1			5.4	6.6			2321
AD-56003.1			4.2	4.4			2307
AD-56004.1			54.0	68.5			2346
AD-56005.1			60.2	62.2			2391
AD-56047.1			24.7	28.2			635
AD-56048.1			7.1	7.4			2306
AD-56049.1			73.0	62.6			2200
AD-56050.1			96.4	102.1			2206
AD-56051.1			17.4	23.0			2314
AD-56052.1			85.1	102.5			2397
AD-56006.1			8.1	10.7			2334

	10nM Avg	10nM SD	0.1nM Avg	0.1nM SD	0.01nM Avg	0.01nM SD	Start relative to NM_000029.3
AD-56007.1			17.8	19.1			1738
AD-56008.1			5.4	4.8			2304
AD-56009.1			12.2	14.4			2328
AD-56010.1			62.1	69.0			1891
AD-56011.1			35.3	40.3			2326
AD-56053.1			5.0	6.7			1810
AD-56054.1			30.9	35.5			1591
AD-56055.1			61.4	50.9			1740
AD-56056.1			83.6	94.0			1887
AD-56057.1			85.7	97.9			606
AD-56058.1			68.6	87.4			1413
AD-56012.1			35.0	47.1			1739
AD-56013.1			49.2	57.6			2296
AD-56014.1			54.4	60.3			1737
AD-56015.1			42.2	46.7			1892
AD-56016.1			11.2	15.6			1249
AD-56017.1			10.6	12.9			834
AD-56059.1			37.3	45.2			1248
AD-56060.1			94.1	94.3			2497
AD-56061.1			99.8	94.6			878
AD-56062.1			19.2	32.2			2325
AD-56063.1			102.2	102.8			911
AD-56064.1			80.2	92.3			644
AD-56018.1			72.0	74.5			2452
AD-56019.1			25.2	27.7			2291
AD-56020.1			10.2	15.3			2329
AD-56021.1			36.0	40.9			658
AD-56022.1			37.5	52.7			1602
AD-56065.1			56.5	71.9			2299
AD-56066.1			12.3	18.9			1572
AD-56067.1			64.9	81.8			741
AD-56068.1			68.6	82.1			1250
AD-56069.1			48.9	72.7			1277

Table 6- AGT IC_{50} data in Hep3B Cells

Duplex Name	IC_{50} (nM)
AD-52431	5.719
AD-52432	>10nM
AD-52433	0.057
AD-52437	>10nM

AD-52438	0.063
AD-52439	0.192
AD-52443	0.504
AD-52444	>10nM
AD-52445	0.183
AD-52449	0.211
AD-52450	2.052
AD-52451	0.318
AD-52455	>10nM
AD-52456	1.569
AD-52461	>10nM
AD-52462	0.242
AD-52463	0.112
AD-52467	>10nM
AD-52468	>10nM
AD-52469	0.540
AD-52473	>10nM
AD-52474	0.323
AD-55983	0.017
AD-55983	0.020
AD-55989	0.017
AD-55989	0.019
AD-56016	0.018
AD-56016	0.019
AD-56017	0.027
AD-56017	0.031
AD-56053	0.007
AD-56053	0.009

Table 7. Unmodified Sense and Antisense Strand Sequences of AGT dsRNAs (21/23mers)

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO.
UM AD-60803.1	830-850	A-122599.1	CGGGAUGCUGGCCAACUUCUU	479	A-122600.1	828-850	AAGAAGUUGGCCAGCAUCCCGAC	517
UM AD-60775.1	843-863	A-122541.1	AACUUCUUGGGCUUCCGUAUA	480	A-122542.1	841-863	UAUACGGAAGCCCAAGAAGUUGG	518
UM AD-60779.1	855-875	A-122605.1	UUCCGUAUAUAUGGCAUGCAA	481	A-122606.1	853-875	UUGCAUGCCAUAUAUACGGAAGC	519
UM AD-60797.1	857-877	A-122581.1	CCGUAUAUAUGGCAUGCACAA	482	A-122582.1	855-877	UUGUGCAUGCCAUAUAUACGGAA	520
UM AD-60806.1	880-900	A-122585.1	AGCUAUGGGGCGUGGUCCAUA	483	A-122586.1	878-900	UAUGGACCACGCCCCAUAGCUCA	521
UM AD-60787.1	912-932	A-122577.1	CUCUCCCCAACGGCUGUCUUU	484	A-122578.1	910-932	AAAGACAGCCGUUGGGGAGAGGA	522
UM AD-60807.1	913-933	A-122601.1	UCUCCCCAACGGCUGUCUUUA	485	A-122602.1	911-933	UAAAGACAGCCGUUGGGGAGAGG	523
UM AD-60794.1	1276-1296	A-122611.1	UGCAGGCUGUGACAGGAUGGA	486	A-122612.1	1274-1296	UCCAUCCUGUCACAGCCUGCAUG	524
UM AD-60796.1	1568-1588	A-122565.1	CCUGGACAAGGUGGAGGGUCU	487	A-122566.1	1566-1588	AGACCCUCCACCUUGUCCAGGUC	525
UM AD-60778.1	1572-1592	A-122589.1	GACAAGGUGGAGGGUCUCACU	488	A-122590.1	1570-1592	AGUGAGACCCUCCACCUUGUCCA	526
UM AD-60792.1	1574-1594	A-122579.1	CAAGGUGGAGGGUCUCACUUU	489	A-122580.1	1572-1594	AAAGUGAGACCCUCCACCUUGUC	527
UM AD-60772.1	1594-1614	A-122571.1	UCCAGCAAAACUCCCUCAACU	490	A-122572.1	1592-1614	AGUUGAGGGAGUUUUGCUGGAAA	528
UM AD-60773.1	1603-1623	A-122587.1	ACUCCCUCAACUGGAUGAAGA	491	A-122588.1	1601-1623	UCUUCAUCCAGUUGAGGGAGUUU	529
UM AD-60782.1	1737-1757	A-122575.1	CUGAACCUGCAAAAAUUGAGA	492	A-122576.1	1735-1757	UCUCAAUUUUUGCAGGUUCAGCU	530
UM AD-60800.1	1739-1759	A-122551.1	GAACCUGCAAAAAUUGAGCAA	493	A-122552.1	1737-1759	UUGCUCAAUUUUUGCAGGUUCAG	531
UM AD-60785.1	1741-1761	A-122545.1	ACCUGCAAAAAUUGAGCAAUA	494	A-122546.1	1739-1761	UAUUGCUCAAUUUUUGCAGGUUC	532
UM AD-60802.1	1742-1762	A-122583.1	CCUGCAAAAAUUGAGCAAUGA	495	A-122584.1	1740-1762	UCAUUGCUCAAUUUUUGCAGGUU	533
UM AD-60799.1	1812-1832	A-122613.1	GCGGAUGAGAGAGAGCCCACA	496	A-122614.1	1810-1832	UGUGGGCUCUCUCUCAUCCGCUU	534
UM AD-60781.1	1894-1914	A-122559.1	UGUUUGCUGUGUAUGAUCAAA	497	A-122560.1	1892-1914	UUUGAUCAUACACAGCAAACAGG	535

Duplex Name	Position relative to NM_000029.3	Sense Name	Sense Sequence	SEQ ID NO.	Antisense Name	Position relative to NM_000029.3	Antisense Sequence	SEQ ID NO.
UM AD-60793.1	2072-2092	A-122595.1	CACCCCCAGUCUCCCACCUUU	498	A-122596.1	2070-2092	AAAGGUGGGAGACUGGGGGUGAC	536
UM AD-60784.1	2081-2101	A-122607.1	UCUCCCACCUUUUUCUUCUAAU	499	A-122608.1	2079-2101	AUUAGAAGAAAAAGGUGGGAGACU	537
UM AD-60777.1	2084-2104	A-122573.1	CCCACCUUUUUCUUCUAAUGAA	500	A-122574.1	2082-2104	UUCAUUAGAAGAAAAAGGUGGGAG	538
UM AD-60795.1	2270-2290	A-122549.1	UCCAAAAAAGAAUUCCAACCGA	501	A-122550.1	2268-2290	UCGGUUGGAAUUCUUUUUUGGAAC	539
UM AD-60783.1	2281-2301	A-122591.1	UUCCAACCGACCAGCUUGUUU	502	A-122592.1	2279-2301	AAACAAGCUGGUCGGUUGGAAUU	540
UM AD-60788.1	2286-2306	A-122593.1	ACCGACCAGCUUGUUUGUGAA	503	A-122594.1	2284-2306	UUCACAAACAAGCUGGUCGGUUG	541
UM AD-60789.1	2291-2311	A-122609.1	CCAGCUUGUUUGUGAAACAAA	504	A-122610.1	2289-2311	UUUGUUUCACAAACAAGCUGGUC	542
UM AD-60770.1	2292-2312	A-122539.1	CAGCUUGUUUGUGAAACAAAA	505	A-122540.1	2290-2312	UUUUGUUUCACAAACAAGCUGGU	543
UM AD-60776.1	2309-2329	A-122557.1	AAAAAAAGUGUUCCCUUUUCAA	506	A-122558.1	2307-2329	UUGAAAAGGGAACACUUUUUUGU	544
UM AD-60798.1	2316-2336	A-122597.1	UGUUCCCUUUUUCAAGUUGAGA	507	A-122598.1	2314-2336	UCUCAACUUGAAAAGGGAACACU	545
UM AD-60801.1	2328-2348	A-122567.1	AAGUUGAGAACAAAAAAUUGGA	508	A-122568.1	2326-2348	UCCAAUUUUUUGUUCUCAACUUGA	546
UM AD-60791.1	2329-2349	A-122563.1	AGUUGAGAACAAAAAUUGGGU	509	A-122564.1	2327-2349	ACCCAAUUUUUUGUUCUCAACUUG	547
UM AD-60771.1	2334-2354	A-122555.1	AGAACAAAAAAUUGGGUUUUAA	510	A-122556.1	2332-2354	UUAAAACCCAAUUUUUUGUUCUCA	548
UM AD-60780.1	2335-2355	A-122543.1	GAACAAAAAAUUGGGUUUUAAA	511	A-122544.1	2333-2355	UUUAAAACCCAAUUUUUUGUUCUC	549
UM AD-60786.1	2386-2406	A-122561.1	GUUUGUAUUUAGUGUCUUGAA	512	A-122562.1	2384-2406	UUCAAGACACUAAAUACAAAACCG	550
UM AD-60790.1	2387-2407	A-122547.1	UUUGUAUUUAGUGUCUUGAAU	513	A-122548.1	2385-2407	AUUCAAGACACUAAAUACAAAACC	551
UM AD-60774.1	2399-2419	A-122603.1	GUCUUGAAUGUAAGAACAUGA	514	A-122604.1	2397-2419	UCAUGUUCUUACAUUCAAGACAC	552
UM AD-60804.1	2400-2420	A-122553.1	UCUUGAAUGUAAGAACAUGAA	515	A-122554.1	2398-2420	UUCAUGUUCUUACAUUCAAGACA	553
UM AD-60805.1	2452-2472	A-122569.1	UUCCACAGAUGCUUGUGAUUU	516	A-122570.1	2450-2472	AAAUCACAAGCAUCUGUGGAAAA	554

Table 8. Modified Sense and Antisense Strand Sequences of AGT dsRNAs (21/23mers)

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Antisense Sequence	SEQ ID NO
AD-60770.1	A-122539.1	CfsasGfcUfuGfuUfUfGfuGfaAfaCfaAfaAfL96	555	A-122540.1	usUfsuUfgUfuUfcAfcaaAfcAfaGfcUfgsgsu	593
AD-60771.1	A-122555.1	AfsgsAfaCfaAfaAfAfUfuGfgGfuUfuUfaAfL96	556	A-122556.1	usUfsaAfaAfcCfcAfauuUfuUfgUfuCfuscsa	594
AD-60772.1	A-122571.1	UfscsCfaGfcAfaAfAfCfuCfcCfuCfaAfcUfL96	557	A-122572.1	asGfsuUfgAfgGfgAfguuUfuGfcUfgGfasasa	595
AD-60773.1	A-122587.1	AfscsUfcCfcUfcAfAfCfuGfgAfuGfaAfgAfL96	558	A-122588.1	usCfsuUfcAfuCfcAfguuGfaGfgGfaGfususu	596
AD-60774.1	A-122603.1	GfsusCfuUfgAfaUfGfUfaAfgAfaCfaUfgAfL96	559	A-122604.1	usCfsaUfgUfuCfuUfacaUfuCfaAfgAfcsasc	597
AD-60775.1	A-122541.1	AfsasCfuUfcUfuGfGfGfcUfuCfcGfuAfuAfL96	560	A-122542.1	usAfsuAfcGfgAfaGfcccAfaGfaAfgUfusgsg	598
AD-60776.1	A-122557.1	AfsasAfaAfaGfuGfUfUfcCfcUfuUfuCfaAfL96	561	A-122558.1	usUfsgAfaAfaGfgGfaacAfcUfuUfuUfusgsu	599
AD-60777.1	A-122573.1	CfscsCfaCfcUfuUfUfCfuUfcUfaAfuGfaAfL96	562	A-122574.1	usUfscAfuUfaGfaAfgaaAfaGfgUfgGfgsasg	600
AD-60778.1	A-122589.1	GfsasCfaAfgGfuGfGfAfgGfgUfcUfcAfcUfL96	563	A-122590.1	asGfsuGfaGfaCfcCfuccAfcCfuUfgUfcscsa	601
AD-60779.1	A-122605.1	UfsusCfcGfuAfuAfUfAfuGfgCfaUfgCfaAfL96	564	A-122606.1	usUfsgCfaUfgCfcAfuauAfuAfcGfgAfasgsc	602
AD-60780.1	A-122543.1	GfsasAfcAfaAfaAfUfUfgGfgUfuUfuAfaAfL96	565	A-122544.1	usUfsuAfaAfaCfcCfaauUfuUfuGfuUfcsusc	603
AD-60781.1	A-122559.1	UfsgsUfuUfgCfuGfUfGfuAfuGfaUfcAfaAfL96	566	A-122560.1	usUfsuGfaUfcAfuAfcacAfgCfaAfaCfasgsg	604
AD-60782.1	A-122575.1	CfsusGfaAfcCfuGfCfAfaAfaAfuUfgAfgAfL96	567	A-122576.1	usCfsuCfaAfuUfuUfugcAfgGfuUfcAfgscsu	605
AD-60783.1	A-122591.1	UfsusCfcAfaCfcGfAfCfcAfgCfuUfgUfuUfL96	568	A-122592.1	asAfsaCfaAfgCfuGfgucGfgUfuGfgAfasusu	606
AD-60784.1	A-122607.1	UfscsUfcCfcAfcCfUfUfuUfcUfuCfuAfaUfL96	569	A-122608.1	asUfsuAfgAfaGfaAfaagGfuGfgGfaGfascsu	607
AD-60785.1	A-122545.1	AfscsCfuGfcAfaAfAfAfuUfgAfgCfaAfuAfL96	570	A-122546.1	usAfsuUfgCfuCfaAfuuuUfuGfcAfgGfususc	608
AD-60786.1	A-122561.1	GfsusUfuGfuAfuUfUfAfgUfgUfcUfuGfaAfL96	571	A-122562.1	usUfscAfaGfaCfaCfuaaAfuAfcAfaAfcscsg	609

Duplex Name	Sense Name	Sense Sequence	SEQ ID NO	Antisense Name	Antisense Sequence	SEQ ID NO
AD-60787.1	A-122577.1	CfsusCfuCfcCfcAfaAfCfgGfcUfgUfcUfuUfL96	572	A-122578.1	asAfsaGfaCfaGfcCfguuGfgGfgAfgAfgsgsa	610
AD-60788.1	A-122593.1	AfscsCfgAfcCfaGfCfUfuGfuUfuGfuGfaAfL96	573	A-122594.1	usUfscAfcAfaAfcAfagcUfgGfuCfgGfususg	611
AD-60789.1	A-122609.1	CfscsAfgCfuUfgUfUfUfgUfgAfaAfcAfaAfL96	574	A-122610.1	usUfsuGfuUfuCfaCfaaaCfaAfgCfuGfgsusc	612
AD-60790.1	A-122547.1	UfsusUfgUfaUfuUfAfGfuGfuCfuUfgAfaUfL96	575	A-122548.1	asUfsuCfaAfgAfcAfcuaAfaUfaCfaAfascsc	613
AD-60791.1	A-122563.1	AfsgsUfuGfaGfaAfCfAfaAfaAfuUfgGfgUfL96	576	A-122564.1	asCfscCfaAfuUfuUfuguUfcUfcAfaCfususg	614
AD-60792.1	A-122579.1	CfsasAfgGfuGfgAfGfGfgUfcUfcAfcUfuUfL96	577	A-122580.1	asAfsaGfuGfaGfaCfccuCfcAfcCfuUfgsusc	615
AD-60793.1	A-122595.1	CfsasCfcCfcCfaGfUfCfuCfcCfaCfcUfuUfL96	578	A-122596.1	asAfsaGfgUfgGfgAfgacUfgGfgGfgUfgsasc	616
AD-60794.1	A-122611.1	UfsgsCfaGfgCfuGfUfGfaCfaGfgAfuGfgAfL96	579	A-122612.1	usCfscAfuCfcUfgUfcacAfgCfcUfgCfasusg	617
AD-60795.1	A-122549.1	UfscsCfaAfaAfaGfAfAfuUfcCfaAfcCfgAfL96	580	A-122550.1	usCfsgGfuUfgGfaAfuucUfuUfuUfgGfasasc	618
AD-60796.1	A-122565.1	CfscsUfgGfaCfaAfGfGfuGfgAfgGfgUfcUfL96	581	A-122566.1	asGfsaCfcCfuCfcAfccuUfgUfcCfaGfgsusc	619
AD-60797.1	A-122581.1	CfscsGfuAfuAfuAfUfGfgCfaUfgCfaCfaAfL96	582	A-122582.1	usUfsgUfgCfaUfgCfcauAfuAfuAfcGfgsasa	620
AD-60798.1	A-122597.1	UfsgsUfuCfcCfuUfUfUfcAfaGfuUfgAfgAfL96	583	A-122598.1	usCfsuCfaAfcUfuGfaaaAfgGfgAfaCfascsu	621
AD-60799.1	A-122613.1	GfscsGfgAfuGfaGfAfGfaGfaGfcCfcAfcAfL96	584	A-122614.1	usGfsuGfgGfcUfcUfcucUfcAfuCfcGfcsusu	622
AD-60800.1	A-122551.1	GfsasAfcCfuGfcAfAfAfaAfuUfgAfgCfaAfL96	585	A-122552.1	usUfsgCfuCfaAfuUfuuuGfcAfgGfuUfcsasg	623
AD-60801.1	A-122567.1	AfsasGfuUfgAfgAfAfCfaAfaAfaUfuGfgAfL96	586	A-122568.1	usCfscAfaUfuUfuUfguuCfuCfaAfcUfusgsa	624
AD-60802.1	A-122583.1	CfscsUfgCfaAfaAfAfUfuGfaGfcAfaUfgAfL96	587	A-122584.1	usCfsaUfuGfcUfcAfauuUfuUfgCfaGfgsusu	625
AD-60803.1	A-122599.1	CfsgsGfgAfuGfcUfGfGfcCfaAfcUfuCfuUfL96	588	A-122600.1	asAfsgAfaGfuUfgGfccaGfcAfuCfcCfgsasc	626
AD-60804.1	A-122553.1	UfscsUfuGfaAfuGfUfAfaGfaAfcAfuGfaAfL96	589	A-122554.1	usUfscAfuGfuUfcUfuacAfuUfcAfaGfascsa	627
AD-60805.1	A-122569.1	UfsusCfcAfcAfgAfUfGfcUfuGfuGfaUfuUfL96	590	A-122570.1	asAfsaUfcAfcAfaGfcauCfuGfuGfgAfasasa	628
AD-60806.1	A-122585.1	AfsgsCfuAfuGfgGfGfCfgUfgGfuCfcAfuAfL96	591	A-122586.1	usAfsuGfgAfcCfaCfgccCfcAfuAfgCfuscsa	629
AD-60807.1	A-122601.1	UfscsUfcCfcCfaAfCfGfgCfuGfuCfuUfuAfL96	592	A-122602.1	usAfsaAfgAfcAfgCfcguUfgGfgGfaGfasgsg	630

Table 9. AGT single dose screen in Hep3B cells (21/23mers)

Duplex Name	10nM Avg	10nM SD	0.1nM Avg	0.1nM SD	Start position relative to NM_000029.3
AD-60770.1	4.7	0.7	27.4	7.4	2292
AD-60771.1	4.6	1.2	10.9	5.9	2334
AD-60772.1	14.8	7.9	63.7	13.2	1594
AD-60773.1	43.9	8.7	88.8	5.4	1603
AD-60774.1	64.0	3.8	79.1	4.2	2399
AD-60775.1	8.4	2.8	62.2	8.8	843
AD-60776.1	5.9	2.8	11.1	5.1	2309
AD-60777.1	4.3	1.7	26.7	5.3	2084
AD-60778.1	11.5	7.4	52.5	15.5	1572
AD-60779.1	5.2	2.8	24.1	4.1	855
AD-60780.1	5.7	2.3	12.0	5.2	2335
AD-60781.1	6.9	2.1	18.5	3.1	1894
AD-60782.1	9.2	5.0	47.0	8.6	1737
AD-60783.1	15.9	9.0	35.7	7.6	2281
AD-60784.1	5.6	1.0	12.3	2.5	2081
AD-60785.1	6.1	0.9	29.7	13.7	1741
AD-60786.1	56.9	5.4	74.0	5.1	2386
AD-60787.1	94.4	0.7	104.4	6.0	912
AD-60788.1	10.5	3.6	49.8	4.8	2286
AD-60789.1	5.2	2.0	25.3	16.0	2291
AD-60790.1	70.4	3.3	86.3	19.7	2387
AD-60791.1	7.8	3.7	33.4	18.0	2329
AD-60792.1	17.0	3.3	72.8	9.0	1574
AD-60793.1	18.4	5.6	58.3	12.5	2072
AD-60794.1	54.3	11.5	101.6	4.3	1276
AD-60795.1	6.2	3.4	36.3	8.6	2270
AD-60796.1	41.6	3.3	100.9	8.6	1568
AD-60797.1	72.5	2.8	97.1	6.1	857
AD-60798.1	13.2	4.8	29.1	16.4	2316
AD-60799.1	29.7	7.5	86.2	4.2	1812
AD-60800.1	31.0	7.5	81.8	11.2	1739
AD-60801.1	10.9	2.2	35.4	11.3	2328
AD-60802.1	14.8	5.5	52.8	9.7	1742
AD-60803.1	29.2	10.9	71.4	9.6	830
AD-60804.1	39.2	2.9	75.6	6.1	2400
AD-60805.1	60.3	10.1	97.4	2.3	2452
AD-60806.1	89.3	11.8	92.8	6.5	880
AD-60807.1	64.1	3.7	91.5	10.1	913

Table 10 - AGT IC_{50} data in Hep3B Cells (21/23mers)

Duplex Name	IC_{50} (nM)
AD-60771.1	0.028
AD-60776.1	0.033
AD-60780.1	0.038
AD-60784.1	0.045
AD-60781.1	0.089

Example 2. *In Vivo* AGT Silencing - Amelioration of Preeclamptic Sequelae

Transgenic female Sprague-Dawley rats harboring the complete genomic human AGT gene (*e.g.,* [TGR(hAGT)L1623] (see, *e.g.,* Bohlender J, , *et al.* (1996) *Hypertension* 27: 535–540 and Bohlender J, , *et al.* (2000) *J Am Soc Nephrol* 11: 2056–2061)) were surgically implemented with a device for measuring blood pressure by telemetry. Subsequent to recovery from the procedure, these rats were mated with transgenic male Sprague-Dawley rats harboring the entire genomic human REN gene (*e.g.,* [TGR(hREN)L10J] (see, *e.g.*, Bohlender J, *et al.* (1997) *Hypertension* 29: 428–434 and Bohlender J, , *et al.* (2000) *J Am Soc Nephrol* 11: 2056–2061)). The female progeny of this cross (referred to herein as "PE rats") are a model of preeclampsia and develop albuminuria and intrauterine growth restriction (IUGR), and have a blood pressure spike beginning around gestation day 13 (see, *e.g.,* Figure 2A).

Beginning on day 3 of gestation, a subset of pregnant PE rats was administered 10 mg/kg siRNA targeting hAGT (AD-60771). A second subset of pregnant PE rats were left untreated as a control. Dosing continued every third day to gestation day 15. Rats were sacrificed on about day 19 of gestation, and blood and tissue samples were collected from the mothers and the fetuses.

Maternal blood bressure was monitored throughout the experiment *via* surgically implemented devices for measuring blood pressure by telemetry. Figure 2A shows that following administration of AD-60771, maternal mean arterial blood pressure was significantly lowered. In addition, as determined by ELISA analysis of serum albumin, maternal albuminuria was significantly reduced following administration of AD-60771 (Figure 2B). These two conditions are the hallmarks of preeclampsia. The reduced blood pressure reduces cardiovascular events associated with the disease, while reduced albuminuria is indicative of improved renal function.

Preeclampsia is also associated with reduced placental size, possibly related to poor perfusion. As a result of the condition, fetal growth is impaired. Following maternal administration of AD-60771, however, uteroplacental unit weight (Figure

3A) and fetal weight (Figure 3B) were increased, and there was normalization of the fetal brain:liver ratio (Figure 3C), all indicative of a more normal placental and fetal development.

As determined by RT-qPCR analysis of mRNA expression of hAGT in maternal liver and placenta, it was shown that, while there is substantial silencing of hAGT in the maternal liver (Figure 4A), there was no significant silencing in the placenta (Figure 4B). This indicates a lack of penetration of the iRNA into the placenta.

In addition, analysis of four maternal liver samples, four placenta samples, and eight fetal liver samples demonstrated that the exposure of the fetal liver to the iRNA was about 1.2 ng siRNA/g (below the limit of detection, 1.3 ng siRNA/g tissue) of tissue and that exposure of the maternal liver to the iRNA was about 265-fold greater than the exposure of the placenta to the iRNA (Figure 5). Tissue exposure was determined by stem-loop qPCR, as previously described (see, *e.g.,* Landesman, Y., *et al.* (2010) *Silence* 1:16.

Thus, maternal treatment with an iRNA targeting hAGT is superior to maternal treatment with small-molecule renin-angiotensin inhibitors, such as ACE inhibitors, and angiotensin receptor blockers, as these compounds cross the placenta and are fetotoxic.

As the placenta acts as the conduit for nutrients to the fetus, and waste removal from the fetus, its composition is critical. Accordingly, placental pathology was evaluated (*i.e.,* by measuring the area of tissue slices immunohistochemically stained for cytokeratin). Figure 6 demonstrates that while the maternal portion of the placenta (the mesometrial triangle; Figure 6D) and the trophospongium (a uniform layer of cells which are precursors of differentiated trophoblasts; Figure 6E) were unchanged by administration of AD-60771, overall placental size was increased (Figures 6B, 6C, and 6F and Figure 6A for reference). In particular, the size of the labyrinth, which is the site of nutritional exchange between fetal and maternal blood, was increased by maternal treatment with AD-60771 (Figure 6G).

The anti-angiogenic soluble fms-like tyrosine kinase-1 (sFLT1) and the angiogenic placental growth factor (PLGF), which are regulated by angiotensins, play a key role in preeclampsia, being released from the placenta into the maternal blood stream and causing endothelial dysfunction. sFlt-1, is largely released from the placenta into the maternal blood stream and causes endothelial dysfunction. PLGF is placental derived, and promotes angiogenesis. The ratio of sFlt-1:PLGF is diagnostic, with a higher sFlt-1:PLGF associated with more severe disease.

Evaluation of the mRNA expression of sFLT1 and PLGF by RT-qPCR analysis demonstrated that the levels of both sFLT1 and PLGF were significantly reduced in the maternal kidney (Figures 7A and 7B, respectively), but remained unchanged in the placenta (Figures 7C and 7D, respectively) following maternal administration of AD-60771. However, as sFlt-1 was reduced to a greater extent than PLGF in the maternal kidney, the serum sFlt-1:PLGF ratio may be improved.

Agonistic autoantibodies to the angiotensin II receptor type I (AT1) have been identified in preeclamptic women. When pregnant rodents are exposed to AT1 autoantibodies, a preeclampsia-like syndrome develops. As activation of AT1 is associated with vasopressor effects as well as aldosterone secretion and sFlt-1 production, reduction of AT1 autoantibodies would be expected to reduce the preeclamptic phenotype. Accordingly, the level of production of agonistic autoantibodies to the AT1 receptor (AT1-AA) may also be evaluated by biochromatography and subsequent bioassay of isolated antibodies. AT1-AA levels were measured as has been described (see, *e.g.,* Dechend, *et al.* (2005) *Hypertension* 45:742–746) by assessing the impact of isolated, purified AT1-AA antibodies on the spontaneous beating rate of neonatal rat cardiomyocytes. Figure 8 demonstrates that there was a significant reduction in the level of AT1-AA following administration of AD-60771 to pregnant PE rats.

Example 3. *In Vivo* AGT Silencing in a Transgenic Rat Model of Preeclampsia

The AD-60771 duplex was tested for the ability to silence hAGT expression in pregnant PE rats, described in the previous example. Beginning on day 3 of gestation, a subset of pregnant PE rats was administered 10 mg/kg siRNA targeting hAGT (AD-60771). Liver and blood were collected at gestation day 21 and the levels of hAGT and rAGT protein and mRNA were assayed and compared to the levels of hAGT and rAGT protein and mRNA present in untreated, pregnant transgenic rats, pregnant Sprague-Dawley rats, and non-pregnant Sprague-Dawley rats. The results of these assays are shown in Figures 9A and 9B and demonstrate that there was an 80% reduction of circulating AT2 and a 95% reduction of circulating hAT1 in the pregnant PE rats treated with AD-60771 as compared to control pregnant PE rats. A reduction of about 45% of rat AT2 was also observed in the pregnant PE rats treated with AD-60771 as compared to control pregnant PE rats. A 95% silencing of hepatic AGT mRNA was observed in the pregnant PE rats treated with AD-60771 as compared to control pregnant PE rats. Figures 9A and 9B also demonstrate that there was a

significant reduction in the serum level of AT1 and AT2 following administration of AD-60771 to pregnant PE rats.

Table 11. Unmodified Sense and Antisense Strand Sequences of AGT dsRNAs (21/23mers)

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-67864.1	A-135936.1	CGGGCAGCAGGGUCAGAAA	631	A-135937.1	UUUCUGACCCUGCUGCCCG	828	10-28
AD-67865.1	A-135938.1	UCAGAAGUGGCCCCCGUGU	632	A-135939.1	ACACGGGGGCCACUUCUGA	829	22-40_as
AD-67866.1	A-135940.1	CCCGUGUUGCCUAAGCAAA	633	A-135941.1	UUUGCUUAGGCAACACGGG	830	34-52_G19A_as
AD-67867.1	A-135948.1	UGCACCUCCGGCCUGCAUA	634	A-135949.1	UAUGCAGGCCGGAGGUGCA	831	76-94_G19A_as
AD-67868.1	A-135950.1	UGCAUGUCCCUGUGGCCUA	635	A-135951.1	UAGGCCACAGGGACAUGCA	832	89-107
AD-67869.1	A-135952.1	UGUGGCCUCUUGGGGGUAA	636	A-135953.1	UUACCCCCAAGAGGCCACA	833	99-117
AD-67870.1	A-135958.1	GGUCAGAAGGCCUGGGUGA	637	A-135959.1	UCACCCAGGCCUUCUGACC	834	132-150_G19A_as
AD-67871.1	A-135960.1	UGGGUGGUUGGCCUCAGGA	638	A-135961.1	UCCUGAGGCCAACCACCCA	835	144-162
AD-67872.1	A-135962.1	CCUCAGGCUGUCACACACA	639	A-135963.1	UGUGUGUGACAGCCUGAGG	836	155-173
AD-67873.1	A-135964.1	CACACACCUAGGGAGAUGA	640	A-135965.1	UCAUCUCCCUAGGUGUGUG	837	166-184
AD-67874.1	A-135966.1	AGGGAGAUGCUCCCGUUUA	641	A-135967.1	UAAACGGGAGCAUCUCCCU	838	175-193
AD-67875.1	A-135968.1	CCGUUUCUGGGAACCUUGA	642	A-135969.1	UCAAGGUUCCCAGAAACGG	839	187-205_G19A_as
AD-67876.1	A-135970.1	AACCUUGGCCCCGACUCCU	643	A-135971.1	AGGAGUCGGGGCCAAGGUU	840	198-216_as
AD-67877.1	A-135972.1	CGACUCCUGCAAACUUCGA	644	A-135973.1	UCGAAGUUUGCAGGAGUCG	841	209-227_G19A_as
AD-67878.1	A-135974.1	AACUUCGGUAAAUGUGUAA	645	A-135975.1	UUACACAUUUACCGAAGUU	842	220-238_as
AD-67879.1	A-135976.1	UGUGUAACUCGACCCUGCA	646	A-135977.1	UGCAGGGUCGAGUUACACA	843	232-250_as
AD-67880.1	A-135978.1	ACCCUGCACCGGCUCACUA	647	A-135979.1	UAGUGAGCCGGUGCAGGGU	844	243-261
AD-67881.1	A-135980.1	GCUCACUCUGUUCAGCAGU	648	A-135981.1	ACUGCUGAACAGAGUGAGC	845	254-272_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-67882.1	A-135982.1	UUCAGCAGUGAAACUCUGA	649	A-135983.1	UCAGAGUUUCACUGCUGAA	846	264-282
AD-67883.1	A-135984.1	AAACUCUGCAUCGAUCACU	650	A-135985.1	AGUGAUCGAUGCAGAGUUU	847	274-292_as
AD-67884.1	A-135986.1	CGAUCACUAAGACUUCCUA	651	A-135987.1	UAGGAAGUCUUAGUGAUCG	848	285-303_G19A_as
AD-67885.1	A-135990.1	GAGGUCCCAGCGUGAGUGU	652	A-135991.1	ACACUCACGCUGGGACCUC	849	307-325_as
AD-67886.1	A-135994.1	UUCUGGCAUCUGUCCUUCU	653	A-135995.1	AGAAGGACAGAUGCCAGAA	850	329-347_as
AD-67887.1	A-135996.1	CCUUCUGGCCAGCCUGUGA	654	A-135997.1	UCACAGGCUGGCCAGAAGG	851	342-360_G19A_as
AD-67888.1	A-135998.1	AGCCUGUGGUCUGGCCAAA	655	A-135999.1	UUUGGCCAGACCACACAGGCU	852	352-370_G19A_as
AD-67889.1	A-136000.1	GGCCAAGUGAUGUAACCCU	656	A-136001.1	AGGGUUACAUCACUUGGCC	853	364-382_as
AD-67890.1	A-136002.1	UGUAACCCUCCUCUCCAGA	657	A-136003.1	UCUGGAGAGGAGGGUUACA	854	374-392
AD-67891.1	A-136004.1	UCUCCAGCCUGUGCACAGA	658	A-136005.1	UCUGUGCACAGGCUGGAGA	855	385-403_G19A_as
AD-67892.1	A-136006.1	UGCACAGGCAGCCUGGGAA	659	A-136007.1	UUCCCAGGCUGCCUGUGCA	856	396-414_as
AD-67893.1	A-136008.1	CCUGGGAACAGCUCCAUCA	660	A-136009.1	UGAUGGAGCUGUUCCCAGG	857	407-425
AD-67894.1	A-136010.1	UCCAUCCCCACCCCUCAGA	661	A-136011.1	UCUGAGGGGUGGGGAUGGA	858	419-437
AD-67895.1	A-136012.1	CCCUCAGCUAUAAAUAGGA	662	A-136013.1	UCCUAUUUAUAGCUGAGGG	859	430-448_G19A_as
AD-67896.1	A-136014.1	UAAAUAGGGCAUCGUGACA	663	A-136015.1	UGUCACGAUGCCCUAUUUA	860	440-458
AD-67897.1	A-136016.1	AUCGUGACCCGGCCGGGGA	664	A-136017.1	UCCCCGGCCGGGUCACGAU	861	450-468_G19A_as
AD-67898.1	A-136018.1	CCGGGGGAAGAAGCUGCCA	665	A-136019.1	UGGCAGCUUCUUCCCCCGG	862	462-

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
							480_G19A_as
AD-67899.1	A-136020.1	AGCUGCCGUUGUUCUGGGU	666	A-136021.1	ACCCAGAACAACGGCAGCU	863	473-491_as
AD-67900.1	A-136022.1	UUCUGGGUACUACAGCAGA	667	A-136023.1	UCUGCUGUAGUACCCAGAA	864	484-502_as
AD-67901.1	A-136024.1	UACAGCAGAAGGGUAUGCA	668	A-136025.1	UGCAUACCCUUCUGCUGUA	865	494-512_G19A_as
AD-67902.1	A-136026.1	UAUGCGGAAGCGAGCACCA	669	A-136027.1	UGGUGCUCCGCUUCCGCAUA	866	507-525
AD-67903.1	A-136028.1	CGAGCACCCCAGUCUGAGA	670	A-136029.1	UCUCAGACUGGGGUGCUCG	867	517-535_as
AD-67904.1	A-136032.1	CUCCUGCCGGUGUGAGCCU	671	A-136033.1	AGGCUCACACCGGCAGGAG	868	539-557_as
AD-67905.1	A-136034.1	UGUGAGCCUGAGGGCCACA	672	A-136035.1	UGUGGCCCUCAGGCUCACA	869	549-567
AD-67906.1	A-136036.1	GGGCCACCAUCCUCUGCCU	673	A-136037.1	AGGCAGAGGAUGGUGGCCC	870	560-578_as
AD-67907.1	A-136038.1	CUGCCUCCUGGCCUGGGCU	674	A-136039.1	AGCCCAGGCCAGGAGGCAG	871	573-591_as
AD-67908.1	A-136042.1	CCUGGCUGCAGGUGACCGA	675	A-136043.1	UCGGUCACCUGCAGCCAGG	872	594-612_G19A_as
AD-67909.1	A-136044.1	UGACCGGGUGUACAUACAA	676	A-136045.1	UUGUAUGUACACCCGGUCA	873	606-624
AD-67910.1	A-136046.1	UACAUACACCCCUUCCACA	677	A-136047.1	UGUGGAAGGGGUGUAUGUA	874	616-634
AD-67911.1	A-136048.1	UUCCACCUCGUCAUCCACA	678	A-136049.1	UGUGGAUGACGAGGUGGAA	875	628-646_as
AD-67912.1	A-136050.1	UCAUCCACAAUGAGAGUAA	679	A-136051.1	UUACUCUCAUUGUGGAUGA	876	638-656
AD-67913.1	A-136056.1	AAAGGCCAAUGCCGGGAAA	680	A-136057.1	UUUCCCGGCAUUGGCCUUU	877	672-690_G19A_as
AD-67914.1	A-136058.1	CCGGGAAGCCCAAAGACCA	681	A-136059.1	UGGUCUUUGGGCUUCCCGG	878	683-701
AD-67915.1	A-136060.1	AAAGACCCCACCUUCAUAA	682	A-136061.1	UUAUGAAGGUGGGGUCUUU	879	694-712
AD-67916.1	A-136062.1	CCUUCAUACCUGCUCCAAU	683	A-136063.1	AUUGGAGCAGGUAUGAAGG	880	704-722_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-67917.1	A-136064.1	CUCCAAUUCAGGCCAAGAA	684	A-136065.1	UUCUUGGCCUGAAUUGGAG	881	716-734
AD-67918.1	A-136066.1	AGGCCAAGACAUCCCCUGU	685	A-136067.1	ACAGGGGAUGUCUUGGCCU	882	725-743_as
AD-67919.1	A-136068.1	UCCCCUGUGGAUGAAAAGA	686	A-136069.1	UCUUUUCAUCCACAGGGGA	883	736-754_G19A_as
AD-67920.1	A-136070.1	AAAAGGCCCUACAGGACCA	687	A-136071.1	UGGUCCUGUAGGGCCUUUU	884	749-767_as
AD-67921.1	A-136072.1	UACAGGACCAGCUGGUGCU	688	A-136073.1	AGCACCAGCUGGUCCUGUA	885	758-776_as
AD-67922.1	A-136078.1	UUGACACCGAAGACAAGUU	689	A-136079.1	AACUUGUCUUCGGUGUCAA	886	791-809_as
AD-67923.1	A-136080.1	ACAAGUUGAGGGCCGCAAU	690	A-136081.1	AUUGCGGCCCUCAACUUGU	887	803-821_as
AD-67924.1	A-136082.1	GCCGCAAUGGUCGGGAUGA	691	A-136083.1	UCAUCCCGACCAUUGCGGC	888	814-832
AD-67925.1	A-136084.1	CGGGAUGCUGGCCAACUUA	692	A-136085.1	UAAGUUGGCCAGCAUCCCG	889	825-843
AD-67926.1	A-136086.1	CAACUUCUUGGGCUUCCGU	693	A-136087.1	ACGGAAGCCCAAGAAGUUG	890	837-855_as
AD-67927.1	A-136088.1	GGCUUCCGUAUAUAUGGCA	694	A-136089.1	UGCCAUAUAUACGGAAGCC	891	847-865_as
AD-67928.1	A-136090.1	UAUGGCAUGCACAGUGAGA	695	A-136091.1	UCUCACUGUGCAUGCCAUA	892	859-877
AD-67929.1	A-136092.1	ACAGUGAGCUAUGGGGCGU	696	A-136093.1	ACGCCCCCAUAGCUCACUGU	893	869-887_as
AD-67930.1	A-136098.1	CGUCCUCUCCCCAACGGCU	697	A-136099.1	AGCCGUUGGGGAGAGGACG	894	903-921_as
AD-67931.1	A-136102.1	UUUGGCACCCUGGCCUCUA	698	A-136103.1	UAGAGGCCAGGGUGCCAAA	895	925-943
AD-67932.1	A-136104.1	CUGGCCUCUCUCUAUCUGA	699	A-136105.1	UCAGAUAGAGAGAGGCCAG	896	934-952_G19A_as
AD-67933.1	A-136106.1	UAUCUGGGAGCCUUGGACA	700	A-136107.1	UGUCCAAGGCUCCCAGAUA	897	946-964
AD-67934.1	A-136108.1	UUGGACCACACAGCUGACA	701	A-136109.1	UGUCAGCUGUGUGGUCCAA	898	958-976_as
AD-67935.1	A-136110.1	ACAGCUGACAGGCUACAGA	702	A-136111.1	UCUGUAGCCUGUCAGCUGU	899	967-985_G19A_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-67936.1	A-136112.1	UACAGGCAAUCCUGGGUGU	703	A-136113.1	ACACCCAGGAUUGCCUGUA	900	980-998_as
AD-67937.1	A-136114.1	UCCUGGGUGUUCCUUGGAA	704	A-136115.1	UUCCAAGGAACACCCAGGA	901	989-1007_as
AD-67938.1	A-136116.1	UUGGAAGGACAAGAACUGA	705	A-136117.1	UCAGUUCUUGUCCUUCCAA	902	1002-1020
AD-67939.1	A-136118.1	AGAACUGCACCUCCCGGCU	706	A-136119.1	AGCCGGGAGGUGCAGUUCU	903	1013-1031_as
AD-67940.1	A-136122.1	UGCGCACAAGGUCCUGUCU	707	A-136123.1	AGACAGGACCUUGUGCGCA	904	1035-1053_as
AD-67947.1	A-136126.1	CUGCAGGCUGUACAGGGCA	708	A-136127.1	UGCCCUGUACAGCCUGCAG	905	1057-1075
AD-67948.1	A-136128.1	UACAGGGCCUGCUAGUGGA	709	A-136129.1	UCCACUAGCAGGCCCUGUA	906	1067-1085
AD-67949.1	A-136130.1	UAGUGGCCCAGGGCAGGGA	710	A-136131.1	UCCCUGCCCUGGGCCACUA	907	1079-1097
AD-67950.1	A-136132.1	AGGGCAGGGCUGAUAGCCA	711	A-136133.1	UGGCUAUCAGCCCUGCCCU	908	1088-1106_as
AD-67951.1	A-136134.1	UAGCCAGGCCCAGCUGCUA	712	A-136135.1	UAGCAGCUGGGCCUGGCUA	909	1101-1119_G19A_as
AD-67952.1	A-136136.1	AGCUGCUGCUGUCCACGGU	713	A-136137.1	ACCGUGGACAGCAGCAGCU	910	1112-1130_as
AD-67954.1	A-136140.1	UGGGCGUGUUCACAGCCCA	714	A-136141.1	UGGGCUGUGAACACGCCCA	911	1133-1151
AD-67955.1	A-136142.1	CACAGCCCCAGGCCUGCAA	715	A-136143.1	UUGCAGGCCUGGGGCUGUG	912	1143-1161
AD-67956.1	A-136144.1	CUGCACCUGAAGCAGCCGU	716	A-136145.1	ACGGCUGCUUCAGGUGCAG	913	1156-1174_as
AD-67957.1	A-136146.1	AGCAGCCGUUUGUGCAGGA	717	A-136147.1	UCCUGCACAAACGGCUGCU	914	1166-1184_G19A_as
AD-67958.1	A-136148.1	UGCAGGGCCUGGCUCUCUA	718	A-136149.1	UAGAGAGCCAGGCCCUGCA	915	1178-1196_as
AD-67959.1	A-136150.1	UGGCUCUCUAUACCCCUGU	719	A-136151.1	ACAGGGGUAUAGAGAGCCA	916	1187-1205_as
AD-67960.1	A-136152.1	ACCCCUGUGGUCCUCCCAA	720	A-136153.1	UUGGGAGGACCACAGGGGU	917	1198-1216
AD-67962.1	A-136156.1	CUGGACUUCACAGAACUGA	721	A-136157.1	UCAGUUCUGUGAAGUCCAG	918	1222-1240_G19A_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-67963.1	A-136158.1	AGAACUGGAUGUUGCUGCU	722	A-136159.1	AGCAGCAACAUCCAGUUCU	919	1233-1251_as
AD-67964.1	A-136160.1	UUGCUGCUGAGAAGAUUGA	723	A-136161.1	UCAAUCUUCUCAGCAGCAA	920	1244-1262_as
AD-67965.1	A-136162.1	AGAAGAUUGACAGGUUCAU	724	A-136163.1	AUGAACCUGUCAAUCUUCU	921	1253-1271_as
AD-67966.1	A-136164.1	AGGUUCAUGCAGGCUGUGA	725	A-136165.1	UCACAGCCUGCAUGAACCU	922	1264-1282_as
AD-67967.1	A-136166.1	GCUGUGACAGGAUGGAAGA	726	A-136167.1	UCUUCCAUCCUGUCACAGC	923	1276-1294_as
AD-67968.1	A-136168.1	UGGAAGACUGGCUGCUCCA	727	A-136169.1	UGGAGCAGCCAGUCUUCCA	924	1288-1306
AD-67970.1	A-136172.1	AUGGGAGCCAGUGUGGACA	728	A-136173.1	UGUCCACACUGGCUCCCAU	925	1309-1327_as
AD-67971.1	A-136174.1	UGUGGACAGCACCCUGGCU	729	A-136175.1	AGCCAGGGUGCUGUCCACA	926	1320-1338_as
AD-67972.1	A-136176.1	CCUGGCUUUCAACACCUAA	730	A-136177.1	UUAGGUGUUGAAAGCCAGG	927	1332-1350
AD-67973.1	A-136178.1	CAACACCUACGUCCACUUA	731	A-136179.1	UAAGUGGACGUAGGUGUUG	928	1341-1359
AD-67974.1	A-136180.1	CACUUCCAAGGGAAGAUGA	732	A-136181.1	UCAUCUUCCCUUGGAAGUG	929	1354-1372_as
AD-67975.1	A-136182.1	GGGAAGAUGAAGGGCUUCU	733	A-136183.1	AGAAGCCCUUCAUCUUCCC	930	1363-1381_as
AD-67976.1	A-136184.1	GCUUCUCCCUGCUGGCCGA	734	A-136185.1	UCGGCCAGCAGGGAGAAGC	931	1376-1394_as
AD-67978.1	A-136188.1	CCAGGAGUUCUGGGUGGAA	735	A-136189.1	UUCCACCCAGAACUCCUGG	932	1398-1416
AD-67979.1	A-136190.1	UGGGUGGACAACAGCACCU	736	A-136191.1	AGGUGCUGUUGUCCACCCA	933	1408-1426_as
AD-67980.1	A-136192.1	ACAGCACCUCAGUGUCUGU	737	A-136193.1	ACAGACACUGAGGUGCUGU	934	1418-1436_as
AD-67981.1	A-136194.1	UGUCUGUUCCCAUGCUCUA	738	A-136195.1	UAGAGCAUGGGAACAGACA	935	1430-1448
AD-67982.1	A-136196.1	CAUGCUCUCUGGCAUGGGA	739	A-136197.1	UCCCAUGCCAGAGAGCAUG	936	1440-1458
AD-67983.1	A-136198.1	AUGGGCACCUUCCAGCACU	740	A-136199.1	AGUGCUGGAAGGUGCCCAU	937	1453-1471_as
AD-67984.1	A-136200.1	UUCCAGCACUGGAGUGACA	741	A-136201.1	UGUCACUCCAGUGCUGGAA	938	1462-1480_as
AD-67986.1	A-136204.1	AGGACAACUUCUCGGUGAA	742	A-136205.1	UUCACCGAGAAGUUGUCCU	939	1484-1502

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-67987.1	A-136206.1	UCGGUGACUCAAGUGCCCU	743	A-136207.1	AGGGCACUUGAGUCACCGA	940	1495-1513_as
AD-67988.1	A-136208.1	UGCCCUUCACUGAGAGCGA	744	A-136209.1	UCGCUCUCAGUGAAGGGCA	941	1508-1526
AD-67989.1	A-136210.1	UGAGAGCGCCUGCCUGCUA	745	A-136211.1	UAGCAGGCAGGCGCUCUCA	942	1518-1536_G19A_as
AD-67990.1	A-136212.1	CCUGCUGCUGAUCCAGCCU	746	A-136213.1	AGGCUGGAUCAGCAGCAGG	943	1530-1548_as
AD-67991.1	A-136214.1	AUCCAGCCUCACUAUGCCU	747	A-136215.1	AGGCAUAGUGAGGCUGGAU	944	1540-1558_as
AD-67992.1	A-136216.1	UAUGCCUCUGACCUGGACA	748	A-136217.1	UGUCCAGGUCAGAGGCAUA	945	1552-1570_as
AD-67993.1	A-136218.1	ACCUGGACAAGGUGGAGGA	749	A-136219.1	UCCUCCACCUUGUCCAGGU	946	1562-1580_G19A_as
AD-67994.1	A-136220.1	UGGAGGGUCUCACUUUCCA	750	A-136221.1	UGGAAAGUGAGACCCUCCA	947	1574-1592_as
AD-67995.1	A-136222.1	CACUUUCCAGCAAAACUCA	751	A-136223.1	UGAGUUUUGCUGGAAAGUG	948	1584-1602
AD-67996.1	A-136224.1	AAAACUCCCUCAACUGGAU	752	A-136225.1	AUCCAGUUGAGGGAGUUUU	949	1595-1613_as
AD-67997.1	A-136226.1	AACUGGAUGAAGAAACUAU	753	A-136227.1	AUAGUUUCUUCAUCCAGUU	950	1606-1624_as
AD-67998.1	A-136228.1	AAACUAUCUCCCCGGACCA	754	A-136229.1	UGGUCCGGGGAGAUAGUUU	951	1618-1636_as
AD-67999.1	A-136230.1	CCGGACCAUCCACCUGACA	755	A-136231.1	UGUCAGGUGGAUGGUCCGG	952	1629-1647
AD-68001.1	A-136234.1	UGCCCCAACUGGUGCUGCA	756	A-136235.1	UGCAGCACCAGUUGGGGCA	953	1649-1667_as
AD-68002.1	A-136236.1	UGCUGCAAGGAUCUUAUGA	757	A-136237.1	UCAUAAGAUCCUUGCAGCA	954	1661-1679_as
AD-68003.1	A-136238.1	UCUUAUGACCUGCAGGACA	758	A-136239.1	UGUCCUGCAGGUCAUAAGA	955	1672-1690
AD-68004.1	A-136240.1	UGCAGGACCUGCUCGCCCA	759	A-136241.1	UGGGCGAGCAGGUCCUGCA	956	1682-1700_as
AD-68005.1	A-136242.1	UCGCCCAGGCUGAGCUGCA	760	A-136243.1	UGCAGCUCAGCCUGGGCGA	957	1694-1712
AD-68006.1	A-136244.1	UGAGCUGCCCGCCAUUCUA	761	A-136245.1	UAGAAUGGCGGGCAGCUCA	958	1704-1722_G19A_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-68009.1	A-136250.1	UGCAAAAAAUUGAGCAAUGA	762	A-136251.1	UCAUUGCUCAAUUUUUGCA	959	1739-1757_as
AD-68010.1	A-136252.1	AGCAAUGACCGCAUCAGGA	763	A-136253.1	UCCUGAUGCGGUCAUUGCU	960	1750-1768_G19A_as
AD-68011.1	A-136254.1	CAUCAGGGUGGGGGAGGUA	764	A-136255.1	UACCUCCCCCCACCCUGAUG	961	1761-1779_G19A_as
AD-68012.1	A-136256.1	GGGGAGGUGCUGAACAGCA	765	A-136257.1	UGCUGUUCAGCACCUCCCC	962	1771-1789_as
AD-68013.1	A-136258.1	AACAGCAUUUUUUUUUGAGA	766	A-136259.1	UCUCAAAAAAAAAAUGCUGUU	963	1783-1801
AD-68014.1	A-136260.1	UUUUUGAGCUUGAAGCGGA	767	A-136261.1	UCCGCUUCAAGCUCAAAAAA	964	1793-1811_as
AD-68017.1	A-136266.1	AGAGUCUACCCAACAGCUU	768	A-136267.1	AAGCUGUUGGGUAGACUCU	965	1827-1845_as
AD-68018.1	A-136268.1	CAACAGCUUAACAAGCCUA	769	A-136269.1	UAGGCUUGUUAAGCUGUUG	966	1837-1855_G19A_as
AD-68019.1	A-136270.1	CAAGCCUGAGGUCUUGGAA	770	A-136271.1	UUCCAAGACCUCAGGCUUG	967	1848-1866_G19A_as
AD-68020.1	A-136272.1	CUUGGAGGUGACCCUGAAA	771	A-136273.1	UUUCAGGGUCACCUCCAAG	968	1860-1878
AD-68021.1	A-136274.1	ACCCUGAACCGCCCAUUCA	772	A-136275.1	UGAAUGGGCGGUUCAGGGU	969	1870-1888
AD-68022.1	A-136276.1	GCCCAUUCCUGUUUGCUGU	773	A-136277.1	ACAGCAAACAGGAAUGGGC	970	1880-1898_as
AD-68025.1	A-136284.1	CACUUCCUGGGCCGCGUGA	774	A-136285.1	UCACGCGGCCCAGGAAGUG	971	1924-1942_G19A_as
AD-68026.1	A-136286.1	CGCGUGGCCAACCCGCUGA	775	A-136287.1	UCAGCGGGUUGGCCACGCG	972	1936-1954_as
AD-68027.1	A-136288.1	ACCCGCUGAGCACAGCAUA	776	A-136289.1	UAUGCUGUGCUCAGCGGGU	973	1946-1964_G19A_as
AD-68028.1	A-136290.1	ACAGCAUGAGGCCAGGGCA	777	A-136291.1	UGCCCUGGCCUCAUGCUGU	974	1957-1975
AD-68029.1	A-136292.1	CAGGGCCCCAGAACACAGU	778	A-136293.1	ACUGUGUUCUGGGGCCCUG	975	1969-1987_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-68032.1	A-136298.1	UCUGCCCCUGGCCUUUGAA	779	A-136299.1	UUCAAAGGCCAGGGGCAGA	976	2001-2019_G19A_as
AD-68033.1	A-136300.1	UUUGAGGCAAAGGCCAGCA	780	A-136301.1	UGCUGGCCUUUGCCUCAAA	977	2014-2032_as
AD-68034.1	A-136302.1	AGGCCAGCAGCAGAUAACA	781	A-136303.1	UGUUAUCUGCUGCUGGCCU	978	2024-2042_as
AD-68035.1	A-136304.1	AGAUAACAACCCCGGACAA	782	A-136305.1	UUGUCCGGGGUUGUUAUCU	979	2035-2053_as
AD-68036.1	A-136306.1	CCGGACAAAUCAGCGAUGU	783	A-136307.1	ACAUCGCUGAUUUGUCCGG	980	2046-2064_as
AD-68037.1	A-136308.1	AGCGAUGUGUCACCCCCAA	784	A-136309.1	UUGGGGGUGACACAUCGCU	981	2057-2075_G19A_as
AD-68084.2	A-136314.1	UUCUAAUGAGUCGACUUUA	785	A-136315.1	UAAAGUCGACUCAUUAGAA	982	2090-2108_G19A_as
AD-68085.2	A-136320.1	GUUUCUCCUUGGUCUAAGU	786	A-136321.1	ACUUAGACCAAGGAGAAAC	983	2124-2142_as
AD-68086.2	A-136328.1	AGCCUGCAGCGGCACAAAU	787	A-136329.1	AUUUGUGCCGCUGCAGGCU	984	2167-2185_as
AD-68087.2	A-136330.1	CACAAAUGCACCUCCCAGU	788	A-136331.1	ACUGGGAGGUGCAUUUGUG	985	2179-2197_as
AD-68088.2	A-136332.1	ACCUCCCAGUUUGCUGGGU	789	A-136333.1	ACCCAGCAAACUGGGAGGU	986	2188-2206_as
AD-68089.2	A-136334.1	UGCUGGGUUUAUUUUAGAA	790	A-136335.1	UUCUAAAAUAAACCCAGCA	987	2199-2217_G19A_as
AD-68090.2	A-136340.1	CAAGAACCAGUGUUUAGCA	791	A-136341.1	UGCUAAACACUGGUUCUUG	988	2234-2252_G19A_as
AD-68091.2	A-136354.1	AGUGUUCCCUUUUCAAGUU	792	A-136355.1	AACUUGAAAAGGGAACACU	989	2309-2327_as
AD-68092.2	A-136356.1	UUCAAGUUGAGAACAAAAA	793	A-136357.1	UUUUUGUUCUCAACUUGAA	990	2320-2338_as
AD-68093.2	A-136358.1	CAAAAAUUGGGUUUUAAAA	794	A-136359.1	UUUUAAAACCCAAUUUUUG	991	2333-2351_as
AD-68094.2	A-136362.1	AAAGUAUACAUUUUUGCAU	795	A-136363.1	AUGCAAAAAUGUAUACUUU	992	2354-2372_as
AD-68095.2	A-136368.1	UUUAGUGUCUUGAAUGUAA	796	A-136369.1	UUACAUUCAAGACACUAAA	993	2388-2406_as

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-68096.2	A-136370.1	GAAUGUAAGAACAUGACCU	797	A-136371.1	AGGUCAUGUUCUUACAUUC	994	2399-2417_as
AD-68097.2	A-136374.1	UGUAGUGUCUGUAAUACCU	798	A-136375.1	AGGUAUUACAGACACUACA	995	2421-2439_as
AD-68098.2	A-136376.1	UGUAAUACCUUAGUUUUUU	799	A-136377.1	AAAAAACUAAGGUAUUACA	996	2430-2448_as
AD-68099.2	A-136378.1	UUUUUUCCACAGAUGCUUA	800	A-136379.1	UAAGCAUCUGUGGAAAAAA	997	2443-2461_G19A_as
AD-68100.2	A-136382.1	UUUUUGAACAAUACGUGAA	801	A-136383.1	UUCACGUAUUGUUCAAAAA	998	2465-2483_as
AD-68101.2	A-136392.1	ACCAUAGCUGGUUAUUUCU	802	A-136393.1	AGAAAUAACCAGCUAUGGU	999	2519-2537_as
AD-68102.2	A-136394.1	UUAUUUCUCCCUUGUGUUA	803	A-136395.1	UAACACAAGGGAGAAAUAA	1000	2530-2548_as
AD-68116.1	A-136312.1	UCCCACCUUUUCUUCUAAU	804	A-136313.1	AUUAGAAGAAAAGGUGGGA	1001	2078-2096_as
AD-68117.1	A-136316.1	UCGACUUUGAGCUGGAAAG	805	A-136317.1	CUUUCCAGCUCAAAGUCGA	1002	2100-2118_as
AD-68118.1	A-136318.1	CUGGAAAGCAGCCGUUUCU	806	A-136319.1	AGAAACGGCUGCUUUCCAG	1003	2111-2129_as
AD-68119.1	A-136322.1	UGGUCUAAGUGUGCUGCAU	807	A-136323.1	AUGCAGCACACUUAGACCA	1004	2133-2151_as
AD-68120.1	A-136324.1	GCUGCAUGGAGUGAGCAGU	808	A-136325.1	ACUGCUCACUCCAUGCAGC	1005	2145-2163_as
AD-68121.1	A-136326.1	UGAGCAGUAGAAGCCUGCA	809	A-136327.1	UGCAGGCUUCUACUGCUCA	1006	2156-2174_as
AD-68122.1	A-136336.1	UUAGAGAAUGGGGGUGGGA	810	A-136337.1	UCCCACCCCCAUUCUCUAA	1007	2212-2230_G19A_as
AD-68123.1	A-136338.1	GGGUGGGGAGGCAAGAACA	811	A-136339.1	UGUUCUUGCCUCCCCACCC	1008	2223-2241
AD-68124.1	A-136342.1	UGUUUAGCGCGGGACUACU	812	A-136343.1	AGUAGUCCCGCGCUAAACA	1009	2244-2262_as
AD-68125.1	A-136344.1	GGACUACUGUUCCAAAAAG	813	A-136345.1	CUUUUUGGAACAGUAGUCC	1010	2255-2273_as
AD-68126.1	A-136350.1	AGCUUGUUUGUGAAACAAA	814	A-136351.1	UUUGUUUCACAAACAAGCU	1011	2288-2306_as
AD-68127.1	A-136352.1	AAACAAAAAAAGUGUUCCCU	815	A-136353.1	AGGGAACACUUUUUUUGUUU	1012	2300-2318_as
AD-68128.1	A-136360.1	UUUUAAAAUUAAAGUAUAA	816	A-136361.1	UUAUACUUUAAUUUUAAAAA	1013	2344-2362

Duplex Name	Sense Oligo Name	Sequence	SEQ ID NO.	Antisense Oligo Name	Sequence	SEQ ID NO.	Location on NM_000029.3
AD-68129.1	A-136364.1	UUUUGCAUUGCCUUCGGUU	817	A-136365.1	AACCGAAGGCAAUGCAAAA	1014	2365-2383_as
AD-68130.1	A-136366.1	UUCGGUUUGUAUUUAGUGU	818	A-136367.1	ACACUAAAUACAAACCGAA	1015	2377-2395_as
AD-68131.1	A-136372.1	AACAUGACCUCCGUGUAGU	819	A-136373.1	ACUACACGGAGGUCAUGUU	1016	2408-2426_as
AD-68132.1	A-136380.1	CAGAUGCUUGUGAUUUUUA	820	A-136381.1	UAAAAAUCACAAGCAUCUG	1017	2452-2470_G19A_as
AD-68133.1	A-136384.1	UACGUGAAAGAUGCAAGCA	821	A-136385.1	UGCUUGCAUCUUUCACGUA	1018	2476-2494_as
AD-68134.1	A-136386.1	UGCAAGCACCUGAAUUUCU	822	A-136387.1	AGAAAUUCAGGUGCUUGCA	1019	2487-2505_as
AD-68135.1	A-136388.1	GAAUUUCUGUUUGAAUGCA	823	A-136389.1	UGCAUUCAAACAGAAAUUC	1020	2498-2516_G19A_as
AD-68136.1	A-136390.1	UUUGAAUGCGGAACCAUAA	824	A-136391.1	UUAUGGUUCCGCAUUCAAA	1021	2507-2525_G19A_as
AD-68137.1	A-136396.1	UUGUGUUAGUAAUAAACGU	825	A-136397.1	ACGUUUAUUACUAACACAA	1022	2541-2559_as
AD-68138.1	A-136398.1	AUAAACGUCUUGCCACAAU	826	A-136399.1	AUUGUGGCAAGACGUUUAU	1023	2552-2570_as
AD-68139.1	A-136400.1	UGCCACAAUAAGCCUCCAA	827	A-136401.1	UUGGAGGCUUAUUGUGGCA	1024	2562-2580_as

Table 12. AGT single dose screen in Hep3B cells (21/23mers)

Duplex Name	10nM Avg	10 nM SD	0.1 nM Avg	0.1nM SD
AD-67864.1	86.08	0.42	100.66	4.93
AD-67865.1	90.98	0.44	97.56	4.30
AD-67866.1	107.85	3.17	108.20	1.59
AD-67867.1	96.24	5.18	96.22	4.24
AD-67868.1	92.25	0.45	93.87	0.92
AD-67869.1	107.24	8.40	96.54	3.78
AD-67870.1	89.43	1.75	96.84	0.47
AD-67871.1	100.66	4.93	96.91	5.22
AD-67872.1	92.27	2.26	87.75	7.73
AD-67873.1	118.49	6.38	105.63	3.10
AD-67874.1	98.36	8.18	99.57	1.46
AD-67875.1	98.55	2.89	100.76	14.27
AD-67876.1	98.951	5.33	105.24	0.51
AD-67877.1	104.94	5.14	100.97	2.47
AD-67878.1	101.79	7.47	100.61	0.98
AD-67879.1	99.66	6.34	101.66	0.49
AD-67880.1	99.23	1.94	93.79	9.63
AD-67881.1	95.84	0.93	104.16	2.04
AD-67882.1	97.52	1.43	98.09	9.60
AD-67883.1	94.53	1.85	95.88	3.75
AD-67884.1	110.16	5.39	105.25	1.54
AD-67885.1	101.70	4.48	97.94	5.75
AD-67886.1	107.09	2.09	102.03	3.00
AD-67887.1	95.51	0.46	94.24	4.15
AD-67888.1	105.98	1.55	101.03	5.44
AD-67889.1	89.42	0.87	102.44	5.52
AD-67890.1	96.51	0.94	99.34	6.81
AD-67891.1	89.73	0.43	102.01	0.99
AD-67892.1	85.81	3.36	91.97	3.60
AD-67893.1	104.89	2.05	93.25	3.65
AD-67894.1	95.95	6.57	100.61	0.98
AD-67895.1	87.61	3.43	92.99	5.92
AD-67896.1	102.36	0.50	102.37	1.50
AD-67897.1	89.23	6.55	101.66	1.49
AD-67898.1	87.68	6.01	97.89	3.83
AD-67899.1	10.98	1.28	28.08	7.87
AD-67900.1	16.91	2.47	42.49	5.81
AD-67901.1	51.36	1.00	73.53	10.77

Duplex Name	10nM Avg	10 nM SD	0.1 nM Avg	0.1nM SD
AD-67902.1	32.91	6.25	49.54	4.60
AD-67903.1	8.23	3.73	25.89	8.71
AD-67904.1	76.02	3.35	92.35	5.88
AD-67905.1	99.22	0.97	103.21	7.58
AD-67906.1	12.68	6.52	31.29	0.76
AD-67907.1	25.24	0.86	68.71	0.67
AD-67908.1	15.32	6.82	41.71	0.40
AD-67909.1	57.21	2.52	81.72	1.60
AD-67910.1	11.66	3.10	54.68	6.68
AD-67911.1	40.57	0.39	60.72	4.16
AD-67912.1	21.45	0.84	50.16	2.70
AD-67913.1	44.86	5.26	69.55	5.78
AD-67914.1	13.41	4.82	14.58	2.84
AD-67915.1	38.73	3.41	62.81	7.67
AD-67916.1	5.21	2.70	19.28	6.84
AD-67917.1	16.92	1.57	50.03	3.91
AD-67918.1	52.71	4.38	95.29	6.53
AD-67919.1	86.98	0.85	96.94	6.17
AD-67920.1	28.31	8.20	62.46	8.84
AD-67921.1	40.44	1.38	65.06	20.38
AD-67922.1	37.99	0.93	68.09	5.00
AD-67923.1	9.52	0.97	31.95	1.09
AD-67924.1	20.28	2.28	53.38	6.78
AD-67925.1	15.78	1.46	35.24	4.82
AD-67926.1	12.85	0.88	28.20	0.41
AD-67927.1	39.78	2.72	70.72	17.16
AD-67928.1	48.92	8.11	76.56	4.12
AD-67929.1	95.53	3.27	103.52	6.08
AD-67930.1	7.70	3.25	38.13	1.12
AD-67931.1	62.59	2.14	83.32	7.74
AD-67932.1	12.85	4.97	48.21	4.95
AD-67933.1	75.51	4.06	99.92	1.95
AD-67934.1	95.55	4.21	95.85	1.87
AD-67935.1	6.92	0.06	26.43	22.43
AD-67936.1	30.62	3.29	64.66	5.06
AD-67937.1	11.89	1.33	46.23	25.91
AD-67938.1	84.08	4.94	94.19	0.46
AD-67939.1	49.09	0.24	76.31	13.39
AD-67940.1	77.85	0.76	90.12	5.29
AD-67947.1	81.74	5.60	89.68	3.07

Duplex Name	10nM Avg	10 nM SD	0.1 nM Avg	0.1nM SD
AD-67948.1	57.40	3.93	75.94	12.96
AD-67949.1	89.04	1.30	98.84	4.35
AD-67950.1	30.38	6.93	50.01	4.40
AD-67951.1	57.60	12.32	84.26	2.89
AD-67952.1	30.08	9.84	71.83	1.76
AD-67954.1	63.41	2.17	83.16	5.29
AD-67955.1	66.78	1.30	88.74	2.60
AD-67956.1	48.82	4.54	84.38	7.02
AD-67957.1	66.79	1.96	96.46	3.78
AD-67958.1	11.88	6.31	28.49	7.58
AD-67959.1	50.08	5.87	78.05	1.14
AD-67960.1	53.33	9.104	72.41	9.90
AD-67962.1	17.29	5.41	54.30	13.17
AD-67963.1	19.63	2.11	49.27	15.43
AD-67964.1	14.83	0.14	46.79	6.40
AD-67965.1	15.94	9.26	36.16	16.09
AD-67966.1	41.84	9.95	80.28	3.54
AD-67967.1	20.10	2.94	45.85	6.71
AD-67968.1	24.10	0.47	45.77	0.22
AD-67970.1	41.61	6.09	59.36	1.16
AD-67971.1	92.20	3.16	97.48	4.29
AD-67972.1	24.48	3.46	60.84	2.68
AD-67973.1	67.49	2.31	93.19	4.56
AD-67974.1	22.421	0.76	62.87	17.33
AD-67975.1	20.05	2.157	52.74	5.93
AD-67976.1	19.21	5.30	54.84	6.96
AD-67978.1	17.36	1.10	60.49	14.96
AD-67979.1	104.18	7.14	104.08	3.06
AD-67980.1	17.85	4.84	43.65	9.34
AD-67981.1	28.91	4.09	63.61	0.62
AD-67982.1	91.54	0.44	103.34	
AD-67983.1	76.45	1.87	97.09	0.95
AD-67984.1	23.20	0.34	75.39	8.84
AD-67986.1	10.16	2.32	43.00	0.21
AD-67987.1	82.21	0.80	90.90	10.66
AD-67988.1	22.56	7.80	59.12	9.52
AD-67989.1	34.16	10.22	67.14	9.83
AD-67990.1	24.33	3.68	36.35	3.20
AD-67991.1	81.13	3.97	100.55	3.94
AD-67992.1	56.20	3.30	97.78	1.91

Duplex Name	10nM Avg	10 nM SD	0.1 nM Avg	0.1nM SD
AD-67993.1	29.38	5.01	78.86	13.08
AD-67994.1	20.30	4.44	30.93	
AD-67995.1	13.97	2.72	37.27	5.82
AD-67996.1	14.48	0.49	30.62	6.25
AD-67997.1	35.60	7.78	70.86	12.09
AD-67998.1	29.38	5.01	62.37	15.13
AD-67999.1	58.52	6.58	86.27	9.70
AD-68001.1	39.90	11.75	68.76	5.38
AD-68002.1	70.36	2.41	87.50	1.61
AD-68003.1	31.65	2.78	86.01	2.10
AD-68004.1	23.47	1.60	42.71	1.04
AD-68005.1	30.41	6.21	68.42	1.00
AD-68006.1	20.44	8.64	41.45	5.87
AD-68009.1	26.59	6.45	50.87	12.58
AD-68010.1	18.01	2.98	41.65	11.68
AD-68011.1	48.64	4.28	75.01	10.99
AD-68012.1	21.28	0.41	66.82	13.98
AD-68013.1	101.46	9.93	109.28	4.28
AD-68014.1	43.62	7.44	71.82	0.35
AD-68017.1	16.05	11.61	38.14	14.23
AD-68018.1	14.74	0.57	62.02	9.38
AD-68019.1	20.85	3.66	84.24	1.23
AD-68020.1	31.12	4.86	70.58	16.45
AD-68021.1	18.98	3.8	56.30	10.96
AD-68022.1	16.41	9.93	27.87	15.96
AD-68025.1	86.91	1.70	99.51	3.41
AD-68026.1	26.43	9.50	73.34	1.79
AD-68027.1	39.43	0.38	72.57	1.42
AD-68028.1	56.98	3.34	80.52	
AD-68029.1	49.97	3.42	85.43	2.93
AD-68032.1	71.12	3.48	91.96	6.30
AD-68033.1	102.29	2.50	99.13	0.97
AD-68034.1	15.54	3.32	32.03	3.91
AD-68035.1	19.40	6.88	49.77	6.32
AD-68036.1	16.23	8.62	29.22	4.28
AD-68037.1	20.40	5.24	49.31	9.13
AD-68084.2	15.14	3.24	42.67	5.63
AD-68085.2	17.11	5.52	30.76	11.20
AD-68086.2	8.96	0	21.05	2.98
AD-68087.2	22.54	14.44	26.79	37.89

Duplex Name	10nM Avg	10 nM SD	0.1 nM Avg	0.1nM SD
AD-68088.2	34.54	2.19	76.58	1.87
AD-68089.2	27.02	5.91	59.45	13.85
AD-68090.2	19.90	0.97	35.94	7.00
AD-68091.2	15.18	0.74	32.19	3.77
AD-68092.2	13.21	0.25	40.48	1.38
AD-68093.2	13.94	3.11	52.91	25.17
AD-68094.2	48.22	7.06	89.18	25.43
AD-68095.2	83.02	5.69	81.51	1.19
AD-68096.2	74.34	5.82	75.78	1.21
AD-68097.2	88.32	4.32	86.30	7.18
AD-68098.2	69.49	0.34	69.49	1.02
AD-68099.2	95.96	3.76	51.05	72.19
AD-68100.2	81.51	1.19	92.05	3.60
AD-68101.2	76.34	2.99	74.83	5.13
AD-68102.2	71.02	4.52	76.99	6.78
AD-68116.1	9.94	0.38	31.41	3.53
AD-68117.1	18.24	0.62	51.01	7.96
AD-68118.1	16.61	0.32	31.54	7.50
AD-68119.1	48.03	3.76	77.61	12.49
AD-68120.1	20.17	11.80	72.58	10.63
AD-68121.1	16.25	4.55	57.64	25.65
AD-68122.1	57.36	5.33	97.32	4.76
AD-68123.1	15.84	1.24	45.55	2.00
AD-68124.1	24.62	8.40	51.57	19.72
AD-68125.1	18.71	9.38	35.98	6.14
AD-68126.1	13.13	6.42	47.97	1.41
AD-68127.1	41.04	12.66	85.58	2.93
AD-68128.1	62.20	16.27	107.38	9.46
AD-68129.1	79.00		81.25	3.18
AD-68130.1	72.97	2.50	88.00	3.88
AD-68131.1	134.88	9.24	92.09	5.41
AD-68132.1	81.05	5.95	89.85	3.96
AD-68133.1	85.28	2.50	104.25	2.04
AD-68134.1	62.63	0.92	83.94	6.98
AD-68135.1	72.95	0.35	79.05	3.87
AD-68136.1	74.86	10.60	88.88	
AD-68137.1	85.08	6.24	90.50	4.87
AD-68138.1	76.05	1.11	76.34	2.99
AD-68139.1	102.25	8.01	99.42	6.81

Example 4: *In Vivo* AGT Silencing in a mouse expressing hAGT

A series of experiments were performed to assess hAGT target knockdown in mice expressing human AGT (hAGT) from an AAV8 expression vector which has strong liver tropism. Briefly, mice were infected with 1 x 10^{11} AAV8 particles containing an expression construct for hAGT under the control of a constitutive promoter. Two weeks after infection, mice were administered a single 3.0 mg/kg, 1.0 mg/kg, 0.3 mg/kg, or 0.1 mg/kg dose of an siRNA targeting hAGT (AD-67327.2 or AD-67335.2), or PBS as a control (n=4 per group). The nucleotide sequences of the agents assessed in these experiments are provided in Table 13.

Table 13. Modified Sense and Antisense Strand Sequences of AGT dsRNAs (21/23mers)

Duplex Name	Location on NM_000029.3	Sense Strand/ Antisense Strand	Sense Sequence/Antisense Sequence	SEQ ID NO.	Parent Duplex
AD-67327	2081-2101	A-134527	uscsucccAfcCfUfUfuucuucuaauL96	1025	AD-60784
	2079-2101	A-134528	asUfsuagAfagaaaagGfuGfggagascsu	1026	
AD-67335	1894-1914	A-134536	usgsuuugCfuGfUfGfuaugaucaaaL96	1027	AD-60781
	1892-1914	A-134538	usUfsugaUfcAfUfacacAfgCfaaacasgsg	1028	

At days 0, 3, 7, and 14, after administration of the agents, blood samples were collected and serum was prepared to determine the level of hAGT mRNA expression relative to the prebleed level of hAGT. The results of these experiments are shown in Table 14.

Table 14. hAGT single dose dose-response screen in hAGT expressing mice

Duplex	Dose mpk	Day 0		Day 3		Day 7		Day 14	
		Avg	SD	Avg	SD	Avg	SD	Avg	SD
	PBS	1.00	0.00	1.29	0.28	0.91	0.17	0.65	0.05
AD-67327	3	1.00	0.00	0.42	0.09	0.16	0.04	0.11	0.04
	1	1.00	0.00	0.63	0.05	0.44	0.04	0.31	0.06
	0.3	1.00	0.00	1.04	0.13	0.90	0.12	0.77	0.06
	0.1	1.00	0.00	0.91	0.06	0.88	0.07	0.74	0.15
AD-67335	3	1.00	0.00	0.58	0.14	0.42	0.13	0.37	0.10
	1	1.00	0.00	0.59	0.41	0.64	0.03	0.56	0.12

	0.3	1.00	0.00	1.06	0.28	0.81	0.14	0.80	0.07
	0.1	1.00	0.00	1.18	0.18	1.02	0.10	0.85	0.08

Example 5: *In Vivo* AGT Silencing in a mouse expressing hAGT

A series of experiments were performed to assess hAGT target knockdown in mice expressing hAGT from an AAV8 expression vector which has a strong liver tropism. Briefly, mice were infected with 1 x 10^{11} AAV8 particles containing an expression construct for hAGT under the control of a constitutive promoter. Two weeks after infection with the AAV8 virus, mice were administered a single 1 mg/kg dose of an siRNA targeting hAGT, or PBS as a control (n=3 per group). The nucleotide sequences of the duplexes assessed in these experiments are provided in Table 15.

Table 15. Modified Sense and Antisense Strand Sequences of AGT dsRNAs (21/23mers)

Duplex Name	Location on NM_000029.3	Sense Strand/ Antisense Strand	Sense Sequence/Antisense Sequence	SEQ ID NO	Parent Duplex
AD-68577	855-875	A-137778	ususccguAfuAfUfAfuggcaugcaaL96	1029	AD-60779
	853-875	A-137779	usUfsgcaUfgCfCfauauAfuAfcggaasgsc	1030	
AD-68581	1741-1761	A-137784	ascscugcAfaAfAfAfuugagcaauaL96	1031	AD-56029
	1739-1761	A-137785	usAfsuugCfuCfAfauuuUfuGfcaggususc	1032	
AD-68582	1741-1761	A-137784	ascscugcAfaAfAfAfuugagcaauaL96	1033	AD-56029
	1739-1761	A-137786	usAfsuugCfucaauuuUfuGfcaggususc	1034	
AD-67335	1894-1914	A-134536	usgsuuugCfuGfUfGfuaugaucaaaL96	1035	AD-60781
	1892-1914	A-134538	usUfsugaUfcAfUfacacAfgCfaaacasgsg	1036	
AD-67327	2081-2101	A-134527	uscsucccAfcCfUfUfuucuucuaauL96	1037	AD-52474
	2079-2101	A-134528	asUfsuagAfagaaaagGfuGfggagascsu	1038	
AD-68575	2084-2104	A-137775	cscscaccUfuUfUfCfuucuaaugaaL96	1039	AD-60777
	2082-2104	A-137776	usUfscauUfaGfAfagaaAfaGfgugggsasg	1040	
AD-68576	2084-2104	A-137775	cscscaccUfuUfUfCfuucuaaugaaL96	1041	AD-60777
	2082-2104	A-137777	usUfscauUfagaagaaAfaGfgugggsasg	1042	
AD-68583	2291-2311	A-137787	cscsagcuUfgUfUfUfgugaaacaaaL96	1043	AD-56019
	2289-2311	A-137788	usUfsuguUfuCfAfcaaaCfaAfgcuggsusc	1044	
AD-68584	2291-2311	A-137787	cscsagcuUfgUfUfUfgugaaacaaaL96	1045	AD-56019
	2289-2311	A-137789	usUfsuguUfucacaaaCfaAfgcuggsusc	1046	
AD-67313	2309-2329	A-134509	asasaaaaGfuGfUfUfcccuuuucaaL96	1047	AD-60776
	2307-2329	A-134510	usUfsgaaAfagggaacAfcUfuuuuusgsu	1048	
AD-67314	2309-2329	A-134509	asasaaaaGfuGfUfUfcccuuuucaaL96	1049	AD-60776
	2307-2329	A-134511	usUfsgaaAfaGfGfgaacAfcUfuuuuusgsu	1050	

Seven days after administration of the agents, blood samples were collected and serum was prepared to determine the level of hAGT mRNA expression relative to the prebleed level of hAGT. The results of these experiments are provided in Table 16.

Table 16. hAGT single dose dose-response screen in hAGT expressing mice

Duplex	Average	SD
PBS	98.6	8.7
AD-68577	65.1	7.7
AD-68581	53.1	3.3
AD-68582	44.8	11.1
AD-67335	60.5	3.1
AD-67327	43.0	1.0
AD-68575	48.0	9.4
AD-68576	47.4	5.9
AD-68583	51.3	7.7
AD-68584	61.0	2.1
AD-67313	70.8	7.6
AD-67314	66.2	5.7

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. Such equivalents are intended to be encompassed by the scope of the following claims.

We claim:

1. A double-stranded ribonucleic acid (RNAi) agent for inhibiting expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:1, and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:2,

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

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

2. A double-stranded ribonucleic acid (RNAi) agent for inhibiting expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region,

wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101; 803-843; 834-859; 803-859; 803-875; 834-875; 847-875; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1892-1914; 1894-1914;1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2078-2107; 2078-2011; 2080-2098; 2081-2099; 2081-2104; 2081-2011; 2082-2100; 2084-2102; 2084-2011; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2291-2311; 2291-2318; 2291-2315; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2304-2329; 2306-2324; 2307-2325; 2309-2327; 2309-2329; 2309-2342; 2309-2350; 2309-2358; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide

sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2, and

wherein the antisense strand is substantially complementary to the sense strand.

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

4. The double-stranded RNAi agent of claim 2, wherein said sense strand is conjugated to a ligand attached at the 3'-terminus.

5. The double-stranded RNAi agent of any one of claims 1-4, wherein all of the nucleotides of said sense strand and all of the nucleotides of said antisense strand are modified nucleotides.

6. The double-stranded RNAi agent of any one of claims 1-4, wherein said sense strand and said antisense strand comprise a region of complementarity which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the sequences listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15.

7. The double-stranded RNAi agent of any one of claims 1 and 3-6, wherein at least one of said modified nucleotides is selected from the group consisting of a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an unlocked nucleotide, a conformationally restricted nucleotide, a constrained ethyl nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a nucleotide comprising a 5'-phosphorothioate group, and a terminal nucleotide linked to a cholesteryl derivative or a dodecanoic acid bisdecylamide group.

8. The double-stranded RNAi agent of any one of claims 1-7, wherein at least one strand comprises a 3' overhang of at least 1 nucleotide.

9. The double-stranded RNAi agent of any one of claims 1-7, wherein at least one strand comprises a 3' overhang of at least 2 nucleotides.

10. A double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand and an antisense strand forming a double-stranded region, wherein said antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein said double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

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

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

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y'; and

wherein the sense strand is conjugated to at least one ligand.

11. The double-stranded RNAi agent of claim 10, wherein i is 0; j is 0; i is 1; j is 1; both i and j are 0; or both i and j are 1.

12. The double-stranded RNAi agent of claim 10, wherein k is 0; l is 0; k is 1; l is 1; both k and l are 0; or both k and l are 1.

13. The double-stranded RNAi agent of claim 10, wherein XXX is complementary to X'X'X', YYY is complementary to Y'Y'Y', and ZZZ is complementary to Z'Z'Z'.

14. The double-stranded RNAi agent of claim 10, wherein the YYY motif occurs at or near the cleavage site of the sense strand.

15. The double-stranded RNAi agent of claim 10, wherein the Y′Y′Y′ motif occurs at the 11, 12 and 13 positions of the antisense strand from the 5'-end.

16. The double-stranded RNAi agent of claim 15, wherein the Y′ is 2′-O-methyl.

17. The double-stranded RNAi agent of claim 10, wherein formula (III) is represented by formula (IIIa):

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

antisense: 3' $n_{p'}$-$N_{a'}$- Y′Y′Y′- $N_{a'}$- $n_{q'}$ 5' (IIIa).

18. The double-stranded RNAi agent of claim 10, wherein formula (III) is represented by formula (IIIb):

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

antisense: 3' $n_{p'}$-$N_{a'}$- Y′Y′Y′-$N_{b'}$-Z′Z′Z′- $N_{a'}$- $n_{q'}$ 5' (IIIb)

wherein each N_b and N_b′ independently represents an oligonucleotide sequence comprising 1-5 modified nucleotides.

19. The double-stranded RNAi agent of claim 10, wherein formula (III) is represented by formula (IIIc):

sense: 5' n_p -N_a –X X X -N_b -Y Y Y -N_a - n_q 3'

antisense: 3' $n_{p'}$-$N_{a'}$- X′X′X′-$N_{b'}$- Y′Y′Y′- $N_{a'}$- $n_{q'}$ 5' (IIIc)

wherein each N_b and N_b′ independently represents an oligonucleotide sequence comprising 1-5 modified nucleotides.

20. The double-stranded RNAi agent of claim 10, wherein formula (III) is represented by formula (IIId):

sense: 5' n_p -N_a –X X X- N_b -Y Y Y -N_b -Z Z Z -N_a - n_q 3'

antisense: 3' $n_{p'}$-$N_{a'}$- X′X′X′- $N_{b'}$-Y′Y′Y′-$N_{b'}$-Z′Z′Z′- $N_{a'}$- $n_{q'}$ 5'

(IIId)

wherein each N_b and N_b′ independently represents an oligonucleotide sequence comprising 1-5 modified nucleotides and each N_a and N_a′ independently represents an oligonucleotide sequence comprising 2-10 modified nucleotides.

21. The double-stranded RNAi agent of any one of claims 1-4 or 10, wherein the double-stranded region is 15-30 nucleotide pairs in length.

22. The double-stranded RNAi agent of claim 21, wherein the double-stranded region is 17-23 nucleotide pairs in length.

23. The double-stranded RNAi agent of claim 21, wherein the double-stranded region is 17-25 nucleotide pairs in length.

24. The double-stranded RNAi agent of claim 21, wherein the double-stranded region is 23-27 nucleotide pairs in length.

25. The double-stranded RNAi agent of claim 21, wherein the double-stranded region is 19-21 nucleotide pairs in length.

26. The double-stranded RNAi agent of claim 21, wherein the double-stranded region is 21-23 nucleotide pairs in length.

27. The double-stranded RNAi agent of any one of claims 1-4 and 10, wherein each strand has 15-30 nucleotides.

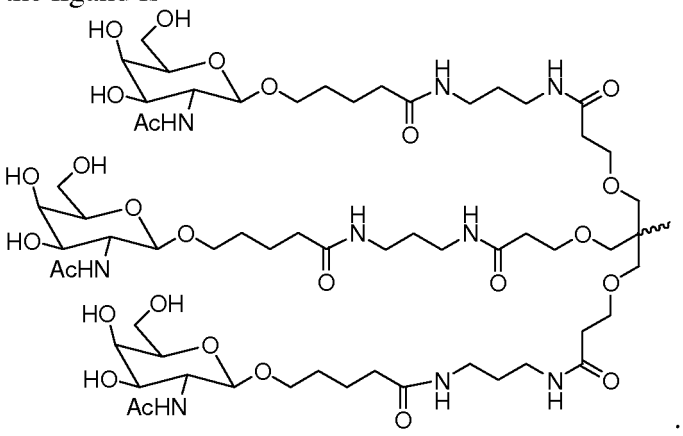
28. The double-stranded RNAi agent of any one of claims 1-4 and 10, wherein each strand has 19-30 nucleotides.

29. The double-stranded RNAi agent of claim 10, wherein the modifications on the nucleotides are selected from the group consisting of LNA, CRN,cET, UNA, HNA, CeNA, 2′-methoxyethyl, 2′-O-alkyl, 2′-O-allyl, 2′-C-allyl, 2′-fluoro, 2′-deoxy, 2'-hydroxyl, and combinations thereof.

30. The double-stranded RNAi agent of claim 29, wherein the modifications on the nucleotides are 2′-O-methyl or 2′-fluoro modifications.

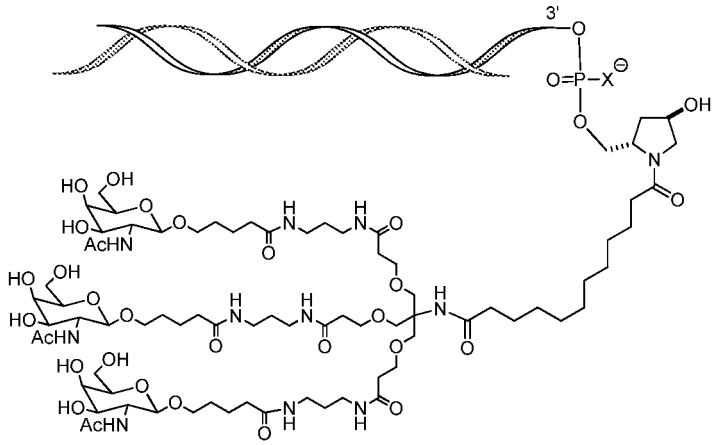
31. The double-stranded RNAi agent of any one of claims 1, 4, and 10, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

32. The double-stranded RNAi agent of any one of claims 1, 4, and 10, wherein the ligand is



33. The double-stranded RNAi agent of any one of claims 1, 4, and 10, wherein the ligand is attached to the 3′ end of the sense strand.

34. The double-stranded RNAi agent of claim 33, wherein the RNAi agent is conjugated to the ligand as shown in the following schematic



wherein X is O or S.

35. The double-stranded RNAi agent of any one of claims 1-4 and 10, wherein said RNAi agent further comprises at least one phosphorothioate or methylphosphonate internucleotide linkage.

36. The double-stranded RNAi agent of claim 35, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the 3'-terminus of one strand.

37. The double-stranded RNAi agent of claim 36, wherein said strand is the antisense strand.

38. The double-stranded RNAi agent of claim 36, wherein said strand is the sense strand.

39. The double-stranded RNAi agent of claim 35, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the 5'-terminus of one strand.

40. The double-stranded RNAi agent of claim 39, wherein said strand is the antisense strand.

41. The double-stranded RNAi agent of claim 39, wherein said strand is the sense strand.

42. The double-stranded RNAi agent of claim 35, wherein the phosphorothioate or methylphosphonate internucleotide linkage is at the both the 5'- and 3'-terminus of one strand.

43. The double-stranded RNAi agent of claim 42, wherein said strand is the antisense strand.

44. The double-stranded RNAi agent of claim 35, wherein said RNAi agent comprises 6-8 phosphorothioate internucleotide linkages.

45. The double-stranded RNAi of claim 44, wherein the antisense strand comprises two phosphorothioate internucleotide linkages at the 5'-terminus and two phosphorothioate internucleotide linkages at the 3'-terminus, and the sense strand comprises at least two phosphorothioate internucleotide linkages at either the 5'-terminus or the 3'-terminus.

46. The double-stranded RNAi agent of any one of claims 1-4 and 10, wherein the base pair at the 1 position of the 5′-end of the antisense strand is an AU base pair.

47. The double-stranded RNAi agent of claim 10, wherein the Y nucleotides contain a 2′-fluoro modification.

48. The double-stranded RNAi agent of claim 10, wherein the Y′ nucleotides contain a 2′-O-methyl modification.

49. The double-stranded RNAi agent of claim 10, wherein p′>0.

50. The double-stranded RNAi agent of claim 10, wherein p′=2.

51. The double-stranded RNAi agent of claim 50, wherein q'=0, p=0, q=0, and p' overhang nucleotides are complementary to the target mRNA.

52. The double-stranded RNAi agent of claim 50, wherein q'=0, p=0, q=0, and p' overhang nucleotides are non-complementary to the target mRNA.

53. The double-stranded RNAi agent of claim 50, wherein the sense strand has a total of 21 nucleotides and the antisense strand has a total of 23 nucleotides.

54. The double-stranded RNAi agent of any one of claims 49-53, wherein at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage.

55. The double-stranded RNAi agent of claim 54, wherein all n_p' are linked to neighboring nucleotides via phosphorothioate linkages.

56. The double-stranded RNAi agent of any one of claims 1-4 and 10, wherein said RNAi agent is selected from the group of RNAi agents listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15.

57. A double-stranded ribonucleic acid (RNAi) agent for inhibiting expression of angiotensinogen (AGT),

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

wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:1, and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:2,

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

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

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

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

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

58. The double-stranded RNAi agent of claim 57, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101; 803-843; 834-859; 803-859; 803-875; 834-875; 847-875; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1892-1914; 1894-1914;1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2078-2107; 2078-2011; 2080-2098; 2081-2099; 2081-2104; 2081-2011; 2082-2100; 2084-2102; 2084-2011; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2291-2311; 2291-2318; 2291-2315; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2304-2329; 2306-2324; 2307-2325; 2309-2327; 2309-2329; 2309-2342; 2309-2350; 2309-2358; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3

nucleotides from the nucleotides at the corresponding position of the nucleotide sequence of SEQ ID NO:2, and

wherein the antisense strand is substantially complementary to the sense strand.

59. The double-stranded RNAi agent of claim 57 or 58, wherein all of the nucleotides of said sense strand and all of the nucleotides of said antisense strand comprise a modification.

60. A double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein said antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein said double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

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

XXX, YYY, ZZZ, X'X'X', Y'Y'Y', and Z'Z'Z' each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2'-O-methyl or 2'-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y'; and

wherein the sense strand is conjugated to at least one ligand.

61. A double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein said antisense strand

comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein said double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

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

n_p′ >0 and at least one n_p′ is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a′ independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b′ independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b′ differ from the modification on Y′; and

wherein the sense strand is conjugated to at least one ligand.

62. A double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein said antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein said double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

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

n_p' >0 and at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y′; and

wherein the sense strand is conjugated to at least one ligand, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

63. A double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein said antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein said double-stranded RNAi agent is represented by formula (III):

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

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

wherein:

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

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

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

n_p' >0 and at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

each N_b and N_b' independently represents an oligonucleotide sequence comprising 0-10 nucleotides which are either modified or unmodified or combinations thereof;

XXX, YYY, ZZZ, X′X′X′, Y′Y′Y′, and Z′Z′Z′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

modifications on N_b differ from the modification on Y and modifications on N_b' differ from the modification on Y′;

wherein the sense strand comprises at least one phosphorothioate linkage; and

wherein the sense strand is conjugated to at least one ligand, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

64. A double-stranded ribonucleic acid (RNAi) agent capable of inhibiting the expression of angiotensinogen (AGT) in a cell, wherein said double-stranded RNAi agent comprises a sense strand complementary to an antisense strand, wherein said antisense strand comprises a region complementary to part of an mRNA encoding AGT, wherein each strand is about 14 to about 30 nucleotides in length, wherein said double-stranded RNAi agent is represented by formula (III):

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

antisense: 3' n_p'-N_a'- Y′Y′Y′- N_a'- n_q' 5' (IIIa)

wherein:

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

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

$n_p' > 0$ and at least one n_p' is linked to a neighboring nucleotide via a phosphorothioate linkage;

each N_a and N_a' independently represents an oligonucleotide sequence comprising 0-25 nucleotides which are either modified or unmodified or combinations thereof, each sequence comprising at least two differently modified nucleotides;

YYY and Y′Y′Y′ each independently represent one motif of three identical modifications on three consecutive nucleotides, and wherein the modifications are 2′-O-methyl or 2′-fluoro modifications;

wherein the sense strand comprises at least one phosphorothioate linkage; and

wherein the sense strand is conjugated to at least one ligand, wherein the ligand is one or more GalNAc derivatives attached through a bivalent or trivalent branched linker.

65. A double-stranded ribonucleic acid (RNAi) agent comprising a sense strand and an antisense strand, said sense strand and said antisense strand comprising sequences

selected from the group consisting of any one of the agents listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15.

66. A composition comprising a modified antisense polynucleotide agent, wherein said agent is capable of inhibiting the expression of AGT in a cell, and comprises a sequence complementary to a sense sequence selected from the group of the sequences listed in any one of Tables 3, 4, 7, 8, 11, 13, and 15, wherein the polynucleotide is about 14 to about 30 nucleotides in length.

67. A vector containing the double-stranded RNAi agent of claim 2.

68. A cell containing the double-stranded RNAi agent of any one of claims 1-4, 10, 57, 58, and 60-65.

69. A pharmaceutical composition comprising the double-stranded RNAi agent of any one of claims 1-4, 10, 57, 58, and 60-65, or the composition comprising a modified antisense polynucleotide agent of claim 66, or the vector of claim 67.

70. The pharmaceutical composition of claim 69, wherein double-stranded RNAi agent is administered in an unbuffered solution.

71. The pharmaceutical composition of claim 70, wherein said unbuffered solution is saline or water.

72. The pharmaceutical composition of claim 69, wherein said double-stranded RNAi agent is administered with a buffer solution.

73. The pharmaceutical composition of claim 72, wherein said buffer solution comprises acetate, citrate, prolamine, carbonate, or phosphate or any combination thereof.

74. The pharmaceutical composition of claim 73, wherein said buffer solution is phosphate buffered saline (PBS).

75. A method of inhibiting angiotensinogen (AGT) expression in a cell, the method comprising:

(a) contacting the cell with the double-stranded RNAi agent of any one of claims 1-4, 10, 57, 58, and 60-65, or the composition comprising a modified antisense polynucleotide agent of claim 66, the vector of claim 67, or the pharmaceutical composition of any one of claims 69-74; and

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

76. The method of claim 75, wherein said cell is within a subject.

77. The method of claim 76, wherein the subject is a human.

78. The method of claim 77, wherein the subject suffers from an angiotensinogen-associated disease.

79. The method of any one of claims 75-78, wherein the AGT expression is inhibited by at least about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 98% or about 100%.

80. A method of treating a subject having a angiotensinogen (AGT)-associated disorder, comprising administering to the subject a therapeutically effective amount of the double-stranded RNAi agent of any one of claims 1-4, 10, 57, 58, and 60-65, or the composition comprising a modified antisense polynucleotide agent of claim 66, the vector of claim 67, or the pharmaceutical composition of any one of claims 69-74, thereby treating said subject.

81. A method of treating a subject having a angiotensinogen (AGT)-associated disorder, comprising subcutaneously administering to the subject a therapeutically effective amount of a double-stranded ribonucleic acid (RNAi) agent,

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

wherein said sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:1, and said antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from the nucleotide sequence of SEQ ID NO:2,

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

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

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

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

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

82. The method of claim 81, wherein the sense strand comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from nucleotides 2801-2101; 803-843; 834-859; 803-859; 803-875; 834-875; 847-875; 1247-1271; 1566-1624; 1570-1624; 1584-1624; 1584-1624; 1584-1621; 2035-2144; 2070-2144; 2070-2103; 2201-2223; 2227-2360; 2227-2304; 2290-2318; 2304-2350; 2304-2326; 2320-2342; 2333-2360; 2333-2358; 485-503; 517-535; 560-578; 635-653; 803-821; 814-832; 822-840; 825-843; 834-852; 837-855; 841-859; 855-873; 967-985; 1247-1265; 1248-1266; 1249-1267; 1251-1269; 1253-1271; 1566-1584; 1570-1588; 1572-1590; 1574-1592; 1584-1602; 1587-1605; 1591-1609; 1592-1610; 1595-1613; 1601-1619; 1602-1620; 1605-1623; 1729-1747; 1738-1756; 1739-1757; 1741-1769; 1767-1785; 1810-1828; 1827-1845; 1880-1989; 1892-1914; 1894-1914;1894-2012; 2035-2053; 2046-2064; 2057-2075; 2070-2088; 2072-2090; 2078-2096; 2078-2107; 2078-2011; 2080-2098; 2081-2099; 2081-2104; 2081-2011; 2082-2100; 2084-2102; 2084-2011; 2090-2108; 2100-2118; 2111-2129; 2124-2142; 2125-2143; 2167-2185; 2179-2197; 2201-2219; 2202-2220; 2203-2221; 2204-2222; 2227-2245; 2230-2248; 2234-2252; 2244-2264; 2255-2273; 2266-2284; 2268-2286; 2270-2288; 2279-2297; 2281-2299; 2283-2301; 2284-2302; 2285-2303; 2286-2304; 2288-2306; 2290-2308; 2291-2309; 2291-2311; 2291-2318; 2291-2315; 2292-2310; 2294-2312; 2296-2314; 2299-2317; 2304-2322; 2304-2329; 2306-2324; 2307-2325; 2309-2327; 2309-2329; 2309-2342; 2309-2350; 2309-2358; 2314-2332; 2316-2334; 2317-2335; 2320-2338; 2321-2339; 2323-2341; 2325-2343; 2326-2344; 2328-2346; 2329-2347; 2331-2349; 2333-2351; 2334-2352; 2335-2353; 2339-2357; 2340-2358; or 2341-2359 of the nucleotide sequence of SEQ ID NO:1 and the antisense strand comprises at least 15 contiguous nucleotides differing by no more than 3

nucleotides from the ncueltodes at the corresponding position of the nucleotide sequence of SEQ ID NO:2, and

wherein the antisense strand is substantially complementary to the sense strand.

83. The method of claim 81 or 82, wherein all of the nucleotides of said sense strand and all of the nucleotides of said antisense strand comprise a modification.

84. The method of any one of claims 81-83, wherein the subject is a human.

85. The method of any one of claims 81-83, wherein the angiotensinogen-associated disease is selected from the group consisting of hypertension, borderline hypertension, primary hypertension, secondary hypertension, hypertensive emergency, hypertensive urgency, isolated systolic or diastolic hypertension, pregnancy-associated hypertension, diabetic hypertension, resistant hypertension, refractory hypertension, paroxysmal hypertension, renovascular hypertension, Goldblatt hypertension, ocular hypertension, glaucoma, pulmonary hypertension, portal hypertension, systemic venous hypertension, systolic hypertension, labile hypertension; hypertensive heart disease, hypertensive nephropathy, atherosclerosis, arteriosclerosis, vasculopathy, diabetic nephropathy, diabetic retinopathy, chronic heart failure, cardiomyopathy, diabetic cardiac myopathy,glomerulosclerosis, coarctation of the aorta, aortic aneurism, ventricular fibrosis, Cushing's syndrome, and other glucocorticoid excess states including chronic steroid therapy, pheochromocytoma, reninoma, secondary aldosteronism and other mineralocorticoid excess states, sleep apnea, thyroid/parathyroid disease, heart failure, myocardial infarction, angina, stroke, diabetes mellitus, renal disease, renal failure, systemic sclerosis, intrauterine growth restriction (IUGR) , and fetal growth restriction.

86. The method of any one of claims 81-83, wherein the angiotensinogen-associated disease is pregnancy-associated hypertension.

87. The method of any one of claims 81-83, wherein the double-stranded RNAi agent is administered at a dose of about 0.01 mg/kg to about 10 mg/kg or about 0.5 mg/kg to about 50 mg/kg.

88. The method of claim 87, wherein the double-stranded RNAi agent is administered at a dose of about 10 mg/kg to about 30 mg/kg.

89. The method of claim 87, wherein the double-stranded RNAi agent is administered at a dose of about 3 mg/kg.

90. The method of claim 87, wherein the double-stranded RNAi agent is administered at a dose of about 10 mg/kg.

91. The method of claim 87, wherein the double-stranded RNAi agent is administered at a dose of about 0.5 mg/kg twice per week.

92. The method of claim 87, wherein the double-stranded RNAi agent is administered at a dose of about 10 mg/kg every other week.

93. The method of claim 87, wherein the double-stranded RNAi agent is administered at a dose of about 0.5-1 mg/kg once per week.

94. The method of claim 87, wherein the double-stranded RNAi agent is administered subcutaneously.

95. The method of claim 87, wherein the double-stranded RNAi agent is administered intravenously.

96. The method of claim 87, wherein said RNAi agent is administered in two or more doses.

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

98. The method of claim 96, wherein said RNAi agent is administered twice per week.

99. The method of claim 96, wherein said RNAi agent is administered every other week.

100. The method of any one of claims 81-83, further comprising administering to the subject an additional therapeutic agent.

101. The method of claim 100, wherein the additional therapeutic agent is selected from the group consisting of a diuretic, an angiotensin converting enzyme (ACE) inhibitor, an angiotensin II receptor antagonist, a beta-blocker, a vasodialator, a calcium channel blocker, an aldosterone antagonist, an alpha$_2$-agonist, a renin inhibitor, an alpha-blocker, a peripheral acting adrenergic agent, a selective D1 receptor partial agonist, a nonselective alpha-adrenergic antagonist, a synthetic, steroidal antimineralocorticoid agent, or a combination of any of the foregoing, and a hypertension therapeutic agent formulated as a combination of agents.