COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF TRANSTHYRETIN

Field of the Invention

The invention relates to a double-stranded ribonucleic acid (dsRNA) targeting a transthyretin (TTR) gene, and methods of using the dsRNA to inhibit expression of TTR.

Cross Reference to Related Applications

This application claims the benefit of U.S. Provisional Application Serial No. 61/106,956, filed October 20, 2008; U.S. Provisional Application Serial No. 61/115,738, filed November 18, 2008; U.S. Provisional Application Serial No. 61/156,670, filed March 2, 2009; U.S. Provisional Application Serial No. 61/185,545, filed June 9, 2009; U.S. Provisional Application Serial No. 61/242,783, filed September 15, 2009; and U.S. Provisional Application Serial No. 61/244,794, filed September 22, 2009, all of which are incorporated herein by reference, in their entirety, for all purposes.

Reference to Sequence Listing

This application includes a Sequence Listing submitted electronically as a text file named _____.txt, created on _____, 2009, with a size of _____ bytes. The sequence listing is incorporated by reference.

Background of the Invention

Transthyretin (TTR) is a secreted thyroid hormone-binding protein. TTR binds and transports retinol binding protein (RBP)/ Vitamin A, and serum thyroxine (T4) in plasma and cerebrospinal fluid.

Both normal-sequence TTR and variant-sequence TTR cause amyloidosis. Normal-sequence TTR causes cardiac amyloidosis in people who are elderly and is termed senile systemic amyloidosis (SSA) (also called senile cardiac amyloidosis (SCA)). SSA often is accompanied by microscopic deposits in many other organs. TTR mutations accelerate the process of TTR amyloid formation and are the most important risk factor for the development of clinically significant TTR amyloidosis (also called ATTR (amyloidosis-transthyretin type)). More than 85 amyloidogenic TTR variants are known to cause systemic familial amyloidosis. The liver is the major site of TTR expression. Other significant sites of expression include the choroid plexus, retina and pancreas.

TTR amyloidosis manifests in various forms. When the peripheral nervous system is affected more prominently, the disease is termed familial amyloidotic polyneuropathy (FAP).

When the heart is primarily involved but the nervous system is not, the disease is called familial amyloidotic cardiomyopathy (FAC). A third major type of TTR amyloidosis is called leptomeningeal/CNS (Central Nervous System) amyloidosis.

Double-stranded RNA molecules (dsRNA) have been shown to block gene expression in a highly conserved regulatory mechanism known as RNA interference (RNAi). WO 99/32619 (Fire *et al.*) disclosed the use of a dsRNA of at least 25 nucleotides in length to inhibit the expression of genes in *C. elegans*. dsRNA has also been shown to degrade target RNA in other organisms, including plants (see, *e.g.*, WO 99/53050, Waterhouse *et al.*; and WO 99/61631, Heifetz *et al.*), *Drosophila* (see, *e.g.*, Yang, D., *et al.*, *Curr. Biol.* (2000) 10:1191-1200), and mammals (see WO 00/44895, Limmer; and DE 101 00 586.5, Kreutzer *et al.*).

U.S. 20070207974 discloses functional and hyperfunctional siRNAs. U.S. 20090082300 discloses antisense molecules directed against TTR. U.S. Pat. No. 7,250,496 discloses microRNAs directed against TTR.

Summary of the Invention

In one embodiment, the invention provides a double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR), wherein said dsRNA comprises a sense strand and an antisense strand, the antisense strand comprising a region complementary to a part of a mRNA encoding transthyretin (TTR), wherein said region of complementarity is less than 30 nucleotides in length and the antisense strand comprises 15 or more contiguous nucleotides of SEQ ID NO:170, SEQ ID NO:450, SEQ ID NO:730, or SEQ ID NO:1010. In a related embodiment, the sense strand comprises 15 or more contiguous nucleotides of SEQ ID NO:169, SEQ ID NO:449, SEQ ID NO:729, or SEQ ID NO:1009. In yet another related embodiment, the sense strand consists of SEQ ID NO:449 and the antisense strand consists of SEQ ID NO:450. In yet another related embodiment, the sense strand consists of SEQ ID NO:729 and the antisense strand consists of SEQ ID NO:730. In still another related embodiment, the sense strand consists of SEQ ID NO:1009 and the antisense strand consists of SEQ ID NO:1010. In yet another related embodiment, the dsRNA comprises a sense strand selected from Tables 3A, 3B, 4, 6A, 6B, 7, and 16, and an antisense strand selected from Tables 3A, 3B, 4, 6A, 6B, 7, and 16.

In certain embodiments, the region of complementarity between the antisense strand of the dsRNA and the mRNA encoding transthyretin is 19 nucleotides in length. In another embodiment, the region of complementarity consists of SEQ ID NO:170. In other embodiments,

each strand of the dsRNA is 19, 20, 21, 22, 23, or 24 nucleotides in length. In still another embodiment, each strand is 21 nucleotides in length.

In certain embodiments, the dsRNA for inhibiting expression of transthyretin does not cleave a TTR mRNA between the adenine nucleotide at position 637 of SEQ ID NO:1331 and the guanine nucleotide at position 638 of SEQ ID NO:1331. In other embodiments, the dsRNA cleaves a TTR mRNA between the guanine nucleotide at position 636 of SEQ ID NO:1331 and the adenine nucleotide at position 637 of SEQ ID NO:1331. In certain embodiments, the dsRNA anneals to a TTR mRNA between the guanine nucleotide at position 628 of SEQ ID NO:1331 and the uracil nucleotide at position 646 of SEQ ID NO: 1331.

In still other related embodiments, the invention provides dsRNA as described above for inhibiting expression of transthyretin wherein the dsRNA comprises one or more modified nucleotides. In related embodiments, at least one modified nucleotide (or nucleotides) is chosen from the group consisting of: a 2'-O-methyl modified nucleotide, a nucleotide comprising a 5'-phosphorothioate group, and a terminal nucleotide linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group. In another related embodiment, the modified nucleotide is chosen from the group of: a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an abasic nucleotide, 2'-amino-modified nucleotide, 2'-alkyl-modified nucleotide, morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide. In certain embodiments, the dsRNA comprises at least one 2'-O-methyl modified nucleotide.

In other embodiments, a dsRNA as described above for inhibiting expression of transthyretin is conjugated to a ligand, or formulated in a lipid formulation. In certain embodiments, the lipid formulation may be a LNP formulation, a LNP01 formulation, a XTC-SNALP formulation, or a SNALP formulation. In related embodiments, the XTC-SNALP formulation is as follows: using 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC) with XTC/DPPC/Cholesterol/PEG-cDMA in a ratio of 57.1/7.1/34.4/1.4 and a lipid:siRNA ratio of about 7. In still other related embodiments, the sense strand of the dsRNA consists of SEQ ID NO:1009 and the antisense strand consists of SEQ ID NO:1010, and the dsRNA is formulated in a XTC-SNALP formulation as follows: using 2,2-Dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (XTC) with a XTC/DPPC/Cholesterol/PEG-cDMA in a ratio of 57.1/7.1/34.4/1.4 and a lipid:siRNA ratio of about 7. Alternatively, a dsRNA such as those described above can be formulated in a LNP09 formulation as follows: using XTC/DSPC/Chol/PEG_{2000}-C14 in a ratio of 50/10/38.5/1.5 mol% and a lipid:siRNA ratio of about 11:1. In another variation, the dsRNA is formulated in a LNP11 formulation as follows: using MC3/DSPC/Chol/PEG_{2000}-C14 in a ratio

of 50/10/38.5/1.5 mol% and a lipid:siRNA ratio of about 11:1. In still another embodiment, the dsRNA is formulated in a LNP09 formulation or a LNP11 formulation and reduces TTR mRNA levels by about 85 to 90% at a dose of 0.3mg/kg, relative to a PBS control group. In yet another embodiment, the dsRNA is formulated in a LNP09 formulation or a LNP11 formulation and reduces TTR mRNA levels by about 50% at a dose of 0.1 mg/kg, relative to a PBS control group. In yet another embodiment, the dsRNA is formulated in a LNP09 formulation or a LNP11 formulation and reduces TTR protein levels in a dose-dependent manner relative to a PBS control group as measured by a western blot. In yet another embodiment, the dsRNA is formulated in a SNALP formulation as follows: using DlinDMA with a DLinDMA/DPPC/Cholesterol/PEG2000-cDMA in a ratio of 57.1/7.1/34.4/1.4 and a lipid:siRNA ratio of about 7.

In certain embodiments, the invention provides a dsRNA such as those described above for inhibiting expression of transthyretin, wherein administration of the dsRNA to a cell results in about 95% inhibition of TTR mRNA expression as measured by a real time PCR assay, wherein the cell is a HepG2 cell or a Hep3B cell, and wherein the concentration of the dsRNA is 10nM. In related embodiments, administration of the dsRNA to a cell results in about 74% inhibition of TTR mRNA expression as measured by a branched DNA assay, wherein the cell is a HepG2 cell or a Hep3B cell, and wherein the concentration of the dsRNA is 10nM. In other related embodiments, the dsRNA has an IC50 of less than 10 pM in a HepG2 cell, wherein the concentration of the dsRNA is 10nM. In still other related embodiments, the dsRNA has an ED50 of about 1 mg/kg. In still other related embodiments, administration of the dsRNA reduces TTR mRNA by about 80% in cynomolgus monkey liver, wherein the concentration of the dsRNA is 3 mg/kg. In still other related embodiments, administration of the dsRNA does not result in immunostimulatory activity in human peripheral blood mononuclear cells (PBMCs) as measured by IFN-alpha and TNF-alpha ELISA assays. In still other related embodiments, administration of the dsRNA reduces liver TTR mRNA levels by about 97% or serum TTR protein levels by about 90%, wherein the concentration of the dsRNA is 6 mg/kg. In still other related embodiments, administration of the dsRNA reduces liver TTR mRNA levels and/or serum TTR protein levels up to 22 days, wherein the concentration of the dsRNA is 6 mg/kg or 3 mg/kg. In still other related embodiments, the dsRNA suppresses serum TTR protein levels up to day 14 post-treatment when administered to a subject in need thereof at 1 mg/kg or 3 mg/kg. In still other related embodiments, the dsRNA reduces TTR expression by 98.9% in a Hep3B cell at a concentration of 0.1nM as measured by real-time PCR. In still other related

embodiments, the dsRNA reduces TTR expression by 99.4% in a Hep3B cell at a concentration of 10nM as measured by real-time PCR.

In other embodiments, the invention provides a double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR), wherein said dsRNA comprises a sense strand and an antisense strand, the antisense strand comprising a region complementary to a part of a mRNA encoding transthyretin (TTR), wherein said region of complementarity is less than 30 nucleotides in length and wherein the dsRNA comprises a sense strand selected from Tables 3A, 3B, 4, 6A, 6B, 7, and 16, and an antisense strand selected from Tables 3A, 3B, 4, 6A, 6B, 7, and 16.

In another embodiment, the invention provides a double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR), wherein said dsRNA comprises an antisense strand comprising a region complementary to 15-30 nucleotides of nucleotides 618-648 of SEQ ID NO: 1331 and wherein said antisense strand base pairs with the guanine at position 628 of SEQ ID NO:1331.

In certain embodiments, the invention provides a cell containing any of the dsRNAs described in the Summary, above. In certain other embodiments, the invention provides a vector comprising a nucleotide sequence that encodes at least one strand of any of the dsRNAs described in the Summary, above. In certain embodiments, the vector is in a cell.

In other embodiments, the invention provides a pharmaceutical composition for inhibiting expression of a TTR gene comprising any of the dsRNAs described in the Summary, above, and a pharmaceutically acceptable carrier. In related embodiments, the invention provides a pharmaceutical composition for inhibiting expression of a TTR gene comprising a dsRNA and a SNALP formulation, wherein the dsRNA comprises an antisense strand which is less than 30 nucleotides in length and comprises 15 or more contiguous nucleotides of SEQ ID NO:170, SEQ ID NO:450, SEQ ID NO:730, or SEQ ID NO:1010, and wherein the SNALP formulation comprises DlinDMA, DPPC, Cholesterol and PEG2000-cDMA in a ratio of 57.1/7.1/34.4/1.4 respectively.

In yet another embodiment, the invention provides a method of inhibiting TTR expression in a cell, the method comprising: (a) contacting the cell with any of dsRNAs described in the Summary, above; and (b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of a TTR gene, thereby inhibiting expression of the TTR gene in the cell.

In yet another embodiment, the invention provides a method of treating a disorder mediated by TTR expression comprising administering to a human in need of such treatment a therapeutically effective amount of any of the dsRNAs describe in the Summary, above. In related embodiments, the dsRNA is administered to the human at about 0.01, 0.1, 0.5, 1.0, 2.5, or 5.0 mg/kg. In yet another related embodiment, the dsRNA is administered to the human at about 1.0 mg/kg. In yet another related embodiment, the human being treated has transthyretin amyloidosis, and/or a liver disorder. In a related embodiment, the human is further provided a liver transplant. In yet another embodiment, administration of the dsRNA reduces TTR mRNA by about 80% in human liver, wherein the concentration of the dsRNA is 3 mg/kg. In yet another related embodiment, administration of the dsRNA does not result in immunostimulatory activity in the human as measured by IFN-alpha and TNF-alpha ELISA assays. In yet another related embodiment, administration of the dsRNA reduces liver TTR mRNA levels by about 97% or serum TTR protein levels by about 90%, wherein the concentration of the dsRNA is 6 mg/kg. In yet another related embodiment, administration of the dsRNA reduces liver TTR mRNA levels and/or serum TTR protein levels up to 22 days, wherein the concentration of the dsRNA is 6 mg/kg or 3 mg/kg. In yet another related embodiment, the dsRNA is formulated in a LNP09 formulation as follows: using XTC/DSPC/Chol/PEG_{2000}-C14 in a ratio of 50/10/38.5/1.5 mol% and a lipid:siRNA ratio of about 11:1. In yet another related embodiment, the dsRNA is formulated in a LNP11 formulation as follows: using MC3/DSPC/Chol/PEG_{2000}-C14 in a ratio of 50/10/38.5/1.5 mol% and a lipid:siRNA ratio of about 11:1. In yet another related embodiment, the dsRNA is formulated in a LNP09 formulation or a LNP11 formulation and reduces TTR mRNA levels by about 85 to 90% at a dose of 0.3mg/kg, relative to a PBC control group. In yet another related embodiment, the dsRNA is formulated in a LNP09 formulation or a LNP11 formulation and reduces TTR mRNA levels by about 50% at a dose of 0.1 mg/kg, relative to a PBC control group. In still another related embodiment, the dsRNA is formulated in a LNP09 formulation or a LNP11 formulation and reduces TTR protein levels in a dose-dependent manner relative to a PBC control group as measured by a western blot. In still another related embodiment, administration of the dsRNA suppresses serum TTR protein levels up to day 14 post-treatment when administered to human at 1 mg/kg or 3 mg/kg. In still another related embodiment, the dsRNA is formulated in a SNALP formulation as follows: using DlinDMA with a DLinDMA/DPPC/Cholesterol/PEG2000-cDMA in a ratio of 57.1/7.1/34.4/1.4 and a lipid:siRNA ratio of about 7.

In another embodiment, the invention provides the use of a dsRNA for treating a disorder mediated by TTR expression comprising administering to a human in need of such treatment a

therapeutically effective amount of any of the dsRNAs described in the Summary, above. In related embodiments, the dsRNA is administered to the human at about 0.01, 0.1, 0.5, 1.0, 2.5, or 5.0 mg/kg. In a particular related embodiment, the dsRNA is administered to the human at about 1.0 mg/kg. In another related embodiment, the human has transthyretin amyloidosis, and/or a liver disorder. In yet another embodiment of the use provided by the invention, the treated human is further provided a liver transplant.

In yet another embodiment, the invention provides the use of a dsRNA in a method for inhibiting TTR expression in a cell, wherein the method comprises (a) contacting the cell with a dsRNA described in the Summary, above; and (b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of a TTR gene, thereby inhibiting expression of the TTR gene in the cell.

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

Description of the Drawings

FIG. 1 is a graph of TNFalpha and IFNalpha levels in cultured human PBMCs following transfection with TTR siRNAs.

FIG. 2A and 2B are dose response curves for AD-18324 and AD-18328, respectively, in HepG2 cells.

FIG. 3 is a dose response curve for AD-18246 in HepG2 cells.

FIG. 4A and FIG. 4B show inhibition of liver mRNA and plasma protein levels, respectively, in transgenic H129-mTTR-KO/iNOS-KO/hTTR mice by an intravenous bolus administration of TTR-dsRNA (AD-18324, AD-18328 and AD-18246) formulated in LNP01.

FIG. 5 is a graph summarizing the measurements of TTR mRNA levels in livers of non-human primates following 15-minute intravenous infusion of TTR-dsRNA (AD-18324 and AD-18328) formulated in SNALP.

FIG. 6A and FIG. 6B show inhibition of human V30M TTR liver mRNA and serum protein levels, respectively, in transgenic mice by an intravenous bolus administration of SNALP-18328. Group means were determined, normalized to the PBS control group, and then plotted. Error bars represent standard deviations. The percentage reduction of the group mean, relative to PBS, is indicated for the SNALP-1955 and SNALP-18328 groups. (*** $p < 0.001$, One-way ANOVA, with Dunn's post-hoc test).

FIG. 7A and FIG. 7B show the durability of reduction of human V30M TTR liver mRNA and serum protein levels, respectively, in transgenic mice over 22 days following a single intravenous bolus administration of SNALP-18328. Group means were determined. TTR/GAPDH mRNA levels were normalized to day 0 levels and plotted. The percent reduction of normalized TTR mRNA levels relative to SNALP-1955 for each time point were calculated and are indicated for the SNALP-18328 groups. (*** $p < 0.001$, One-way ANOVA, with Dunn's post-hoc test).

FIG. 8 shows the timecourse of TTR serum protein levels in non-human primates over 14 days following a single 15-minute intravenous infusion of SNALP-18328.

FIG. 9 shows reduction of TTR-immunoreactivity in various tissues of human V30M TTR/HSF-1 knock-out mice following intravenous bolus administration of SNALP-18328. E, esophagus; S, stomach; I1, intestine/duodenum; I4, intestine/colon; N, nerve; D, dorsal root ganglia.

FIG. 10 shows the measurements of TTR mRNA levels in livers of non-human primates following 15-minute intravenous infusion of XTC-SNALP-18328.

FIGs. 11A and 11B show the measurements of TTR mRNA and serum protein levels, respectively, in livers of non-human primates following 15-minute intravenous infusion of LNP09-18328 or LNP11-18328. FIG.11C shows the timecourse of TTR serum protein levels over 28 days following a 15-minute intravenous infusion of 0.3mg/kg LNP09-18328, as compared to the PBS control group.

FIG. 12 shows the sequence of human TTR mRNA (Ref. Seq. NM_000371.3, SEQ ID NO:1331).

FIGs. 13A and 13B are the sequences of human and rat TTR mRNA, respectively. FIG. 13A is the sequence of human TTR mRNA (Ref. Seq. NM_000371.2, SEQ ID NO:1329). FIG. 13B is the sequence of rat TTR mRNA (Ref. Seq. NM_012681.1, SEQ ID NO:1330).

FIG. 14 shows the nucleotide alignment of NM_000371.3, NM_000371.2, and AD-18328.

FIG. 15 illustrates symptoms and mutations in TTR associated with familial amyloidotic neuropathy, familial amyloidotic cardiomyopathy and CNS amyloidosis.

FIG. 16 shows reduction of TTR mRNA levels in the liver with SNALP-18534 with different infusion durations. Groups of animals (n=4/group) were administered 1 mg/kg SNALP-18534 via a 15-minute, or 1, 2, or 3 hour infusion. Forty-eight hours later, rats were euthanized and livers harvested. TTR and GAPDH mRNA levels were measured from liver

lysates using the Quantigene bDNA assay. The ratio of TTR to GAPDH mRNA levels was calculated for each animal. Group means were determined and normalized to a PBS control group, and then plotted. Error bars represent standard deviations. (*** $p < 0.001$, One-way ANOVA with Bonferroni post- hoc test, relative to PBS).

FIG. 17 shows the measurements of TTR mRNA levels in livers of rats following 15-minute intravenous infusion of LNP07-18534 or LNP08-18534.

FIG. 18 shows *in vivo* inhibition of endogenous TTR mRNA levels in livers of Sprague-Dawley Rats following a 15-min IV infusion of LNP09-18534 or LNP11-18534. Groups of animals (n=4/group) were intravenously administered 0.01, 0.03, 0.1, or 0.3 mg/kg LNP09-18534, LNP-11-18534; or PBS via a 15-minute infusion. Forty-eight hours later, animals were euthanized and livers harvested. TTR and GAPDH mRNA levels were measured from liver biopsy lysates using the Quantigene bDNA assay. The ratio of TTR to GAPDH mRNA levels was calculated for each animal. Group means were determined, normalized to the PBS control group, and then plotted. Error bars represent standard deviations.

Detailed Description of the Invention

The invention provides dsRNAs and methods of using the dsRNAs for inhibiting the expression of a TTR gene in a cell or a mammal where the dsRNA targets a TTR gene. The invention also provides compositions and methods for treating pathological conditions and diseases, such as a TTR amyloidosis, in a mammal caused by the expression of a TTR gene. dsRNA directs the sequence-specific degradation of mRNA through a process known as RNA interference (RNAi).

The dsRNAs of the compositions featured herein include an RNA strand (the antisense strand) having a region which is less than 30 nucleotides in length, generally 19-24 nucleotides in length, and is substantially complementary to at least part of an mRNA transcript of a TTR gene. The use of these dsRNAs enables the targeted degradation of mRNAs of genes that are implicated in pathologies associated with TTR expression in mammals. Very low dosages of TTR dsRNAs in particular can specifically and efficiently mediate RNAi, resulting in significant inhibition of expression of a TTR gene. Using cell-based assays, the present inventors have demonstrated that dsRNAs targeting TTR can specifically and efficiently mediate RNAi, resulting in significant inhibition of expression of a TTR gene. Thus, methods and compositions including these dsRNAs are useful for treating pathological processes that can be mediated by down regulating TTR, such as in the treatment of a liver disorder or a TTR amyloidosis, *e.g.*, FAP.

The methods and compositions containing a TTR dsRNA are useful for treating pathological processes mediated by TTR expression, such as a TTR amyloidosis. In an embodiment, a method of treating a disorder mediated by TTR expression includes administering to a human in need of such treatment a therapeutically effective amount of a dsRNA targeted to TTR. In an embodiment, a dsRNA is administered to the human at about 0.01, 0.1, 0.5, 1.0, 2, 2.5, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 mg/kg.

The following detailed description discloses how to make and use the compositions containing dsRNAs to inhibit the expression of a TTR gene, as well as compositions and methods for treating diseases and disorders caused by the expression of this gene. The pharmaceutical compositions featured in the invention include a dsRNA having an antisense strand comprising a region of complementarity which is less than 30 nucleotides in length, generally 19-24 nucleotides in length, and is substantially complementary to at least part of an RNA transcript of a TTR gene, together with a pharmaceutically acceptable carrier. The compositions featured in the invention also include a dsRNA having an antisense strand having a region of complementarity which is less than 30 nucleotides in length, generally 19-24 nucleotides in length, and is substantially complementary to at least part of an RNA transcript of a TTR gene.

The sense strand of a dsRNA can include 15, 16, 17, 18, 19, 20, 21, or more contiguous nucleotides of SEQ ID NO:169, SEQ ID NO:449, SEQ ID NO:729, or SEQ ID NO:1009. The antisense strand of a dsRNA can include 15, 16, 17, 18, 19, 20, 21, or more contiguous nucleotides of SEQ ID NO:170, SEQ ID NO:450, SEQ ID NO:730, or SEQ ID NO:1010. In an embodiment, the sense strand of a dsRNA can consist of SEQ ID NO:449 or fragments thereof and the antisense strand can consist of SEQ ID NO:450 or fragments thereof. In an embodiment, the sense strand of a dsRNA can consist of SEQ ID NO:729 or fragments thereof and the antisense strand can consist of SEQ ID NO:730 or fragments thereof. In an embodiment, the sense strand of a dsRNA can consist of SEQ ID NO:1009 or fragments thereof and the antisense strand can consist of SEQ ID NO:1010 or fragments thereof.

In an embodiment, a dsRNA can include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more modified nucleotides. In an embodiment, a modified nucleotide can include a 2'-O-methyl modified nucleotide, a nucleotide comprising a 5'-phosphorothioate group, and/or a terminal nucleotide linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group. In an embodiment, a modified nucleotide can include a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an abasic nucleotide, 2'-amino-modified

nucleotide, 2'-alkyl-modified nucleotide, morpholino nucleotide, a phosphoramidate, and/or a non-natural base comprising nucleotide.

In an embodiment, the region of complementary of a dsRNA is at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more nucleotides in length. In an embodiment, the region of complementary includes 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or more contiguous nucleotides of SEQ ID NO:169.

In an embodiment, each strand of a dsRNA is 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more nucleotides in length. In an embodiment, the dsRNA includes a sense strand, or 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotide fragment thereof, selected from Tables 3A, 3B, 4, 6A, 6B, 7, and 16, and an antisense strand, or 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 21 nucleotide fragment thereof, selected from Tables 3A, 3B, 4, 6A, 6B, 7, and 16.

In an embodiment, administration of a dsRNA to a cell results in about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more inhibition of TTR mRNA expression as measured by a real time PCR assay. In an embodiment, administration of a dsRNA to a cell results in about 40% to 45%, 45% to 50%, 50% to 55%, 55% to 60%, 60% to 65%, 65% to 70%, 70% to 75%, 75% to 80%, 80% to 85%, 85% to 90%, 90% to 95% or more inhibition of TTR mRNA expression as measured by a real time PCR assay. In an embodiment, administration of a dsRNA to a cell results in about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more inhibition of TTR mRNA expression as measured by a branched DNA assay. In an embodiment, administration of a dsRNA to a cell results in about 40% to 45%, 45% to 50%, 50% to 55%, 55% to 60%, 60% to 65%, 65% to 70%, 70% to 75%, 75% to 80%, 80% to 85%, 85% to 90%, 90% to 95% or more inhibition of TTR mRNA expression as measured by a branched DNA assay.

In an embodiment, a dsRNA has an IC50 of less than 0.01pM, 0.1pM, 1pM, 5pM, 10 pM, 100pM, or 1000pM. In an embodiment, a dsRNA has an ED50 of about 0.01, 0.1, 1, 5, or 10 mg/kg.

In an embodiment, administration of a dsRNA can reduce TTR mRNA by about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more in cynomolgus monkeys. In an embodiment, administration of a dsRNA reduces liver TTR mRNA levels by about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more or serum TTR protein levels by about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more. In an

embodiment, administration of a dsRNA reduces liver TTR mRNA levels and/or serum TTR protein levels up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more days.

In an embodiment, a dsRNA is formulated in a LNP formulation and reduces TTR mRNA levels by about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more at a dose of 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, or 1 mg/kg, relative to a PBC control group. In an embodiment, a dsRNA is formulated in a LNP formulation and reduces TTR protein levels about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 90%, 95% or more relative to a PBC control group as measured by a western blot. In an embodiment, a dsRNA suppresses serum TTR protein levels up to day 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 post-treatment when administered to a subject in need thereof at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 mg/kg.

Accordingly, in some aspects, pharmaceutical compositions containing a TTR dsRNA and a pharmaceutically acceptable carrier, methods of using the compositions to inhibit expression of a TTR gene, and methods of using the pharmaceutical compositions to treat diseases caused by expression of a TTR gene are featured in the invention.

I. Definitions

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

"G," "C," "A" and "U" each generally stand for a nucleotide that contains guanine, cytosine, adenine, and uracil as a base, respectively. "T" and "dT" are used interchangeably herein and refer to a deoxyribonucleotide wherein the nucleobase is thymine, e.g., deoxyribothymine. However, it will be understood that the term "ribonucleotide" or "nucleotide" or "deoxyribonucleotide" can also refer to a modified nucleotide, as further detailed below, or a surrogate replacement moiety. The skilled person is well aware that guanine, cytosine, adenine, and uracil may be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base may base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine may be replaced in the nucleotide sequences of the invention by a

nucleotide containing, for example, inosine. Sequences comprising such replacement moieties are embodiments of the invention.

As used herein, "transthyretin" ("TTR") refers to a gene in a cell. TTR is also known as ATTR, HsT2651, PALB, prealbumin, TBPA, and transthyretin (prealbumin, amyloidosis type I). The sequence of a human TTR mRNA transcript can be found at NM_000371. The sequence of mouse TTR mRNA can be found at NM_013697.2, and the sequence of rat TTR mRNA can be found at NM_012681.1.

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

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

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

This includes base-pairing of the oligonucleotide or polynucleotide comprising the first nucleotide sequence to the oligonucleotide or polynucleotide comprising the second nucleotide sequence over the entire length of the first and second nucleotide sequence. Such sequences can be referred to as "fully complementary" with respect to each other herein. However, where a first sequence is referred to as "substantially complementary" with respect to a second sequence herein, the two sequences can be fully complementary, or they may form one or more, but generally not more than 4, 3 or 2 mismatched base pairs upon hybridization, while retaining the ability to hybridize under the conditions most relevant to their ultimate application. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the

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

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

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

As used herein, a polynucleotide that is "substantially complementary to at least part of" a messenger RNA (mRNA) refers to a polynucleotide that is substantially complementary to a contiguous portion of the mRNA of interest (*e.g.*, an mRNA encoding TTR) including a 5' UTR, an open reading frame (ORF), or a 3' UTR. For example, a polynucleotide is complementary to at least a part of a TTR mRNA if the sequence is substantially complementary to a non-interrupted portion of an mRNA encoding TTR.

The term "double-stranded RNA" or "dsRNA," as used herein, refers to a complex of ribonucleic acid molecules, having a duplex structure comprising two anti-parallel and substantially complementary, as defined above, nucleic acid strands. In general, the majority of nucleotides of each strand are ribonucleotides, but as described in detail herein, each or both strands can also include at least one non-ribonucleotide, e.g., a deoxyribonucleotide and/or a modified nucleotide. In addition, as used in this specification, "dsRNA" may include chemical modifications to ribonucleotides, including substantial modifications at multiple nucleotides and including all types of modifications disclosed herein or known in the art. Any such modifications, as used in an siRNA type molecule, are encompassed by "dsRNA" for the purposes of this specification and claims.

The two strands forming the duplex structure may be different portions of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between

the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting RNA chain is referred to as a "hairpin loop." Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting structure is referred to as a "linker." The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the dsRNA minus any overhangs that are present in the duplex. In addition to the duplex structure, a dsRNA may comprise one or more nucleotide overhangs. The term "siRNA" is also used herein to refer to a dsRNA as described above.

As used herein, a "nucleotide overhang" refers to the unpaired nucleotide or nucleotides that protrude from the duplex structure of a dsRNA when a 3'-end of one strand of the dsRNA extends beyond the 5'-end of the other strand, or vice versa. "Blunt" or "blunt end" means that there are no unpaired nucleotides at that end of the dsRNA, *i.e.*, no nucleotide overhang. A "blunt ended" dsRNA is a dsRNA that is double-stranded over its entire length, *i.e.*, no nucleotide overhang at either end of the molecule.

The term "antisense strand" refers to the strand of a dsRNA which includes a region that is substantially complementary to a target sequence. As used herein, the term "region of complementarity" refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches are most tolerated in the terminal regions and, if present, are generally in a terminal region or regions, *e.g.*, within 6, 5, 4, 3, or 2 nucleotides of the 5' and/or 3' terminus.

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

As used herein, the term "SNALP" refers to a stable nucleic acid-lipid particle. A SNALP represents a vesicle of lipids coating a reduced aqueous interior comprising a nucleic acid such as a dsRNA or a plasmid from which a dsRNA is transcribed. SNALP are described, *e.g.*, in U.S. Patent Application Publication Nos. 20060240093, 20070135372, and USSN 61/045,228 filed on April 15, 2008. These applications are hereby incorporated by reference.

"Introducing into a cell," when referring to a dsRNA, means facilitating uptake or absorption into the cell, as is understood by those skilled in the art. Absorption or uptake of dsRNA can occur through unaided diffusive or active cellular processes, or by auxiliary agents or devices. The meaning of this term is not limited to cells *in vitro*; a dsRNA may also be

"introduced into a cell," wherein the cell is part of a living organism. In such instance, introduction into the cell will include the delivery to the organism. For example, for *in vivo* delivery, dsRNA can be injected into a tissue site or administered systemically. *In vitro* introduction into a cell includes methods known in the art such as electroporation and lipofection. Further approaches are described herein or known in the art.

The terms "silence," "inhibit the expression of," "down-regulate the expression of," "suppress the expression of" and the like in as far as they refer to a TTR gene, herein refer to the at least partial suppression of the expression of a TTR gene, as manifested by a reduction of the amount of mRNA which may be isolated from a first cell or group of cells in which a TTR gene is transcribed and which has or have been treated such that the expression of a TTR 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 is usually expressed in terms of

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

Alternatively, the degree of inhibition may be given in terms of a reduction of a parameter that is functionally linked to TTR gene expression, *e.g.*, the amount of protein encoded by a TTR gene which is secreted by a cell, or the number of cells displaying a certain phenotype, *e.g.*, apoptosis. In principle, TTR gene silencing may be determined in any cell expressing the target, either constitutively or by genomic engineering, and by any appropriate assay. However, when a reference is needed in order to determine whether a given dsRNA inhibits the expression of a TTR gene by a certain degree and therefore is encompassed by the instant invention, the assays provided in the Examples below shall serve as such reference.

For example, in certain instances, expression of a TTR gene is suppressed by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% by administration of the double-stranded oligonucleotide featured in the invention. In some embodiments, a TTR gene is suppressed by at least about 60%, 70%, or 80% by administration of the double-stranded oligonucleotide featured in the invention. In some embodiments, a TTR gene is suppressed by at least about 85%, 90%, or 95% by administration of the double-stranded oligonucleotide featured in the invention.

As used herein in the context of TTR expression, the terms "treat," "treatment," and the like, refer to relief from or alleviation of pathological processes mediated by TTR expression. In

the context of the present invention insofar as it relates to any of the other conditions recited herein below (other than pathological processes mediated by TTR expression), the terms "treat," "treatment," and the like mean to relieve or alleviate at least one symptom associated with such condition, or to slow or reverse the progression of such condition, such as the slowing the progression of a TTR amyloidosis, such as FAP. Symptoms of TTR amyloidosis include sensory neuropathy (*e.g.* paresthesia, hypesthesia in distal limbs), autonomic neuropathy (*e.g.*, gastrointestinal dysfunction, such as gastric ulcer, or orthostatic hypotension), motor neuropathy, seizures, dementia, myelopathy, polyneuropathy, carpal tunnel syndrome, autonomic insufficiency, cardiomyopathy, vitreous opacities, renal insufficiency, nephropathy, substantially reduced mBMI (modified Body Mass Index), cranial nerve dysfunction, and corneal lattice dystrophy.

As used herein, the phrases "therapeutically effective amount" and "prophylactically effective amount" refer to an amount that provides a therapeutic benefit in the treatment, prevention, or management of pathological processes mediated by TTR expression or an overt symptom of pathological processes mediated by TTR expression. The specific amount that is therapeutically effective can be readily determined by an ordinary medical practitioner, and may vary depending on factors known in the art, such as, for example, the type of pathological processes mediated by TTR expression, the patient's history and age, the stage of pathological processes mediated by TTR expression, and the administration of other anti-pathological processes mediated by TTR expression agents.

As used herein, a "pharmaceutical composition" comprises a pharmacologically effective amount of a dsRNA and a pharmaceutically acceptable carrier. As used herein, "pharmacologically effective amount," "therapeutically effective amount" or simply "effective amount" refers to that amount of an RNA effective to produce the intended pharmacological, therapeutic or preventive result. For example, if a given clinical treatment is considered effective when there is at least a 25% reduction in a measurable parameter associated with a disease or disorder, a therapeutically effective amount of a drug for the treatment of that disease or disorder is the amount necessary to effect at least a 25% reduction in that parameter. For example, a therapeutically effective amount of a dsRNA targeting TTR can reduce TTR serum levels by at least 25%. In another example, a therapeutically effective amount of a dsRNA targeting TTR can improve liver function or renal function by at least 25%.

The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The term specifically excludes cell culture

medium. For drugs administered orally, pharmaceutically acceptable carriers include, but are not limited to pharmaceutically acceptable excipients such as inert diluents, disintegrating agents, binding agents, lubricating agents, sweetening agents, flavoring agents, coloring agents and preservatives. Suitable inert diluents include sodium and calcium carbonate, sodium and calcium phosphate, and lactose, while corn starch and alginic acid are suitable disintegrating agents. Binding agents may include starch and gelatin, while the lubricating agent, if present, will generally be magnesium stearate, stearic acid or talc. If desired, the tablets may be coated with a material such as glyceryl monostearate or glyceryl distearate, to delay absorption in the gastrointestinal tract.

As used herein, a "transformed cell" is a cell into which a vector has been introduced from which a dsRNA molecule may be expressed.

II. Double-stranded ribonucleic acid (dsRNA)

As described in more detail herein, the invention provides double-stranded ribonucleic acid (dsRNA) molecules for inhibiting the expression of a TTR gene in a cell or mammal, *e.g.*, in a human having a TTR amyloidosis, where the dsRNA includes an antisense strand having a region of complementarity which is complementary to at least a part of an mRNA formed in the expression of a TTR gene, and where the region of complementarity is less than 30 nucleotides in length, generally 19-24 nucleotides in length, and where said dsRNA, upon contact with a cell expressing said TTR gene, inhibits the expression of said TTR gene by at least 30% as assayed by, for example, a PCR or branched DNA (bDNA)-based method, or by a protein-based method, such as by Western blot. Expression of a TTR gene can be reduced by at least 30% when measured by an assay as described in the Examples below. For example, expression of a TTR gene in cell culture, such as in Hep3B cells, can be assayed by measuring TTR mRNA levels, such as by bDNA or TaqMan assay, or by measuring protein levels, such as by ELISA assay. The dsRNA of the invention can further include one or more single-stranded nucleotide overhangs.

The dsRNA can be synthesized by standard methods known in the art as further discussed below, *e.g.*, by use of an automated DNA synthesizer, such as are commercially available from, for example, Biosearch, Applied Biosystems, Inc. The dsRNA includes two RNA strands that are sufficiently complementary to hybridize to form a duplex structure. One strand of the dsRNA (the antisense strand) includes a region of complementarity that is substantially complementary, and generally fully complementary, to a target sequence, derived from the sequence of an mRNA formed during the expression of a TTR 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. Generally, the duplex structure is between 15 and 30 or between 25 and 30, or between 18 and 25, or between 19 and 24, or between 19 and 21, or 19, 20, or 21 base pairs in length. In one embodiment the duplex is 19 base pairs in length. In another embodiment the duplex is 21 base pairs in length. When two different siRNAs are used in combination, the duplex lengths can be identical or can differ.

Each strand of the dsRNA of invention is generally between 15 and 30, or between 18 and 25, or 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length. In other embodiments, each is strand is 25-30 nucleotides in length. Each strand of the duplex can be the same length or of different lengths. When two different siRNAs are used in combination, the lengths of each strand of each siRNA can be identical or can differ.

The dsRNA of the invention can include one or more single-stranded overhang(s) of one or more nucleotides. In one embodiment, at least one end of the dsRNA has a single-stranded nucleotide overhang of 1 to 4, generally 1 or 2 nucleotides. In another embodiment, the antisense strand of the dsRNA has 1-10 nucleotides overhangs each at the 3' end and the 5' end over the sense strand. In further embodiments, the sense strand of the dsRNA has 1-10 nucleotides overhangs each at the 3' end and the 5' end over the antisense strand.

A dsRNAs having at least one nucleotide overhang can have unexpectedly superior inhibitory properties than the blunt-ended counterpart. In some embodiments the presence of only one nucleotide overhang strengthens the interference activity of the dsRNA, without affecting its overall stability. A dsRNA having only one overhang has proven particularly stable and effective *in vivo*, as well as in a variety of cells, cell culture mediums, blood, and serum. Generally, the single-stranded overhang is located at the 3'-terminal end of the antisense strand or, alternatively, at the 3'-terminal end of the sense strand. The dsRNA can also have a blunt end, generally located at the 5'-end of the antisense strand. Such dsRNAs can have improved stability and inhibitory activity, thus allowing administration at low dosages, *i.e.*, less than 5 mg/kg body weight of the recipient per day. Generally, the antisense strand of the dsRNA has a nucleotide overhang at the 3'-end, and the 5'-end is blunt. In another embodiment, one or more of the nucleotides in the overhang is replaced with a nucleoside thiophosphate.

In one embodiment, a TTR gene is a human TTR gene. In specific embodiments, the sense strand of the dsRNA is one of the sense sequences from Tables 3A, 3B, 4, 6A, 6B, or 7, and the antisense strand is one of the antisense sequences of Tables 3A, 3B, 4, 6A, 6B, or 7. Alternative antisense agents that target elsewhere in the target sequence provided in Tables 3A,

3B, 4, 6A, 6B, or 7 can readily be determined using the target sequence and the flanking TTR sequence.

The skilled person is well aware that dsRNAs having a duplex structure of between 20 and 23, but specifically 21, base pairs have been hailed as particularly effective in inducing RNA interference (Elbashir *et al.*, EMBO 2001, 20:6877-6888). However, others have found that shorter or longer dsRNAs can be effective as well. In the embodiments described above, by virtue of the nature of the oligonucleotide sequences provided in Tables 3A, 3B, 4, 6A, 6B, and 7, the dsRNAs featured in the invention can include at least one strand of a length described herein. It can be reasonably expected that shorter dsRNAs having one of the sequences of Tables 3A, 3B, 4, 6A, 6B, or 7 minus only a few nucleotides on one or both ends may be similarly effective as compared to the dsRNAs described above. Hence, dsRNAs having a partial sequence of at least 15, 16, 17, 18, 19, 20, or more contiguous nucleotides from one of the sequences of Tables 3, 4, 6 or 7, and differing in their ability to inhibit the expression of a TTR gene in an assay as described herein below by not more than 5, 10, 15, 20, 25, or 30 % inhibition from a dsRNA comprising the full sequence, are contemplated by the invention. Further, dsRNAs that cleave within a desired TTR target sequence can readily be made using the corresponding TTR antisense sequence and a complementary sense sequence.

In addition, the dsRNAs provided in Tables 3A, 3B, 4, 6A, 6B, or 7 identify a site in a TTR that is susceptible to RNAi based cleavage. As such, the present invention further features dsRNAs that target within the sequence targeted by one of the agents of the present invention. As used herein, a second dsRNA is said to target within the sequence of a first dsRNA if the second dsRNA cleaves the message anywhere within the mRNA that is complementary to the antisense strand of the first dsRNA. Such a second dsRNA will generally consist of at least 15 contiguous nucleotides from one of the sequences provided in Tables 3A, 3B, 4, 6A, 6B, or 7 coupled to additional nucleotide sequences taken from the region contiguous to the selected sequence in a TTR gene.

The dsRNA featured in the invention can contain one or more mismatches to the target sequence. In one embodiment, the dsRNA featured in the invention contains no more than 3 mismatches. If the antisense strand of the dsRNA contains mismatches to a target sequence, it is preferable that the area of mismatch not be located in the center of the region of complementarity. If the antisense strand of the dsRNA contains mismatches to the target sequence, it is preferable that the mismatch be restricted to 5 nucleotides from either end, for example 5, 4, 3, 2, or 1 nucleotide from either the 5' or 3' end of the region of complementarity. For example, for a 23 nucleotide dsRNA strand which is complementary to a region of a TTR

gene, the dsRNA generally does not contain any mismatch within the central 13 nucleotides. The methods described within the invention can be used to determine whether a dsRNA containing a mismatch to a target sequence is effective in inhibiting the expression of a TTR gene. Consideration of the efficacy of dsRNAs with mismatches in inhibiting expression of a TTR gene is important, especially if the particular region of complementarity in a TTR gene is known to have polymorphic sequence variation within the population.

Modifications

In yet another embodiment, the dsRNA is chemically modified to enhance stability. The nucleic acids featured in the invention may be synthesized and/or modified by methods well established in the art, such as those described in "Current protocols in nucleic acid chemistry," Beaucage, S.L. *et al.* (Eds.), John Wiley & Sons, Inc., New York, NY, USA, which is hereby incorporated herein by reference. Specific examples of dsRNA compounds useful in this invention include dsRNAs containing modified backbones or no natural internucleoside linkages. As defined in this specification, dsRNAs having modified backbones include those that retain a phosphorus atom in the backbone and 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 dsRNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

Modified dsRNA 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. Pat. 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; and 5,625,050, each of which is herein incorporated by reference

Modified dsRNA 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 ore 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. Pat. Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,64,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; and, 5,677,439, each of which is herein incorporated by reference.

In other suitable dsRNA mimetics, both the sugar and the internucleoside linkage, *i.e.*, the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, a dsRNA 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 a dsRNA 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. Pat. Nos. 5,539,082; 5,714,331; and 5,719,262, each of which is herein incorporated by reference. Further teaching of PNA compounds can be found in Nielsen *et al.*, Science, 1991, 254, 1497-1500.

Other embodiments of the invention are dsRNAs 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. Pat. No. 5,489,677, and the amide backbones of the above-referenced U.S. Pat. No. 5,602,240. Also

preferred are dsRNAs having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506.

Modified dsRNAs may also contain one or more substituted sugar moieties. Preferred dsRNAs comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. Other preferred dsRNAs comprise 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 dsRNA, or a group for improving the pharmacodynamic properties of an dsRNA, and other substituents having similar properties. A preferred modification includes 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. A further preferred modification includes 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--$N(CH_2)_2$, also described in examples herein below.

Other preferred modifications include 2'-methoxy (2'-OCH_3), 2'-aminopropoxy (2'-$OCH_2CH_2CH_2NH_2$) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the dsRNA, 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. DsRNAs may also have sugar mimetics such as cyclobutyl moieties in place of the pentofuranosyl sugar. Representative U.S. patents that teach the preparation of such modified sugar structures include, but are not limited to, U.S. 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, and each of which is herein incorporated by reference in its entirety.

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

the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl anal other 8-substituted adenines and guanines, 5-halo, particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-daazaadenine and 3-deazaguanine and 3-deazaadenine. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, 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. Pat. No. 3,687,808, as well as U.S. Pat. Nos. 4,845,205; 5,130,30; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; and 5,681,941, each of which is herein incorporated by reference, and U.S. Pat. No. 5,750,692, also herein incorporated by reference.

Conjugates

Another modification of the dsRNAs of the invention involves chemically linking to the dsRNA one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the dsRNA. 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-Hphosphonate (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).

Representative U.S. patents that teach the preparation of such dsRNA 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, each of which is herein incorporated by reference.

It is not necessary for all positions in a given compound to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within a dsRNA. The present invention also includes dsRNA compounds which are chimeric compounds. "Chimeric" dsRNA compounds or "chimeras," in the context of this invention, are dsRNA compounds, particularly 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 dsRNAs typically contain at least one region wherein the dsRNA is modified so as to confer upon the dsRNA increased resistance to nuclease degradation, increased cellular uptake, and/or increased binding affinity for the target

nucleic acid. An additional region of the dsRNA may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of dsRNA inhibition of gene expression. Consequently, comparable results can often be obtained with shorter dsRNAs when chimeric dsRNAs are used, compared to phosphorothioate deoxydsRNAs 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. The cleavage site on the target mRNA of a dsRNA can be determined using methods generally known to one of ordinary skill in the art, e.g., the 5'-RACE method described in Soutschek et al., *Nature*; 2004, Vol. 432, pp. 173-178 (which is herein incorporated by reference for all purposes). In an embodiment, using the 5'-RACE method described by Soutschek et al., ALN-18328 was determined to cleave a TTR mRNA between the guanine nucleotide at position 636 of SEQ ID NO:1331 (NM_000371.3) and the adenine nucleotide at position 637 of SEQ ID NO:1331. In an embodiment, it was determined that ALN-18328 does not cleave a TTR mRNA between the adenine nucleotide at position 637 of SEQ ID NO:1331 and the guanine nucleotide at position 638 of SEQ ID NO:1331.

In certain instances, the dsRNA may be modified by a non-ligand group. A number of non-ligand molecules have been conjugated to dsRNAs in order to enhance the activity, cellular distribution or cellular uptake of the dsRNA, and procedures for performing such conjugations are available in the scientific literature. Such non-ligand moieties have included lipid moieties, such as cholesterol (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 dsRNA conjugates have been listed above. Typical conjugation protocols involve the synthesis of dsRNAs bearing an aminolinker at one or more positions of the sequence. The amino group is then reacted with the molecule being conjugated using appropriate coupling or activating reagents. The conjugation reaction may be performed either with the dsRNA still bound to the solid support or following cleavage of the dsRNA in solution phase. Purification of the dsRNA conjugate by HPLC typically affords the pure conjugate.

Vector encoded dsRNAs

In another aspect, TTR dsRNA molecules are 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). These transgenes can be introduced as a linear construct, a circular plasmid, or a viral vector, which can be incorporated and inherited as a transgene integrated into the host genome. 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 strands of a dsRNA can be transcribed by promoters on two separate expression vectors and co-transfected into a target cell. Alternatively each individual strand of the dsRNA can be transcribed by promoters both of which are located on the same expression plasmid. In one embodiment, a dsRNA is expressed as an inverted repeat joined by a linker polynucleotide sequence such that the dsRNA has a stem and loop structure.

The recombinant dsRNA expression vectors are generally DNA plasmids or viral vectors. dsRNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus (for a review, see Muzyczka, *et al.*, *Curr. Topics Micro. Immunol.* (1992) 158:97-129)); adenovirus (see, for example, Berkner, *et al.*, BioTechniques (1998) 6:616), Rosenfeld *et al.* (1991, Science 252:431-434), and Rosenfeld *et al.* (1992), *Cell* 68:143-155)); or alphavirus as well as others known in the art. Retroviruses have been used to introduce a variety of genes into many different cell types, including epithelial cells, *in vitro* and/or *in vivo* (see, *e.g.*, Eglitis, *et al.*, *Science* (1985) 230:1395-1398; Danos and Mulligan, *Proc. NatI. Acad. Sci. USA* (1998) 85:6460-6464; Wilson *et al.*, 1988, Proc. NatI. Acad. Sci. USA 85:3014-3018; Armentano *et al.*, 1990, Proc. NatI. Acad. Sci. USA 87:61416145; Huber *et al.*, 1991, Proc. NatI. Acad. Sci. USA 88:8039-8043; Ferry *et al.*, 1991, Proc. NatI. Acad. Sci. USA 88:8377-8381; Chowdhury *et al.*, 1991, Science 254:1802-1805; van Beusechem. *et al.*, 1992, Proc. Natl.

Acad. Sci. USA 89:7640-19 ; Kay *et al.*, 1992, Human Gene Therapy 3:641-647; Dai *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89:10892-10895; Hwu *et al.*, 1993, J. Immunol. 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO 89/02468; PCT Application WO 89/05345; and PCT Application WO 92/07573). Recombinant retroviral vectors capable of transducing and expressing genes inserted into the genome of a cell can be produced by transfecting the recombinant retroviral genome into suitable packaging cell lines such as PA317 and Psi-CRIP (Comette *et al.*, 1991, Human Gene Therapy 2:5-10; Cone *et al.*, 1984, Proc. Natl. Acad. Sci. USA 81:6349). Recombinant adenoviral vectors can be used to infect a wide variety of cells and tissues in susceptible hosts (*e.g.*, rat, hamster, dog, and chimpanzee) (Hsu *et al.*, 1992, J. Infectious Disease, 166:769), and also have the advantage of not requiring mitotically active cells for infection.

Any viral vector capable of accepting the coding sequences for the dsRNA molecule(s) to be expressed can be used, for example vectors derived from adenovirus (AV); adeno-associated virus (AAV); retroviruses (*e.g*, lentiviruses (LV), Rhabdoviruses, murine leukemia virus); herpes virus, and the like. 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 featured in the invention can be pseudotyped with surface proteins from vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. AAV vectors featured in the invention can be made to target different cells by engineering the vectors to express different capsid protein serotypes. For example, an AAV vector expressing a serotype 2 capsid on a serotype 2 genome is called AAV 2/2. This serotype 2 capsid gene in the AAV 2/2 vector can be replaced by a serotype 5 capsid gene to produce an AAV 2/5 vector. Techniques for constructing AAV vectors which express different capsid protein serotypes are within the skill in the art; see, *e.g.*, Rabinowitz J E *et al.* (2002), J Virol 76:791-801, the entire disclosure of which is herein incorporated by reference.

Selection of recombinant viral vectors suitable for use in the invention, methods for inserting nucleic acid sequences for expressing the dsRNA into the vector, and methods of delivering the viral vector to the cells of interest are within the skill in the art. See, for example, Dornburg R (1995), Gene Therap. 2: 301-310; Eglitis M A (1988), Biotechniques 6: 608-614; Miller A D (1990), Hum Gene Therap. 1: 5-14; Anderson W F (1998), Nature 392: 25-30; and Rubinson D A *et al.*, Nat. Genet. 33: 401-406, the entire disclosures of which are herein incorporated by reference.

Viral vectors can be derived from AV and AAV. In one embodiment, the dsRNA featured in the invention is 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.

A suitable AV vector for expressing the dsRNA 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.

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.

The promoter driving dsRNA expression in either a DNA plasmid or viral vector featured in the invention may be a eukaryotic RNA polymerase I (*e.g.,* ribosomal RNA promoter), RNA polymerase II (*e.g.,* CMV early promoter or actin promoter or U1 snRNA promoter) or generally RNA polymerase III promoter (*e.g.,* U6 snRNA or 7SK RNA promoter) or a prokaryotic promoter, for example the T7 promoter, provided the expression plasmid also encodes T7 RNA polymerase required for transcription from a T7 promoter. The promoter can also direct transgene expression to the pancreas (see, *e.g.*, the insulin regulatory sequence for pancreas (Bucchini *et al.*, 1986, Proc. Natl. Acad. Sci. USA 83:2511-2515)).

In addition, expression of the transgene can be precisely regulated, for example, by using an inducible regulatory sequence and expression systems such as a 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 transgene expression in cells or in mammals include regulation by ecdysone, by estrogen, progesterone, tetracycline, chemical inducers of dimerization, and isopropyl-beta-D1 -thiogalactopyranoside (EPTG). A person skilled in the art would be able to choose the appropriate regulatory/promoter sequence based on the intended use of the dsRNA transgene.

Generally, recombinant vectors capable of expressing dsRNA molecules are delivered as described below, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of dsRNA molecules. Such vectors can be repeatedly administered as

necessary. Once expressed, the dsRNAs bind to target RNA and modulate its function or expression. Delivery of dsRNA 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.

dsRNA expression DNA plasmids are typically transfected into target cells as a complex with cationic lipid carriers (*e.g.,* Oligofectamine) or non-cationic lipid-based carriers (*e.g.,* Transit-TKO^{TM}). Multiple lipid transfections for dsRNA-mediated knockdowns targeting different regions of a single TTR gene or multiple TTR genes 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.

TTR specific dsRNA molecules can also be inserted into vectors and used as gene therapy vectors for human patients. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (see U.S. Patent 5,328,470) or by stereotactic injection (see *e.g.*, Chen *et al.* (1994) Proc. Natl. Acad. Sci. USA 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can include a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

III. Pharmaceutical compositions containing dsRNA

In one embodiment, the invention provides pharmaceutical compositions containing a dsRNA, as described herein, and a pharmaceutically acceptable carrier. The pharmaceutical composition containing the dsRNA is useful for treating a disease or disorder associated with the expression or activity of a TTR gene, such as pathological processes mediated by TTR expression. 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 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 featured herein are administered in dosages sufficient to inhibit expression of TTR genes.

In general, a suitable dose of dsRNA will be in the range of 0.01 to 200.0 milligrams per kilogram body weight of the recipient per day, generally in the range of 1 to 50 mg per kilogram body weight per day. For example, the dsRNA can be administered at 0.0059 mg/kg, 0.01 mg/kg, 0.0295 mg/kg, 0.05 mg/kg, 0.0590 mg/kg, 0.163 mg/kg, 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.543 mg/kg, 0.5900 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, 1 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, 1.5 mg/kg, 1.628 mg/kg, 2 mg/kg, 3 mg/kg, 5.0 mg/kg, 10 mg/kg, 20 mg/kg, 30 mg/kg, 40 mg/kg, or 50 mg/kg per single dose.

In one embodiment, the dosage is between 0.01 and 0.2 mg/kg. For example, the dsRNA can be administered at a dose of 0.01 mg/kg, 0.02 mg/kg, 0.3 mg/kg, 0.04 mg/kg, 0.05 mg/kg, 0.06 mg/kg, 0.07 mg/kg 0.08 mg/kg 0.09 mg/kg , 0.10 mg/kg, 0.11 mg/kg, 0.12 mg/kg, 0.13 mg/kg, 0.14 mg/kg, 0.15 mg/kg, 0.16 mg/kg, 0.17 mg/kg, 0.18 mg/kg, 0.19 mg/kg, or 0.20 mg/kg.

In one embodiment, the dosage is between 0.005 mg/kg and 1.628 mg/kg. For example, the dsRNA can be administered at a dose of 0.0059 mg/kg, 0.0295 mg/kg, 0.0590 mg/kg, 0.163 mg/kg, 0.543 mg/kg, 0.5900 mg/kg, or 1.628 mg/kg.

In one embodiment, the dosage is between 0.2 mg/kg and 1.5 mg/kg. For example, the dsRNA can be administered at a dose of 0.2 mg/kg, 0.3 mg/kg, 0.4 mg/kg, 0.5 mg/kg, 0.6 mg/kg, 0.7 mg/kg, 0.8 mg/kg, 0.9 mg/kg, 1 mg/kg, 1.1 mg/kg, 1.2 mg/kg, 1.3 mg/kg, 1.4 mg/kg, or 1.5 mg/kg.

The pharmaceutical composition may be administered once daily, or the dsRNA may be administered as two, three, or more sub-doses at appropriate intervals throughout the day or even

using continuous infusion or delivery through a controlled release formulation. In that case, the dsRNA 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 dsRNA 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.

The effect of a single dose on TTR levels is 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, or at not more than 5, 6, 7, 8, 9, or 10 week intervals.

The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a composition can include a single treatment or a series of treatments. Estimates of effective dosages and *in vivo* half-lives for the individual dsRNAs 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.

Advances in mouse genetics have generated a number of mouse models for the study of various human diseases, such as pathological processes mediated by TTR expression. Such models are used for *in vivo* testing of dsRNA, as well as for determining a therapeutically effective dose. A suitable mouse model is, for example, a mouse containing a plasmid expressing human TTR. Another suitable mouse model is a transgenic mouse carrying a transgene that expresses human TTR.

The data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of compositions featured in the invention lies generally within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods featured in the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range of the compound or, when appropriate, of the polypeptide product of a target sequence (*e.g.*,

achieving a decreased concentration of the polypeptide) that includes the IC50 (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

The dsRNAs featured in the invention can be administered in combination with other known agents effective in treatment of pathological processes mediated by target gene expression. In any event, the administering physician can adjust the amount and timing of dsRNA administration on the basis of results observed using standard measures of efficacy known in the art or described herein.

Administration

The present invention also includes pharmaceutical compositions and formulations which include the dsRNA compounds featured in the invention. The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be topical, pulmonary, *e.g.*, by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal, oral or parenteral. Parenteral administration includes intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, *e.g.*, intraparenchymal, intrathecal or intraventricular, administration.

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

The present invention includes pharmaceutical compositions that can be delivered by injection directly into the brain. The injection can be by stereotactic injection into a particular region of the brain (*e.g.*, the substantia nigra, cortex, hippocampus, striatum, or globus pallidus), or the dsRNA can be delivered into multiple regions of the central nervous system (*e.g.*, into multiple regions of the brain, and/or into the spinal cord). The dsRNA can also be delivered into diffuse regions of the brain (*e.g.*, diffuse delivery to the cortex of the brain).

In one embodiment, a dsRNA targeting TTR can be delivered by way of a cannula or other delivery device having one end implanted in a tissue, *e.g.*, the brain, *e.g.*, the substantia nigra, cortex, hippocampus, striatum, corpus callosum or globus pallidus of the brain. The cannula can be connected to a reservoir of the dsRNA composition. The flow or delivery can be mediated by a pump, *e.g.*, an osmotic pump or minipump, such as an Alzet pump (Durect, Cupertino, CA). In one embodiment, a pump and reservoir are implanted in an area distant from

the tissue, *e.g.*, in the abdomen, and delivery is effected by a conduit leading from the pump or reservoir to the site of release. Infusion of the dsRNA composition into the brain can be over several hours or for several days, *e.g.*, for 1, 2, 3, 5, or 7 days or more. Devices for delivery to the brain are described, for example, in U.S. Patent Nos. 6,093,180, and 5,814,014.

Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful. Suitable topical formulations include those in which the dsRNAs 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, distearoylphosphatidyl choline) negative (*e.g.*, dimyristoylphosphatidyl glycerol DMPG) and cationic (*e.g.*, dioleoyltetramethylaminopropyl DOTAP and dioleoylphosphatidyl ethanolamine DOTMA). DsRNAs featured in the invention may be encapsulated within liposomes or may form complexes thereto, in particular to cationic liposomes. Alternatively, dsRNAs may be complexed to lipids, in particular to cationic lipids. Suitable fatty acids and esters include but are not limited to arachidonic acid, oleic acid, eicosanoic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a C_{1-10} 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.

Liposomal formulations

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

Liposomes are unilamellar or multilamellar vesicles which have a membrane formed from a lipophilic material and an aqueous interior. The aqueous portion contains the composition to be delivered. Cationic liposomes possess the advantage of being able to fuse to the cell wall.

Non-cationic liposomes, although not able to fuse as efficiently with the cell wall, are taken up by macrophages *in vivo*.

In order to 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. Therefore, it is desirable to use a liposome which is highly deformable and able to pass through such fine pores.

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

Liposomes are useful for the transfer and delivery of active ingredients to the site of action. Because the liposomal membrane is structurally similar to biological membranes, when liposomes are applied to a tissue, the liposomes start to merge with the cellular membranes and as the merging of the liposome and cell progresses, the liposomal contents are emptied into the cell where the active agent may act.

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

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

Liposomes fall into two broad classes. Cationic liposomes are positively charged liposomes which interact with the negatively charged DNA molecules to form a stable complex. The positively charged DNA/liposome complex binds to the negatively charged cell surface and is internalized in an endosome. Due to the acidic pH within the endosome, the liposomes are

ruptured, releasing their contents into the cell cytoplasm (Wang *et al.*, Biochem. Biophys. Res. Commun., 1987, 147, 980-985).

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

Several studies have assessed the topical delivery of liposomal drug formulations to the skin. Application of liposomes containing interferon to guinea pig skin resulted in a reduction of skin herpes sores while delivery of interferon via other means (*e.g.,* as a solution or as an emulsion) were ineffective (Weiner *et al.*, Journal of Drug Targeting, 1992, 2, 405-410). Further, an additional study tested the efficacy of interferon administered as part of a liposomal formulation to the administration of interferon using an aqueous system, and concluded that the liposomal formulation was superior to aqueous administration (du Plessis *et al.*, Antiviral Research, 1992, 18, 259-265).

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

Many liposomes comprising lipids derivatized with one or more hydrophilic polymers, and methods of preparation thereof, are known in the art. Sunamoto *et al.* (Bull. Chem. Soc. Jpn., 1980, 53, 2778) described liposomes comprising a nonionic detergent, $2C_{1215G}$, that contains a PEG moiety. Illum *et al.* (FEBS Lett., 1984, 167, 79) noted that hydrophilic coating of polystyrene particles with polymeric glycols results in significantly enhanced blood half-lives. Synthetic phospholipids modified by the attachment of carboxylic groups of polyalkylene glycols (*e.g.*, PEG) are described by Sears (U.S. Pat. Nos. 4,426,330 and 4,534,899). Klibanov *et al.* (FEBS Lett., 1990, 268, 235) described experiments demonstrating that liposomes comprising phosphatidylethanolamine (PE) derivatized with PEG or PEG stearate have significant increases in blood circulation half-lives. Blume *et al.* (Biochimica et Biophysica Acta, 1990, 1029, 91) extended such observations to other PEG-derivatized phospholipids, *e.g.*, DSPE-PEG, formed from the combination of distearoylphosphatidylethanolamine (DSPE) and PEG. Liposomes having covalently bound PEG moieties on their external surface are described in European Patent No. EP 0 445 131 B1 and WO 90/04384 to Fisher. Liposome compositions containing 1-20 mole percent of PE derivatized with PEG, and methods of use thereof, are described by Woodle *et al.* (U.S. Pat. Nos. 5,013,556 and 5,356,633) and Martin *et al.* (U.S. Pat.

No. 5,213,804 and European Patent No. EP 0 496 813 B1). Liposomes comprising a number of other lipid-polymer conjugates are disclosed in WO 91/05545 and U.S. Pat. No. 5,225,212 (both to Martin *et al.*) and in WO 94/20073 (Zalipsky *et al.*) Liposomes comprising PEG-modified ceramide lipids are described in WO 96/10391 (Choi *et al*). U.S. Pat. No. 5,540,935 (Miyazaki *et al.*) and U.S. Pat. No. 5,556,948 (Tagawa *et al.*) describe PEG-containing liposomes that can be further derivatized with functional moieties on their surfaces.

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

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

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

If the surfactant molecule is not ionized, it is classified as a nonionic surfactant. Nonionic surfactants find wide application in pharmaceutical and cosmetic products and are usable over a wide range of pH values. In general their HLB values range from 2 to about 18 depending on their structure. Nonionic surfactants include nonionic esters such as ethylene glycol esters, propylene glycol esters, glyceryl esters, polyglyceryl esters, sorbitan esters, sucrose esters, and

ethoxylated esters. Nonionic alkanolamides and ethers such as fatty alcohol ethoxylates, propoxylated alcohols, and ethoxylated/propoxylated block polymers are also included in this class. The polyoxyethylene surfactants are the most popular members of the nonionic surfactant class.

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

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

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

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

Nucleic acid lipid particles

In one embodiment, a TTR dsRNA featured in the invention is fully encapsulated in the lipid formulation, e.g., to form a SPLP, pSPLP, SNALP, or other nucleic acid-lipid particle. As used herein, the term "SNALP" refers to a stable nucleic acid-lipid particle, including SPLP. As used herein, the term "SPLP" refers to a nucleic acid-lipid particle comprising plasmid DNA encapsulated within a lipid vesicle. SNALPs and SPLPs typically contain a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of the particle (*e.g.*, a PEG-lipid conjugate). SNALPs and SPLPs are extremely useful for systemic applications, as they exhibit extended circulation lifetimes following intravenous (i.v.) injection and accumulate at distal sites (*e.g.*, sites physically separated from the administration site). SPLPs include "pSPLP," which include an encapsulated condensing agent-nucleic acid complex as set forth in PCT Publication No. WO 00/03683. The particles of the present 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; 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.

The cationic lipid may be, for example, N,N-dioleyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), N-(I -(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(I -(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), N,N-dimethyl-2,3-dioleyloxy)propylamine (DODMA), 1,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA), 1,2-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 may 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 non-cationic lipid may be an anionic lipid or a neutral lipid including, but not limited to, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoylphosphatidylethanolamine (POPE), dioleoyl- phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-l- carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1 -trans PE, 1 -stearoyl-2-oleoyl- phosphatidyethanolamine (SOPE), cholesterol, or a mixture thereof. The non-cationic lipid may be from about 5 mol % to about 90 mol %, about 10 mol %, or about 58 mol % if cholesterol is included, of the total lipid present in the particle.

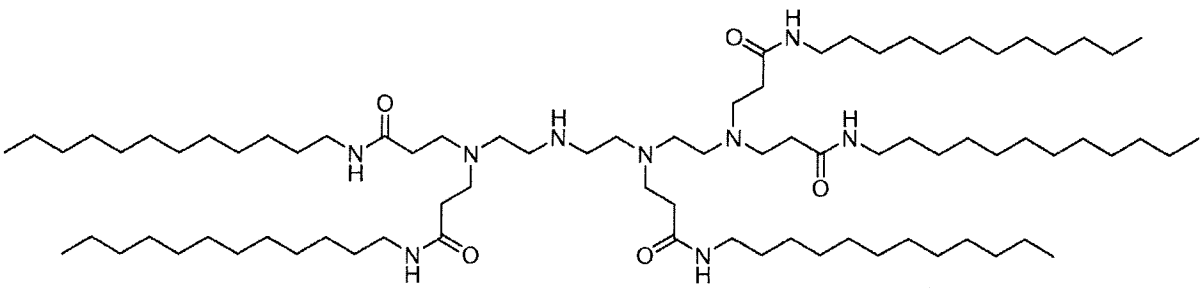
The conjugated lipid that inhibits aggregation of particles may be, for example, a polyethyleneglycol (PEG)-lipid including, without limitation, a PEG-diacylglycerol (DAG), a PEG-dialkyloxypropyl (DAA), a PEG-phospholipid, a PEG-ceramide (Cer), or a mixture thereof. The PEG-DAA conjugate may be, for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

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

LNP01

In one embodiment, the lipidoid ND98·4HCl (MW 1487) (Formula 1), Cholesterol (Sigma-Aldrich), and PEG-Ceramide C16 (Avanti Polar Lipids) can be used to prepare lipid-siRNA 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 siRNA (*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-siRNA 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-siRNA formulations are as follows:

	Cationic Lipid	**cationic lipid/non-cationic lipid/cholesterol/PEG-lipid conjugate Lipid:siRNA ratio**	**Process**
SNALP	1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLinDMA)	DLinDMA/DPPC/Cholesterol/PEG-cDMA (57.1/7.1/34.4/1.4) lipid:siRNA ~ 7:1	
SNALP-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	Extrusion
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	Extrusion
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	In-line mixing
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	In-line mixing

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	In-line mixing
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	In-line mixing
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	In-line mixing
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	In-line mixing

LNP09 formulations and XTC comprising formulations are described, *e.g.*, in U.S. Provisional Serial No. 61/239,686, filed September 3, 2009, which is hereby incorporated by reference. LNP11 formulations and MC3 comprising formulations are described, *e.g.*, in U.S. Provisional Serial No. 61/244,834, filed September 22, 2009, which is hereby incorporated by reference.

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 siRNA concentration in the formulation, as well as the entrapped fraction, is estimated using a dye exclusion assay. A sample of the formulated siRNA 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 siRNA 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" siRNA content (as measured by the signal in the absence of surfactant) from the total siRNA content. Percent entrapped siRNA is typically >85%. For SNALP formulation, the particle size is at least 30 nm, at least 40 nm, at least 50 nm, at least 60 nm, at least 70 nm, at least 80 nm, at least 90 nm, at

least 100 nm, at least 110 nm, and at least 120 nm. The suitable range is typically about at least 50 nm to about at least 110 nm, about at least 60 nm to about at least 100 nm, or about at least 80 nm to about at least 90 nm.

Compositions and formulations for oral administration include powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Thickeners, flavoring agents, diluents, emulsifiers, dispersing aids or binders may be desirable. In some embodiments, oral formulations are those in which dsRNAs featured in the invention are administered in conjunction with one or more penetration enhancers surfactants and chelators. Suitable surfactants include fatty acids and/or esters or salts thereof, bile acids and/or salts thereof. Suitable bile acids/salts include chenodeoxycholic acid (CDCA) and ursodeoxychenodeoxycholic acid (UDCA), cholic acid, dehydrocholic acid, deoxycholic acid, glucholic acid, glycholic acid, glycodeoxycholic acid, taurocholic acid, taurodeoxycholic acid, sodium tauro-24,25-dihydro-fusidate and sodium glycodihydrofusidate. Suitable fatty acids include arachidonic acid, undecanoic acid, oleic acid, lauric acid, caprylic acid, capric acid, myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein, dilaurin, glyceryl 1-monocaprate, 1-dodecylazacycloheptan-2-one, an acylcarnitine, an acylcholine, or a monoglyceride, a diglyceride or a pharmaceutically acceptable salt thereof (*e.g.,* sodium). In some embodiments, combinations of penetration enhancers are used, for example, fatty acids/salts in combination with bile acids/salts. One exemplary combination is the sodium salt of lauric acid, capric acid and UDCA. Further penetration enhancers include polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether. DsRNAs featured in the invention may be delivered orally, in granular form including sprayed dried particles, or complexed to form micro or nanoparticles. DsRNA complexing agents include poly-amino acids; polyimines; polyacrylates; polyalkylacrylates, polyoxethanes, polyalkylcyanoacrylates; cationized gelatins, albumins, starches, acrylates, polyethyleneglycols (PEG) and starches; polyalkylcyanoacrylates; DEAE-derivatized polyimines, pollulans, celluloses and starches. Suitable complexing agents include chitosan, N-trimethylchitosan, poly-L-lysine, polyhistidine, polyornithine, polyspermines, protamine, polyvinylpyridine, polythiodiethylaminomethylethylene P(TDAE), polyaminostyrene (*e.g.,* p-amino), poly(methylcyanoacrylate), poly(ethylcyanoacrylate), poly(butylcyanoacrylate), poly(isobutylcyanoacrylate), poly(isohexylcynaoacrylate), DEAE-methacrylate, DEAE-hexylacrylate, DEAE-acrylamide, DEAE-albumin and DEAE-dextran, polymethylacrylate, polyhexylacrylate, poly(D,L-lactic acid), poly(DL-lactic-co-glycolic acid (PLGA), alginate, and

polyethyleneglycol (PEG). Oral formulations for dsRNAs and their preparation are described in detail in U.S. Patent 6,887,906, 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 may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

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

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

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

Emulsions

The compositions of the present invention may be prepared and formulated as emulsions. Emulsions are typically heterogeneous systems of one liquid dispersed in another in the form of droplets usually exceeding 0.1 μm in diameter (Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199; Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., Volume 1, p. 245; Block in Pharmaceutical Dosage

Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 2, p. 335; Higuchi *et al.*, in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa., 1985, p. 301). Emulsions are often biphasic systems comprising two immiscible liquid phases intimately mixed and dispersed with each other. In general, emulsions may be of either the water-in-oil (w/o) or the oil-in-water (o/w) variety. When an aqueous phase is finely divided into and dispersed as minute droplets into a bulk oily phase, the resulting composition is called a water-in-oil (w/o) emulsion. Alternatively, when an oily phase is finely divided into and dispersed as minute droplets into a bulk aqueous phase, the resulting composition is called an oil-in-water (o/w) emulsion. Emulsions may contain additional components in addition to the dispersed phases, and the active drug which may be present as a solution in either the aqueous phase, oily phase or itself as a separate phase. Pharmaceutical excipients such as emulsifiers, stabilizers, dyes, and anti-oxidants may also be present in emulsions as needed. Pharmaceutical emulsions may also be multiple emulsions that are comprised of more than two phases such as, for example, in the case of oil-in-water-in-oil (o/w/o) and water-in-oil-in-water (w/o/w) emulsions. Such complex formulations often provide certain advantages that simple binary emulsions do not. Multiple emulsions in which individual oil droplets of an o/w emulsion enclose small water droplets constitute a w/o/w emulsion. Likewise a system of oil droplets enclosed in globules of water stabilized in an oily continuous phase provides an o/w/o emulsion.

Emulsions are characterized by little or no thermodynamic stability. Often, the dispersed or discontinuous phase of the emulsion is well dispersed into the external or continuous phase and maintained in this form through the means of emulsifiers or the viscosity of the formulation. Either of the phases of the emulsion may be a semisolid or a solid, as is the case of emulsion-style ointment bases and creams. Other means of stabilizing emulsions entail the use of emulsifiers that may be incorporated into either phase of the emulsion. Emulsifiers may broadly be classified into four categories: synthetic surfactants, naturally occurring emulsifiers, absorption bases, and finely dispersed solids (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 (Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), Marcel Dekker, Inc., New York, N.Y., 1988, volume 1, p. 199). Surfactants are typically amphiphilic and comprise a hydrophilic and a hydrophobic portion. The

ratio of the hydrophilic to the hydrophobic nature of the surfactant has been termed the hydrophile/lipophile balance (HLB) and is a valuable tool in categorizing and selecting surfactants in the preparation of formulations. Surfactants may be classified into different classes based on the nature of the hydrophilic group: nonionic, anionic, cationic and amphoteric (Rieger, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 285).

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

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

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

Since emulsions often contain a number of ingredients such as carbohydrates, proteins, sterols and phosphatides that may readily support the growth of microbes, these formulations often incorporate preservatives. Commonly used preservatives included in emulsion formulations include methyl paraben, propyl paraben, quaternary ammonium salts, benzalkonium chloride, esters of p-hydroxybenzoic acid, and boric acid. Antioxidants are also commonly added to emulsion formulations to prevent deterioration of the formulation.

Antioxidants used may be free radical scavengers such as tocopherols, alkyl gallates, butylated hydroxyanisole, butylated hydroxytoluene, or reducing agents such as ascorbic acid and sodium metabisulfite, and antioxidant synergists such as citric acid, tartaric acid, and lecithin.

The application of emulsion formulations via dermatological, oral and parenteral routes and methods for their manufacture have been reviewed in the literature (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 (Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Idson, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 199). Mineral-oil base laxatives, oil-soluble vitamins and high fat nutritive preparations are among the materials that have commonly been administered orally as o/w emulsions.

In one embodiment of the present invention, the compositions of dsRNAs and nucleic acids are formulated as microemulsions. A microemulsion may be defined as a system of water, oil and amphiphile which is a single optically isotropic and thermodynamically stable liquid solution (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 (Rosoff, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker

(Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 245; Block, in Pharmaceutical Dosage Forms, Lieberman, Rieger and Banker (Eds.), 1988, Marcel Dekker, Inc., New York, N.Y., volume 1, p. 335). Compared to conventional emulsions, microemulsions offer the advantage of solubilizing water-insoluble drugs in a formulation of thermodynamically stable droplets that are formed spontaneously.

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

Microemulsions are particularly of interest from the standpoint of drug solubilization and the enhanced absorption of drugs. Lipid based microemulsions (both o/w and w/o) have been proposed to enhance the oral bioavailability of drugs, including peptides (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 (Constantinides *et al.*, Pharmaceutical Research, 1994, 11, 1385; Ho *et al.*, J. Pharm. Sci., 1996, 85, 138-143). Often microemulsions may form spontaneously when their components are brought together at ambient temperature. This may be particularly advantageous when formulating thermolabile drugs, peptides or dsRNAs. 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 dsRNAs and nucleic acids from the gastrointestinal tract, as well as improve the local cellular uptake of dsRNAs and nucleic acids.

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

Penetration Enhancers

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

Penetration enhancers may be classified as belonging to one of five broad categories, *i.e.*, surfactants, fatty acids, bile salts, chelating agents, and non-chelating non-surfactants (Lee *et al.*, Critical Reviews in Therapeutic Drug Carrier Systems, 1991, p.92). Each of the above mentioned classes of penetration enhancers are described below in greater detail.

Surfactants: In connection with the present invention, 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 dsRNAs 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) (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).

Fatty acids: Various fatty acids and their derivatives which act as penetration enhancers include, for example, oleic acid, lauric acid, capric acid (n-decanoic acid), myristic acid, palmitic acid, stearic acid, linoleic acid, linolenic acid, dicaprate, tricaprate, monoolein (1-monooleoyl-rac-glycerol), dilaurin, caprylic acid, arachidonic acid, glycerol 1-monocaprate, 1-dodecylazacycloheptan-2-one, acylcarnitines, acylcholines, C.sub.1-10 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.*) (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).

Bile salts: The physiological role of bile includes the facilitation of dispersion and absorption of lipids and fat-soluble vitamins (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) (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: 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 dsRNAs 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)(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).

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

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.

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 may be liquid or solid and is selected, with the planned manner of administration in mind, so as to provide for the desired bulk, consistency, *etc.*, when combined with a nucleic acid and the other components of a given pharmaceutical composition. Typical pharmaceutical carriers include, but are not limited

to, binding agents (*e.g.*, pregelatinized maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose, *etc.*); fillers (*e.g.*, lactose and other sugars, microcrystalline cellulose, pectin, gelatin, calcium sulfate, ethyl cellulose, polyacrylates or calcium hydrogen phosphate, *etc.*); lubricants (*e.g.*, magnesium stearate, talc, silica, colloidal silicon dioxide, stearic acid, metallic stearates, hydrogenated vegetable oils, corn starch, polyethylene glycols, sodium benzoate, sodium acetate, *etc.*); disintegrants (*e.g.*, starch, sodium starch glycolate, *etc.*); and wetting agents (*e.g.*, sodium lauryl sulphate, *etc*).

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

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

Other Components

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

In some embodiments, pharmaceutical compositions featured in the invention include (a) one or more dsRNA compounds and (b) one or more anti-cytokine biologic agents which function by a non-RNAi mechanism. Examples of such biologics include, biologics that target IL1β (*e.g.*, anakinra), IL6 (tocilizumab), or TNF (etanercept, infliximab, adlimumab, or certolizumab).

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

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

Methods for treating diseases caused by expression of a TTR gene

The invention relates in particular to the use of a dsRNA targeting TTR and compositions containing at least one such dsRNA for the treatment of a TTR-mediated disorder or disease. For example, a dsRNA targeting a TTR gene can be useful for the treatment of a TTR amyloidosis, such as familial amyloidotic polyneuropathy (FAP), familial amyloidotic cardiomyopathy (FAC), leptomeningeal/CNS amyloidosis, amyloidosis VII form (also known as leptomeningeal or meningocerebrovascular amyloidosis), hyperthyroxinemia, and cardiac amyloidosis (also called senile systemic amyloidosis (SSA) and senile cardiac amyloidosis (SCA)).

FIG. 15 illustrates symptoms and mutations in TTR associated with familial amyloidotic neuropathy, familial amyloidotic cardiomyopathy and CNS amyloidosis. The invention includes compositions and methods for treatment of these diseases and symptoms, and directed to these mutant versions of TTR.

A dsRNA targeting a TTR gene is also used for treatment of symptoms and disorders, such as TTR amyloidosis. Symptoms associated with such amyloidosis include, *e.g.*, seizures, dementia, myelopathy, polyneuropathy, carpal tunnel syndrome, autonomic insufficiency, cardiomyopathy, gastrointestinal dysfunction (*e.g.*, gastric ulcers, diarrhea, constipation, malabsorption), weight loss, hepatomegaly, lymphadenopathy, goiter, vitreous opacities, renal insufficiency (including proteinuria and kidney failure), nephropathy, cranial nerve dysfunction, corneal lattice dystrophy, and congestive heart failure with generalized weakness and difficulties breathing from fluid retention.

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

The invention further relates to the use of a dsRNA or a pharmaceutical composition thereof, *e.g.*, for treating a TTR amyloidosis, 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. In one example, a dsRNA targeting TTR can be administered in combination with a liver transplant. In other examples, a dsRNA targeting TTR can be administered in combination with a pharmaceutical or therapeutic method for treating a symptom of a TTR disease, such as diuretics, ACE (angiotensin converting enzyme) inhibitors, angiotensin receptor blockers (ARBs), or dialysis, *e.g.*, for management of renal function.

The dsRNA and an additional therapeutic agent can be administered in the same combination, *e.g.*, parenterally, or the additional therapeutic agent can be administered as part of a separate composition or by another method described herein.

The invention features a method of administering a dsRNA targeting TTR to a patient having a disease or disorder mediated by TTR expression, such as a TTR amyloidosis, *e.g.*, FAP. Administration of the dsRNA can stabilize and improve peripheral neurological function, for example, in a patient with FAP. Patients can be administered a therapeutic amount of dsRNA, such as 0.1 mg/kg, 0.2 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 1.5 mg/kg, 2.0 mg/kg, or 2.5 mg/kg dsRNA. The dsRNA can be administered by intravenous infusion over a period of time, such as over a 5 minute, 10 minute, 15 minute, 20 minute, 25 minute, 60 minute, 120 minute or 180 minute period. The administration is repeated, for example, on a regular basis, such as biweekly (*i.e.*, every two weeks) for one month, two months, three months, four months or longer. After an initial treatment regimen, the treatments can be administered on a less frequent basis. For example, after administration biweekly for three months, administration can be repeated once per month, for six months or a year or longer. Administration of the dsRNA can reduce TTR levels in the blood or urine of the patient by at least 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80 % or 90% or more.

Before administration of a full dose of the dsRNA, patients can be administered a smaller dose, such as a dose that is 5% of the full dose, and monitored for adverse effects, such as an allergic reaction or a change in liver function. For example, in patients monitored for changes in liver function, a low incidence of LFT (Liver Function Test) change (*e.g.*, a 10-20% incidence of LFT) is acceptable (*e.g.*, a reversible, 3-fold increase in ALT (alanine aminotransferase) and/or AST (aspartate aminotransferase) levels).

Many TTR-associated diseases and disorders are hereditary. Therefore, a patient in need of a TTR dsRNA can be identified by taking a family history. A healthcare provider, such as a doctor, nurse, or family member, can take a family history before prescribing or administering a TTR dsRNA. A DNA test may also be performed on the patient to identify a mutation in the TTR gene, before a TTR dsRNA is administered to the patient.

The patient may have a biopsy performed before receiving a TTR dsRNA. The biopsy can be, for example, on a tissue, such as the gastric mucosa, peripheral nerve, skin, abdominal fat, liver, or kidney, and the biopsy may reveal amyloid plaques, which are indicative of a TTR-mediated disorder. Upon the identification of amyloid plaques, the patient is administered a TTR dsRNA.

Methods for inhibiting expression of a TTR gene

In yet another aspect, the invention provides a method for inhibiting the expression of a TTR gene in a mammal. The method includes administering a composition featured in the invention to the mammal such that expression of the target TTR gene is silenced.

When the organism to be treated is a mammal such as a human, the composition may be administered by any means known in the art including, but not limited to oral or parenteral routes, including intracranial (*e.g.*, intraventricular, intraparenchymal and intrathecal), intravenous, intramuscular, subcutaneous, transdermal, airway (aerosol), nasal, rectal, and topical (including buccal and sublingual) administration. In certain embodiments, the compositions are administered by intravenous infusion or injection.

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

EXAMPLES

Example 1. dsRNA synthesis

Source of reagents

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

siRNA synthesis

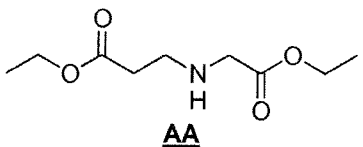
Single-stranded RNAs were produced by solid phase synthesis on a scale of 1 µmole using an Expedite 8909 synthesizer (Applied Biosystems, Applera Deutschland GmbH, Darmstadt, Germany) and controlled pore glass (CPG, 500Å, Proligo Biochemie GmbH, Hamburg, Germany) as solid support. RNA and RNA containing *2'-O*-methyl nucleotides were generated by solid phase synthesis employing the corresponding phosphoramidites and *2'-O*-methyl phosphoramidites, respectively (Proligo Biochemie GmbH, Hamburg, Germany). These building blocks were incorporated at selected sites within the sequence of the oligoribonucleotide chain using standard nucleoside phosphoramidite chemistry such as

described in Current protocols in nucleic acid chemistry, Beaucage, S.L. *et al.* (Edrs.), John Wiley & Sons, Inc., New York, NY, USA. Phosphorothioate linkages were introduced by replacement of the iodine oxidizer solution with a solution of the Beaucage reagent (Chruachem Ltd, Glasgow, UK) in acetonitrile (1%). Further ancillary reagents were obtained from Mallinckrodt Baker (Griesheim, Germany).

Deprotection and purification of the crude oligoribonucleotides by anion exchange HPLC were carried out according to established procedures. Yields and concentrations were determined by UV absorption of a solution of the respective RNA at a wavelength of 260 nm using a spectral photometer (DU 640B, Beckman Coulter GmbH, Unterschleißheim, Germany). Double stranded RNA was generated by mixing an equimolar solution of complementary strands in annealing buffer (20 mM sodium phosphate, pH 6.8; 100 mM sodium chloride), heated in a water bath at 85 - 90°C for 3 minutes and cooled to room temperature over a period of 3 - 4 hours. The annealed RNA solution was stored at –20 °C until use.

For the synthesis of 3'-cholesterol-conjugated siRNAs (herein referred to as -Chol-3'), an appropriately modified solid support was used for RNA synthesis. The modified solid support was prepared as follows:

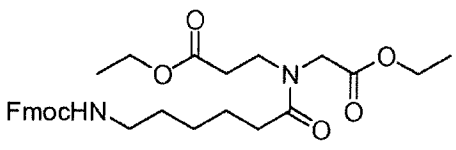
Diethyl-2-azabutane-1,4-dicarboxylate **AA**



AA

A 4.7 M aqueous solution of sodium hydroxide (50 mL) was added into a stirred, ice-cooled solution of ethyl glycinate hydrochloride (32.19 g, 0.23 mole) in water (50 mL). Then, ethyl acrylate (23.1 g, 0.23 mole) was added and the mixture was stirred at room temperature until completion of the reaction was ascertained by TLC. After 19 h the solution was partitioned with dichloromethane (3 x 100 mL). The organic layer was dried with anhydrous sodium sulfate, filtered and evaporated. The residue was distilled to afford AA (28.8 g, 61%).

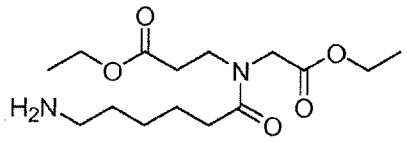
3-{Ethoxycarbonylmethyl-[6-(9H-fluoren-9-ylmethoxycarbonyl-amino)-hexanoyl]-amino}-propionic acid ethyl ester **AB**



AB

Fmoc-6-amino-hexanoic acid (9.12 g, 25.83 mmol) was dissolved in dichloromethane (50 mL) and cooled with ice. Diisopropylcarbodiimde (3.25 g, 3.99 mL, 25.83 mmol) was added to the solution at 0°C. It was then followed by the addition of Diethyl-azabutane-1,4-dicarboxylate (5 g, 24.6 mmol) and dimethylamino pyridine (0.305 g, 2.5 mmol). The solution was brought to room temperature and stirred further for 6 h. Completion of the reaction was ascertained by TLC. The reaction mixture was concentrated under vacuum and ethyl acetate was added to precipitate diisopropyl urea. The suspension was filtered. The filtrate was washed with 5% aqueous hydrochloric acid, 5% sodium bicarbonate and water. The combined organic layer was dried over sodium sulfate and concentrated to give the crude product which was purified by column chromatography (50 % EtOAC/Hexanes) to yield 11.87 g (88%) of AB.

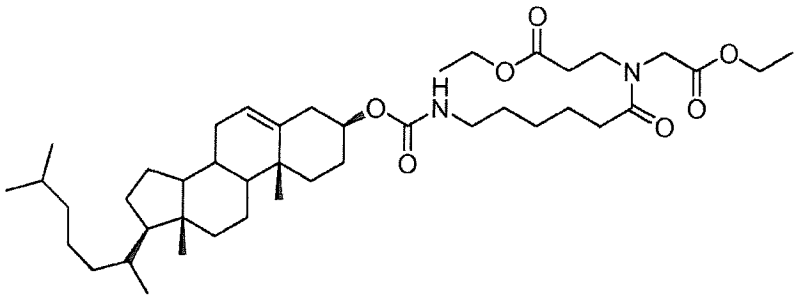
3-[(6-Amino-hexanoyl)-ethoxycarbonylmethyl-amino]-propionic acid ethyl ester **AC**



AC

3-{Ethoxycarbonylmethyl-[6-(9H-fluoren-9-ylmethoxycarbonylamino)-hexanoyl]-amino}-propionic acid ethyl ester AB (11.5 g, 21.3 mmol) was dissolved in 20% piperidine in dimethylformamide at 0°C. The solution was continued stirring for 1 h. The reaction mixture was concentrated under vacuum, water was added to the residue, and the product was extracted with ethyl acetate. The crude product was purified by conversion into its hydrochloride salt.

3-({6-[17-(1,5-Dimethyl-hexyl)-10,13-dimethyl-2,3,4,7,8,9,10,11,12,13,14,15,16,17-tetradecahydro-1H-cyclopenta[a]phenanthren-3-yloxycarbonylamino]-hexanoyl}ethoxycarbonylmethyl-amino)-propionic acid ethyl ester **AD**

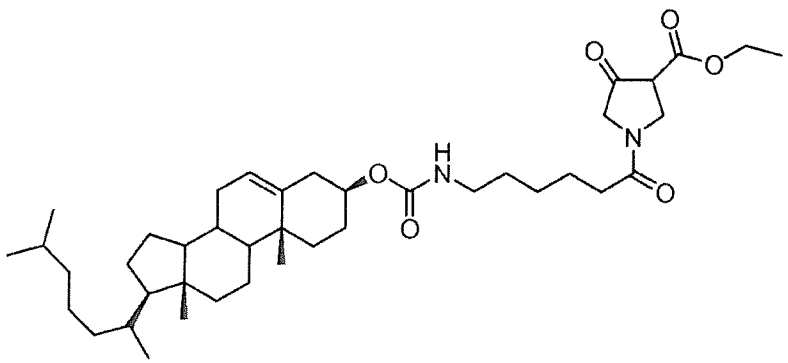


AD

The hydrochloride salt of 3-[(6-Amino-hexanoyl)-ethoxycarbonylmethyl-amino]-propionic acid ethyl ester AC (4.7 g, 14.8 mmol) was taken up in dichloromethane. The suspension was cooled to 0°C on ice. To the suspension diisopropylethylamine (3.87 g, 5.2 mL,

30 mmol) was added. To the resulting solution cholesteryl chloroformate (6.675 g, 14.8 mmol) was added. The reaction mixture was stirred overnight. The reaction mixture was diluted with dichloromethane and washed with 10% hydrochloric acid. The product was purified by flash chromatography (10.3 g, 92%).

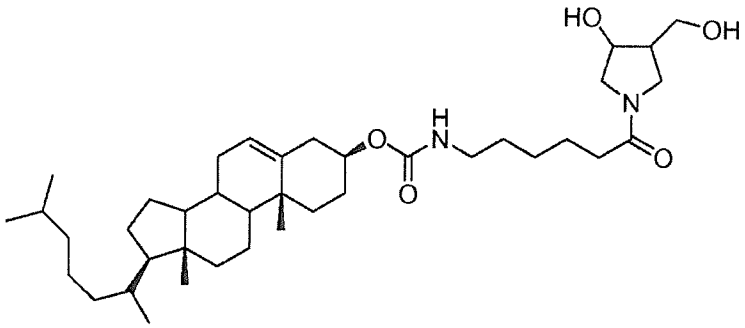
1-{6-[17-(1,5-Dimethyl-hexyl)-10,13-dimethyl-2,3,4,7,8,9,10,11,12,13,14,15,16,17-tetradecahydro-1H-cyclopenta[a] phenanthren-3-yloxycarbonylamino]-hexanoyl}-4-oxo-pyrrolidine-3-carboxylic acid ethyl ester **AE**



AE

Potassium t-butoxide (1.1 g, 9.8 mmol) was slurried in 30 mL of dry toluene. The mixture was cooled to 0°C on ice and 5 g (6.6 mmol) of diester AD was added slowly with stirring within 20 mins. The temperature was kept below 5°C during the addition. The stirring was continued for 30 mins at 0°C and 1 mL of glacial acetic acid was added, immediately followed by 4 g of $NaH_2PO_4 \cdot H_2O$ in 40 mL of water The resultant mixture was extracted twice with 100 mL of dichloromethane each and the combined organic extracts were washed twice with 10 mL of phosphate buffer each, dried, and evaporated to dryness. The residue was dissolved in 60 mL of toluene, cooled to 0°C and extracted with three 50 mL portions of cold pH 9.5 carbonate buffer. The aqueous extracts were adjusted to pH 3 with phosphoric acid, and extracted with five 40 mL portions of chloroform which were combined, dried and evaporated to dryness. The residue was purified by column chromatography using 25% ethylacetate/hexane to afford 1.9 g of b-ketoester (39%).

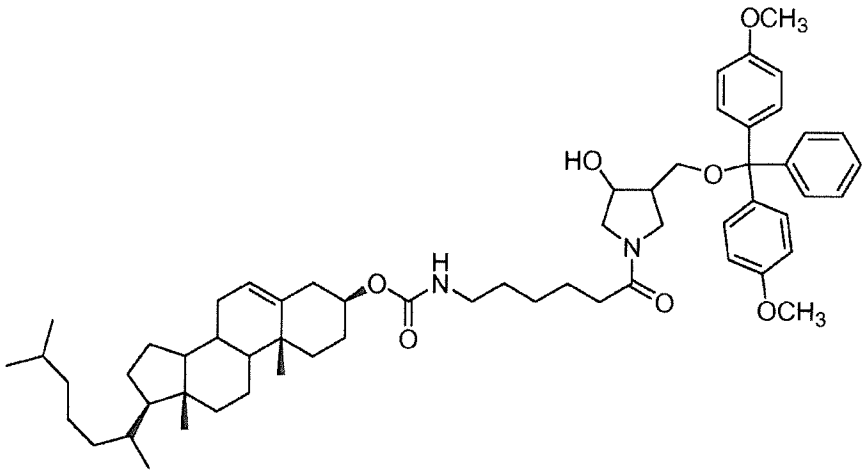
[6-(3-Hydroxy-4-hydroxymethyl-pyrrolidin-1-yl)-6-oxo-hexyl]-carbamic acid 17-(1,5-dimethyl-hexyl)-10,13-dimethyl-2,3,4,7,8,9,10,11,12,13,14,15,16,17-tetradecahydro-1H-cyclopenta[a]phenanthren-3-yl ester **AF**



AF

Methanol (2 mL) was added dropwise over a period of 1 h to a refluxing mixture of b-ketoester AE (1.5 g, 2.2 mmol) and sodium borohydride (0.226 g, 6 mmol) in tetrahydrofuran (10 mL). Stirring was continued at reflux temperature for 1 h. After cooling to room temperature, 1 N HCl (12.5 mL) was added, the mixture was extracted with ethylacetate (3 x 40 mL). The combined ethylacetate layer was dried over anhydrous sodium sulfate and concentrated under vacuum to yield the product which was purified by column chromatography (10% MeOH/$CHCl_3$) (89%).

(6-{3-[Bis-(4-methoxy-phenyl)-phenyl-methoxymethyl]-4-hydroxy-pyrrolidin-1-yl}-6-oxo-hexyl)-carbamic acid 17-(1,5-dimethyl-hexyl)-10,13-dimethyl-2,3,4,7,8,9,10,11,12,13,14,15,16,17-tetradecahydro-1H-cyclopenta[a]phenanthren-3-yl ester **AG**

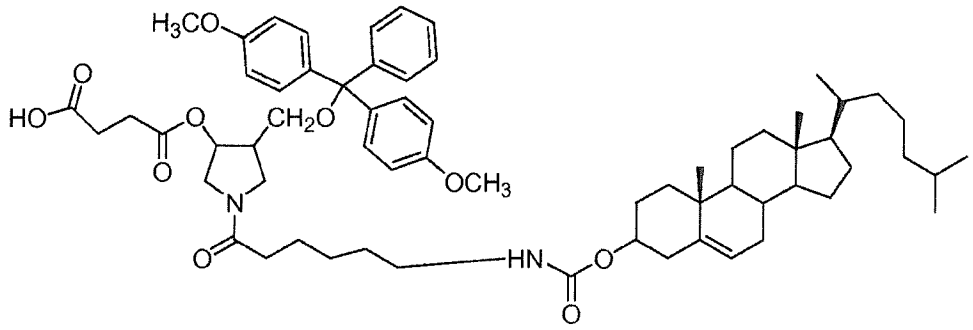


AG

Diol AF (1.25 gm 1.994 mmol) was dried by evaporating with pyridine (2 x 5 mL) *in vacuo*. Anhydrous pyridine (10 mL) and 4,4'-dimethoxytritylchloride (0.724 g, 2.13 mmol) were added with stirring. The reaction was carried out at room temperature overnight. The reaction was quenched by the addition of methanol. The reaction mixture was concentrated under vacuum and to the residue dichloromethane (50 mL) was added. The organic layer was washed with 1M aqueous sodium bicarbonate. The organic layer was dried over anhydrous

sodium sulfate, filtered and concentrated. The residual pyridine was removed by evaporating with toluene. The crude product was purified by column chromatography (2% MeOH/Chloroform, Rf = 0.5 in 5% MeOH/CHCl3) (1.75 g, 95%).

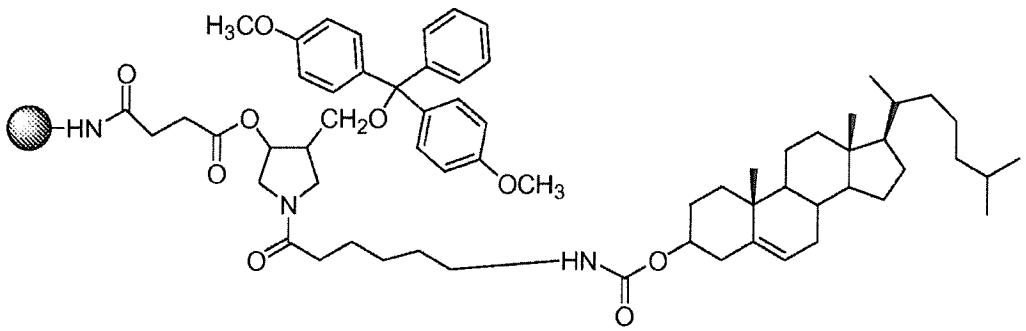
Succinic acid mono-(4-[bis-(4-methoxy-phenyl)-phenyl-methoxymethyl]-1-{6-[17-(1,5-dimethyl-hexyl)-10,13-dimethyl 2,3,4,7,8,9,10,11,12,13,14,15,16,17-tetradecahydro-1H cyclopenta[a]phenanthren-3-yloxycarbonylamino]-hexanoyl}-pyrrolidin-3-yl) ester **AH**



AH

Compound AG (1.0 g, 1.05 mmol) was mixed with succinic anhydride (0.150 g, 1.5 mmol) and DMAP (0.073 g, 0.6 mmol) and dried in a vacuum at 40°C overnight. The mixture was dissolved in anhydrous dichloroethane (3 mL), triethylamine (0.318 g, 0.440 mL, 3.15 mmol) was added and the solution was stirred at room temperature under argon atmosphere for 16 h. It was then diluted with dichloromethane (40 mL) and washed with ice cold aqueous citric acid (5 wt%, 30 mL) and water (2 X 20 mL). The organic phase was dried over anhydrous sodium sulfate and concentrated to dryness. The residue was used as such for the next step.

Cholesterol derivatised CPG **AI**



AI

Succinate AH (0.254 g, 0.242 mmol) was dissolved in a mixture of dichloromethane/acetonitrile (3:2, 3 mL). To that solution DMAP (0.0296 g, 0.242 mmol) in acetonitrile (1.25 mL), 2,2'-Dithio-bis(5-nitropyridine) (0.075 g, 0.242 mmol) in acetonitrile/dichloroethane (3:1, 1.25 mL) were added successively. To the resulting solution

triphenylphosphine (0.064 g, 0.242 mmol) in acetonitrile (0.6 ml) was added. The reaction mixture turned bright orange in color. The solution was agitated briefly using a wrist-action shaker (5 mins). Long chain alkyl amine-CPG (LCAA-CPG) (1.5 g, 61 mM) was added. The suspension was agitated for 2 h. The CPG was filtered through a sintered funnel and washed with acetonitrile, dichloromethane and ether successively. Unreacted amino groups were masked using acetic anhydride/pyridine. The achieved loading of the CPG was measured by taking UV measurement (37 mM/g).

The synthesis of siRNAs bearing a 5'-12-dodecanoic acid bisdecylamide group (herein referred to as "5'-C32-") or a 5'-cholesteryl derivative group (herein referred to as "5'-Chol-") was performed as described in WO 2004/065601, except that, for the cholesteryl derivative, the oxidation step was performed using the Beaucage reagent in order to introduce a phosphorothioate linkage at the 5'-end of the nucleic acid oligomer.

Nucleic acid sequences are represented below using standard nomenclature, and specifically the abbreviations of Table 1.

Table 1: Abbreviations of nucleotide monomers used in nucleic acid sequence representation. It will be understood that these monomers, when present in an oligonucleotide, are mutually linked by 5'-3'-phosphodiester bonds.

Abbreviation	Nucleotide(s)
A	adenosine-3'-phosphate
C	cytidine-3'-phosphate
G	guanosine-3'-phosphate
T	5-methyluridine-3'-phosphate
U	uridine-3'-phosphate
N	any nucleotide (G, A, C, or T)
a	2'-O-methyladenosine-3'-phosphate
c	2'-O-methylcytidine-3'-phosphate
g	2'-O-methylguanosine-3'-phosphate
u	2'-O-methyluridine-3'-phosphate
dT	2'-deoxythymidine-3'-phosphate
sT; sdT	2'-deoxy-thymidine-5'phosphate-phosphorothioate

Example 2A. TTR siRNA Design

Transcripts

siRNA design was carried out to identify siRNAs targeting the gene transthyretin from human (symbol TTR) and rat (symbol Ttr). The design used the TTR transcripts NM_000371.2

(SEQ ID NO:1329) (human) and NM_012681.1 (SEQ ID NO:1330) (rat) from the NCBI Refseq collection. The siRNA duplexes were designed with 100% identity to their respective TTR genes.

siRNA Design and Specificity Prediction

The predicted specificity of all possible 19mers was determined for each sequence. The TTR siRNAs were used in a comprehensive search against the human and rat transcriptomes (defined as the set of NM_ and XM_ records within the NCBI Refseq set) using the FASTA algorithm. The Python script 'offtargetFasta.py' was then used to parse the alignments and generate a score based on the position and number of mismatches between the siRNA and any potential 'off-target' transcript. The off-target score is weighted to emphasize differences in the 'seed' region of siRNAs, in positions 2-9 from the 5' end of the molecule. The off-target score is calculated as follows: mismatches between the oligo and the transcript are given penalties. A mismatch in the seed region in positions 2-9 of the oligo is given a penalty of 2.8; mismatches in the putative cleavage sites 10 and 11 are given a penalty of 1.2, and mismatches in positions 12-19 a penalty of 1. Mismatches in position 1 are not considered. The off-target score for each oligo-transcript pair is then calculated by summing the mismatch penalties. The lowest off-target score from all the oligo-transcript pairs is then determined and used in subsequent sorting of oligos. 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. In picking which oligos to synthesize, off-target scores of the antisense strand were sorted from high to low, and the 144 best (lowest off-target score) oligo pairs from human, and the best 26 pairs from rat were selected.

siRNA sequence selection

A total of 140 sense and 140 antisense human TTR derived siRNA oligos were synthesized and formed into duplexes. A total of 26 sense and 26 antisense rat TTR derived siRNA oligos were synthesized and formed into duplexes. Duplexes included The oligos are presented in Tables 2-4 (human TTR) and Tables 5-7 (rat TTR).

Table 2. Identification numbers for human TTR dsRNAs

See Table 4 for sequences and modifications of oligos.

Duplex #	Sense Oligo #	Antisense Oligo #
AD-18243	A-32153	A-32154
AD-18244	A-32155	A-32156
AD-18245	A-32157	A-32158
AD-18246	A-32159	A-32160
AD-18247	A-32163	A-32164
AD-18248	A-32165	A-32166
AD-18249	A-32167	A-32168
AD-18250	A-32169	A-32170
AD-18251	A-32171	A-32172
AD-18252	A-32175	A-32176
AD-18253	A-32177	A-32178
AD-18254	A-32179	A-32180
AD-18255	A-32181	A-32182
AD-18256	A-32183	A-32184
AD-18257	A-32187	A-32188
AD-18258	A-32189	A-32190
AD-18259	A-32191	A-32192
AD-18260	A-32193	A-32194
AD-18261	A-32195	A-32196
AD-18262	A-32199	A-32200
AD-18263	A-32201	A-32202
AD-18264	A-32203	A-32204
AD-18265	A-32205	A-32206
AD-18266	A-32207	A-32208
AD-18267	A-32211	A-32212
AD-18268	A-32213	A-32214
AD-18269	A-32215	A-32216
AD-18270	A-32217	A-32218
AD-18271	A-32219	A-32220
AD-18272	A-32221	A-32222
AD-18273	A-32223	A-32224
AD-18274	A-32225	A-32226
AD-18275	A-32227	A-32228
AD-18276	A-32229	A-32230
AD-18277	A-32231	A-32232
AD-18278	A-32233	A-32234
AD-18279	A-32235	A-32236
AD-18280	A-32237	A-32238
AD-18281	A-32239	A-32240
AD-18282	A-32241	A-32242
AD-18283	A-32243	A-32244

Duplex #	Sense Oligo #	Antisense Oligo #
AD-18284	A-32247	A-32248
AD-18285	A-32249	A-32250
AD-18286	A-32251	A-32252
AD-18287	A-32253	A-32254
AD-18288	A-32255	A-32256
AD-18289	A-32259	A-32260
AD-18290	A-32261	A-32262
AD-18291	A-32263	A-32264
AD-18292	A-32265	A-32266
AD-18293	A-32267	A-32268
AD-18294	A-32269	A-32270
AD-18295	A-32271	A-32272
AD-18296	A-32273	A-32274
AD-18297	A-32275	A-32276
AD-18298	A-32277	A-32278
AD-18299	A-32279	A-32280
AD-18300	A-32281	A-32282
AD-18301	A-32283	A-32284
AD-18302	A-32285	A-32286
AD-18303	A-32287	A-32288
AD-18304	A-32289	A-32290
AD-18305	A-32291	A-32292
AD-18306	A-32295	A-32296
AD-18307	A-32297	A-32298
AD-18308	A-32299	A-32300
AD-18309	A-32301	A-32302
AD-18310	A-32303	A-32304
AD-18311	A-32307	A-32308
AD-18312	A-32309	A-32310
AD-18313	A-32311	A-32312
AD-18314	A-32313	A-32314
AD-18315	A-32315	A-32316
AD-18316	A-32319	A-32320
AD-18317	A-32321	A-32322
AD-18318	A-32323	A-32324
AD-18319	A-32325	A-32326
AD-18320	A-32327	A-32328
AD-18321	A-32331	A-32332
AD-18322	A-32333	A-32334
AD-18323	A-32335	A-32336
AD-18324	A-32337	A-32338
AD-18325	A-32339	A-32340
AD-18326	A-32341	A-32342
AD-18327	A-32343	A-32344

Duplex #	Sense Oligo #	Antisense Oligo #
AD-18328	A-32345	A-32346
AD-18329	A-32347	A-32348
AD-18330	A-32349	A-32350
AD-18331	A-32351	A-32352
AD-18332	A-32353	A-32354
AD-18333	A-32355	A-32356
AD-18334	A-32357	A-32358
AD-18335	A-32359	A-32360
AD-18336	A-32363	A-32364
AD-18337	A-32367	A-32368
AD-18338	A-32369	A-32370
AD-18339	A-32371	A-32372
AD-18340	A-32373	A-32374
AD-18341	A-32375	A-32376
AD-18342	A-32379	A-32380
AD-18343	A-32381	A-32382
AD-18344	A-32383	A-32384
AD-18345	A-32385	A-32386
AD-18346	A-32387	A-32388
AD-18347	A-32391	A-32392
AD-18348	A-32393	A-32394
AD-18349	A-32395	A-32396
AD-18350	A-32397	A-32398
AD-18351	A-32399	A-32400
AD-18352	A-32401	A-32402
AD-18353	A-32403	A-32404
AD-18354	A-32405	A-32406
AD-18355	A-32407	A-32408
AD-18356	A-32409	A-32410
AD-18357	A-32411	A-32412
AD-18358	A-32415	A-32416
AD-18359	A-32417	A-32418
AD-18360	A-32419	A-32420
AD-18361	A-32421	A-32422
AD-18362	A-32423	A-32424
AD-18363	A-32427	A-32428
AD-18364	A-32429	A-32430
AD-18446	A-32161	A-32162
AD-18447	A-32173	A-32174
AD-18448	A-32185	A-32186
AD-18449	A-32197	A-32198
AD-18450	A-32209	A-32210
AD-18451	A-32245	A-32246
AD-18452	A-32257	A-32258

Duplex #	Sense Oligo #	Antisense Oligo #
AD-18453	A-32293	A-32294
AD-18454	A-32305	A-32306
AD-18455	A-32317	A-32318
AD-18456	A-32329	A-32330
AD-18457	A-32361	A-32362
AD-18458	A-32365	A-32366
AD-18459	A-32377	A-32378
AD-18460	A-32389	A-32390
AD-18461	A-32401	A-32402
AD-18462	A-32413	A-32414
AD-18463	A-32425	A-32426

Table 3A. Sense and antisense strand sequences of human TTR dsRNAs

Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_000371.2, SEQ ID NO:1329)

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
S	100	CCGGUGAAUCCAAGUGUCC	1	CCGGUGAAUCCAAGUGUCCNN	281
as	118	GGACACUUGGAUUCACCGG	2	GGACACUUGGAUUCACCGGNN	282
S	11	ACUCAUUCUUGGCAGGAUG	3	ACUCAUUCUUGGCAGGAUGNN	283
as	29	CAUCCUGCCAAGAAUGAGU	4	CAUCCUGCCAAGAAUGAGUNN	284
S	111	AAGUGUCCUCUGAUGGUCA	5	AAGUGUCCUCUGAUGGUCANN	285
as	129	UGACCAUCAGAGGACACUU	6	UGACCAUCAGAGGACACUUNN	286
S	13	UCAUUCUUGGCAGGAUGGC	7	UCAUUCUUGGCAGGAUGGCNN	287
as	31	GCCAUCCUGCCAAGAAUGA	8	GCCAUCCUGCCAAGAAUGANN	288
s	130	AAGUUCUAGAUGCUGUCCG	9	AAGUUCUAGAUGCUGUCCGNN	289
as	148	CGGACAGCAUCUAGAACUU	10	CGGACAGCAUCUAGAACUUNN	290
s	132	GUUCUAGAUGCUGUCCGAG	11	GUUCUAGAUGCUGUCCGAGNN	291
as	150	CUCGGACAGCAUCUAGAAC	12	CUCGGACAGCAUCUAGAACNN	292
s	135	CUAGAUGCUGUCCGAGGCA	13	CUAGAUGCUGUCCGAGGCANN	293
as	153	UGCCUCGGACAGCAUCUAG	14	UGCCUCGGACAGCAUCUAGNN	294
s	138	GAUGCUGUCCGAGGCAGUC	15	GAUGCUGUCCGAGGCAGUCNN	295
as	156	GACUGCCUCGGACAGCAUC	16	GACUGCCUCGGACAGCAUCNN	296
s	14	CAUUCUUGGCAGGAUGGCU	17	CAUUCUUGGCAGGAUGGCUNN	297
as	32	AGCCAUCCUGCCAAGAAUG	18	AGCCAUCCUGCCAAGAAUGNN	298
s	140	UGCUGUCCGAGGCAGUCCU	19	UGCUGUCCGAGGCAGUCCUNN	299
as	158	AGGACUGCCUCGGACAGCA	20	AGGACUGCCUCGGACAGCANN	300
s	146	CCGAGGCAGUCCUGCCAUC	21	CCGAGGCAGUCCUGCCAUCNN	301
as	164	GAUGGCAGGACUGCCUCGG	22	GAUGGCAGGACUGCCUCGGNN	302
s	152	CAGUCCUGCCAUCAAUGUG	23	CAGUCCUGCCAUCAAUGUGNN	303
as	170	CACAUUGAUGGCAGGACUG	24	CACAUUGAUGGCAGGACUGNN	304
s	164	CAAUGUGGCCGUGCAUGUG	25	CAAUGUGGCCGUGCAUGUGNN	305
as	182	CACAUGCACGGCCACAUUG	26	CACAUGCACGGCCACAUUGNN	306
s	178	AUGUGUUCAGAAAGGCUGC	27	AUGUGUUCAGAAAGGCUGCNN	307
as	196	GCAGCCUUUCUGAACACAU	28	GCAGCCUUUCUGAACACAUNN	308
s	2	CAGAAGUCCACUCAUUCUU	29	CAGAAGUCCACUCAUUCUUNN	309

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
as	20	AAGAAUGAGUGGACUUCUG	30	AAGAAUGAGUGGACUUCUGNN	310
s	21	GGCAGGAUGGCUUCUCAUC	31	GGCAGGAUGGCUUCUCAUCNN	311
as	39	GAUGAGAAGCCAUCCUGCC	32	GAUGAGAAGCCAUCCUGCCNN	312
s	210	GAGCCAUUUGCCUCUGGGA	33	GAGCCAUUUGCCUCUGGGANN	313
as	228	UCCCAGAGGCAAAUGGCUC	34	UCCCAGAGGCAAAUGGCUCNN	314
s	23	CAGGAUGGCUUCUCAUCGU	35	CAGGAUGGCUUCUCAUCGUNN	315
as	41	ACGAUGAGAAGCCAUCCUG	36	ACGAUGAGAAGCCAUCCUGNN	316
s	24	AGGAUGGCUUCUCAUCGUC	37	AGGAUGGCUUCUCAUCGUCNN	317
as	42	GACGAUGAGAAGCCAUCCU	38	GACGAUGAGAAGCCAUCCUNN	318
s	245	AGAGCUGCAUGGGCUCACA	39	AGAGCUGCAUGGGCUCACANN	319
as	263	UGUGAGCCCAUGCAGCUCU	40	UGUGAGCCCAUGCAGCUCUNN	320
s	248	GCUGCAUGGGCUCACAACU	41	GCUGCAUGGGCUCACAACUNN	321
as	266	AGUUGUGAGCCCAUGCAGC	42	AGUUGUGAGCCCAUGCAGCNN	322
s	25	GGAUGGCUUCUCAUCGUCU	43	GGAUGGCUUCUCAUCGUCUNN	323
as	43	AGACGAUGAGAAGCCAUCC	44	AGACGAUGAGAAGCCAUCCNN	324
s	251	GCAUGGGCUCACAACUGAG	45	GCAUGGGCUCACAACUGAGNN	325
as	269	CUCAGUUGUGAGCCCAUGC	46	CUCAGUUGUGAGCCCAUGCNN	326
s	253	AUGGGCUCACAACUGAGGA	47	AUGGGCUCACAACUGAGGANN	327
as	271	UCCUCAGUUGUGAGCCCAU	48	UCCUCAGUUGUGAGCCCAUNN	328
s	254	UGGGCUCACAACUGAGGAG	49	UGGGCUCACAACUGAGGAGNN	329
as	272	CUCCUCAGUUGUGAGCCCA	50	CUCCUCAGUUGUGAGCCCANN	330
s	270	GAGGAAUUUGUAGAAGGGA	51	GAGGAAUUUGUAGAAGGGANN	331
as	288	UCCCUUCUACAAAUUCCUC	52	UCCCUUCUACAAAUUCCUCNN	332
s	276	UUUGUAGAAGGGAUAUACA	53	UUUGUAGAAGGGAUAUACANN	333
as	294	UGUAUAUCCCUUCUACAAA	54	UGUAUAUCCCUUCUACAAANN	334
s	277	UUGUAGAAGGGAUAUACAA	55	UUGUAGAAGGGAUAUACAANN	335
as	295	UUGUAUAUCCCUUCUACAA	56	UUGUAUAUCCCUUCUACAANN	336
s	278	UGUAGAAGGGAUAUACAAA	57	UGUAGAAGGGAUAUACAAANN	337
as	296	UUUGUAUAUCCCUUCUACA	58	UUUGUAUAUCCCUUCUACANN	338
s	281	AGAAGGGAUAUACAAAGUG	59	AGAAGGGAUAUACAAAGUGNN	339
as	299	CACUUUGUAUAUCCCUUCU	60	CACUUUGUAUAUCCCUUCUNN	340
s	295	AAGUGGAAAUAGACACCAA	61	AAGUGGAAAUAGACACCAANN	341
as	313	UUGGUGUCUAUUUCCACUU	62	UUGGUGUCUAUUUCCACUUNN	342
s	299	GGAAAUAGACACCAAAUCU	63	GGAAAUAGACACCAAAUCUNN	343
as	317	AGAUUUGGUGUCUAUUUCC	64	AGAUUUGGUGUCUAUUUCCNN	344
s	300	GAAAUAGACACCAAAUCUU	65	GAAAUAGACACCAAAUCUUNN	345
as	318	AAGAUUUGGUGUCUAUUUC	66	AAGAUUUGGUGUCUAUUUCNN	346
s	303	AUAGACACCAAAUCUUACU	67	AUAGACACCAAAUCUUACUNN	347
as	321	AGUAAGAUUUGGUGUCUAU	68	AGUAAGAUUUGGUGUCUAUNN	348
s	304	UAGACACCAAAUCUUACUG	69	UAGACACCAAAUCUUACUGNN	349
as	322	CAGUAAGAUUUGGUGUCUA	70	CAGUAAGAUUUGGUGUCUANN	350
s	305	AGACACCAAAUCUUACUGG	71	AGACACCAAAUCUUACUGGNN	351
as	323	CCAGUAAGAUUUGGUGUCU	72	CCAGUAAGAUUUGGUGUCUNN	352
s	317	UUACUGGAAGGCACUUGGC	73	UUACUGGAAGGCACUUGGCNN	353
as	335	GCCAAGUGCCUUCCAGUAA	74	GCCAAGUGCCUUCCAGUAANN	354
s	32	UUCUCAUCGUCUGCUCCUC	75	UUCUCAUCGUCUGCUCCUCNN	355
as	50	GAGGAGCAGACGAUGAGAA	76	GAGGAGCAGACGAUGAGAANN	356
s	322	GGAAGGCACUUGGCAUCUC	77	GGAAGGCACUUGGCAUCUCNN	357
as	340	GAGAUGCCAAGUGCCUUCC	78	GAGAUGCCAAGUGCCUUCCNN	358

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
s	326	GGCACUUGGCAUCUCCCCA	79	GGCACUUGGCAUCUCCCCANN	359
as	344	UGGGGAGAUGCCAAGUGCC	80	UGGGGAGAUGCCAAGUGCCNN	360
s	333	GGCAUCUCCCCAUUCCAUG	81	GGCAUCUCCCCAUUCCAUGNN	361
as	351	AUGGAAUGGGGAGAUGCCTT	82	AUGGAAUGGGGAGAUGCCTTNN	362
s	334	GCAUCUCCCCAUUCCAUGA	83	GCAUCUCCCCAUUCCAUGANN	363
as	352	UCAUGGAAUGGGGAGAUGC	84	UCAUGGAAUGGGGAGAUGCNN	364
s	335	CAUCUCCCCAUUCCAUGAG	85	CAUCUCCCCAUUCCAUGAGNN	365
as	353	CUCAUGGAAUGGGGAGAUG	86	CUCAUGGAAUGGGGAGAUGNN	366
s	336	AUCUCCCCAUUCCAUGAGC	87	AUCUCCCCAUUCCAUGAGCNN	367
as	354	GCUCAUGGAAUGGGGAGAU	88	GCUCAUGGAAUGGGGAGAUNN	368
s	338	CUCCCCAUUCCAUGAGCAU	89	CUCCCCAUUCCAUGAGCAUNN	369
as	356	AUGCUCAUGGAAUGGGGAG	90	AUGCUCAUGGAAUGGGGAGNN	370
s	341	CCCAUUCCAUGAGCAUGCA	91	CCCAUUCCAUGAGCAUGCANN	371
as	359	UGCAUGCUCAUGGAAUGGG	92	UGCAUGCUCAUGGAAUGGGNN	372
s	347	CCAUGAGCAUGCAGAGGUG	93	CCAUGAGCAUGCAGAGGUGNN	373
as	365	CACCUCUGCAUGCUCAUGG	94	CACCUCUGCAUGCUCAUGGNN	374
s	352	AGCAUGCAGAGGUGGUAUU	95	AGCAUGCAGAGGUGGUAUUNN	375
as	370	AAUACCACCUCUGCAUGCU	96	AAUACCACCUCUGCAUGCUNN	376
s	354	CAUGCAGAGGUGGUAUUCA	97	CAUGCAGAGGUGGUAUUCANN	377
as	372	UGAAUACCACCUCUGCAUG	98	UGAAUACCACCUCUGCAUGNN	378
s	355	AUGCAGAGGUGGUAUUCAC	99	AUGCAGAGGUGGUAUUCACNN	379
as	373	GUGAAUACCACCUCUGCAU	100	GUGAAUACCACCUCUGCAUNN	380
s	362	GGUGGUAUUCACAGCCAAC	101	GGUGGUAUUCACAGCCAACNN	381
as	380	GUUGGCUGUGAAUACCACC	102	GUUGGCUGUGAAUACCACCNN	382
s	363	GUGGUAUUCACAGCCAACG	103	GUGGUAUUCACAGCCAACGNN	383
as	381	CGUUGGCUGUGAAUACCAC	104	CGUUGGCUGUGAAUACCACNN	384
s	364	UGGUAUUCACAGCCAACGA	105	UGGUAUUCACAGCCAACGANN	385
as	382	UCGUUGGCUGUGAAUACCA	106	UCGUUGGCUGUGAAUACCANN	386
s	365	GGUAUUCACAGCCAACGAC	107	GGUAUUCACAGCCAACGACNN	387
as	383	GUCGUUGGCUGUGAAUACC	108	GUCGUUGGCUGUGAAUACCNN	388
s	366	GUAUUCACAGCCAACGACU	109	GUAUUCACAGCCAACGACUNN	389
as	384	AGUCGUUGGCUGUGAAUAC	110	AGUCGUUGGCUGUGAAUACNN	390
s	367	UAUUCACAGCCAACGACUC	111	UAUUCACAGCCAACGACUCNN	391
as	385	GAGUCGUUGGCUGUGAAUA	112	GAGUCGUUGGCUGUGAAUANN	392
s	370	UCACAGCCAACGACUCCGG	113	UCACAGCCAACGACUCCGGNN	393
as	388	CCGGAGUCGUUGGCUGUGA	114	CCGGAGUCGUUGGCUGUGANN	394
s	390	CCCCGCCGCUACACCAUUG	115	CCCCGCCGCUACACCAUUGNN	395
as	408	CAAUGGUGUAGCGGCGGGG	116	CAAUGGUGUAGCGGCGGGGNN	396
s	4	GAAGUCCACUCAUUCUUGG	117	GAAGUCCACUCAUUCUUGGNN	397
as	22	CCAAGAAUGAGUGGACUUC	118	CCAAGAAUGAGUGGACUUCNN	398
s	412	CCCUGCUGAGCCCCUACUC	119	CCCUGCUGAGCCCCUACUCNN	399
as	430	GAGUAGGGGCUCAGCAGGG	120	GAGUAGGGGCUCAGCAGGGNN	400
s	417	CUGAGCCCCUACUCCUAUU	121	CUGAGCCCCUACUCCUAUUNN	401
as	435	AAUAGGAGUAGGGGCUCAG	122	AAUAGGAGUAGGGGCUCAGNN	402
s	418	UGAGCCCCUACUCCUAUUC	123	UGAGCCCCUACUCCUAUUCNN	403
as	436	GAAUAGGAGUAGGGGCUCA	124	GAAUAGGAGUAGGGGCUCANN	404
s	422	CCCCUACUCCUAUUCCACC	125	CCCCUACUCCUAUUCCACCNN	405
as	440	GGUGGAAUAGGAGUAGGGG	126	GGUGGAAUAGGAGUAGGGGNN	406
s	425	CUACUCCUAUUCCACCACG	127	CUACUCCUAUUCCACCACGNN	407

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
as	443	CGUGGUGGAAUAGGAGUAG	128	CGUGGUGGAAUAGGAGUAGNN	408
s	426	UACUCCUAUUCCACCACGG	129	UACUCCUAUUCCACCACGGNN	409
as	444	CCGUGGUGGAAUAGGAGUA	130	CCGUGGUGGAAUAGGAGUANN	410
s	427	ACUCCUAUUCCACCACGGC	131	ACUCCUAUUCCACCACGGCNN	411
as	445	GCCGUGGUGGAAUAGGAGU	132	GCCGUGGUGGAAUAGGAGUNN	412
s	429	UCCUAUUCCACCACGGCUG	133	UCCUAUUCCACCACGGCUGNN	413
as	447	CAGCCGUGGUGGAAUAGGA	134	CAGCCGUGGUGGAAUAGGANN	414
s	432	UAUUCCACCACGGCUGUCG	135	UAUUCCACCACGGCUGUCGNN	415
as	450	CGACAGCCGUGGUGGAAUA	136	CGACAGCCGUGGUGGAAUANN	416
s	433	AUUCCACCACGGCUGUCGU	137	AUUCCACCACGGCUGUCGUNN	417
as	451	ACGACAGCCGUGGUGGAAU	138	ACGACAGCCGUGGUGGAAUNN	418
s	437	CACCACGGCUGUCGUCACC	139	CACCACGGCUGUCGUCACCNN	419
as	455	GGUGACGACAGCCGUGGUG	140	GGUGACGACAGCCGUGGUGNN	420
s	438	ACCACGGCUGUCGUCACCA	141	ACCACGGCUGUCGUCACCANN	421
as	456	UGGUGACGACAGCCGUGGU	142	UGGUGACGACAGCCGUGGUNN	422
s	439	CCACGGCUGUCGUCACCAA	143	CCACGGCUGUCGUCACCAANN	423
as	457	UUGGUGACGACAGCCGUGG	144	UUGGUGACGACAGCCGUGGNN	424
s	441	ACGGCUGUCGUCACCAAUC	145	ACGGCUGUCGUCACCAAUCNN	425
as	459	GAUUGGUGACGACAGCCGU	146	GAUUGGUGACGACAGCCGUNN	426
s	442	CGGCUGUCGUCACCAAUCC	147	CGGCUGUCGUCACCAAUCCNN	427
as	460	GGAUUGGUGACGACAGCCG	148	GGAUUGGUGACGACAGCCGNN	428
s	449	CGUCACCAAUCCCAAGGAA	149	CGUCACCAAUCCCAAGGAANN	429
as	467	UUCCUUGGGAUUGGUGACG	150	UUCCUUGGGAUUGGUGACGNN	430
s	455	CAAUCCCAAGGAAUGAGGG	151	CAAUCCCAAGGAAUGAGGGNN	431
as	473	CCCUCAUUCCUUGGGAUUG	152	CCCUCAUUCCUUGGGAUUGNN	432
s	491	CCUGAAGGACGAGGGAUGG	153	CCUGAAGGACGAGGGAUGGNN	433
as	509	CCAUCCCUCGUCCUUCAGG	154	CCAUCCCUCGUCCUUCAGGNN	434
s	497	GGACGAGGGAUGGGAUUUC	155	GGACGAGGGAUGGGAUUUCNN	435
as	515	GAAAUCCCAUCCCUCGUCC	156	GAAAUCCCAUCCCUCGUCCNN	436
s	5	AAGUCCACUCAUUCUUGGC	157	AAGUCCACUCAUUCUUGGCNN	437
as	23	GCCAAGAAUGAGUGGACUU	158	GCCAAGAAUGAGUGGACUUNN	438
s	508	GGGAUUUCAUGUAACCAAG	159	GGGAUUUCAUGUAACCAAGNN	439
as	526	CUUGGUUACAUGAAAUCCC	160	CUUGGUUACAUGAAAUCCCNN	440
s	509	GGAUUUCAUGUAACCAAGA	161	GGAUUUCAUGUAACCAAGANN	441
as	527	UCUUGGUUACAUGAAAUCC	162	UCUUGGUUACAUGAAAUCCNN	442
s	514	UCAUGUAACCAAGAGUAUU	163	UCAUGUAACCAAGAGUAUUNN	443
as	532	AAUACUCUUGGUUACAUGA	164	AAUACUCUUGGUUACAUGANN	444
s	516	AUGUAACCAAGAGUAUUCC	165	AUGUAACCAAGAGUAUUCCNN	445
as	534	GGAAUACUCUUGGUUACAU	166	GGAAUACUCUUGGUUACAUNN	446
s	517	UGUAACCAAGAGUAUUCCA	167	UGUAACCAAGAGUAUUCCANN	447
as	535	UGGAAUACUCUUGGUUACA	168	UGGAAUACUCUUGGUUACANN	448
s	518	GUAACCAAGAGUAUUCCAU	169	GUAACCAAGAGUAUUCCAUNN	449
as	536	AUGGAAUACUCUUGGUUAC	170	AUGGAAUACUCUUGGUUACNN	450
s	54	UGCCUUGCUGGACUGGUAU	171	UGCCUUGCUGGACUGGUAUNN	451
as	72	AUACCAGUCCAGCAAGGCA	172	AUACCAGUCCAGCAAGGCANN	452
s	543	UAAAGCAGUGUUUUCACCU	173	UAAAGCAGUGUUUUCACCUNN	453
as	561	AGGUGAAAACACUGCUUUA	174	AGGUGAAAACACUGCUUUANN	454
s	55	GCCUUGCUGGACUGGUAUU	175	GCCUUGCUGGACUGGUAUUNN	455
as	73	AAUACCAGUCCAGCAAGGC	176	AAUACCAGUCCAGCAAGGCNN	456

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
s	551	UGUUUUCACCUCAUAUGCU	177	UGUUUUCACCUCAUAUGCUNN	457
as	569	AGCAUAUGAGGUGAAAACA	178	AGCAUAUGAGGUGAAAACANN	458
s	552	GUUUUCACCUCAUAUGCUA	179	GUUUUCACCUCAUAUGCUANN	459
as	570	UAGCAUAUGAGGUGAAAAC	180	UAGCAUAUGAGGUGAAAACNN	460
s	553	UUUUCACCUCAUAUGCUAU	181	UUUUCACCUCAUAUGCUAUNN	461
as	571	AUAGCAUAUGAGGUGAAAA	182	AUAGCAUAUGAGGUGAAAANN	462
s	555	UUCACCUCAUAUGCUAUGU	183	UUCACCUCAUAUGCUAUGUNN	463
as	573	ACAUAGCAUAUGAGGUGAA	184	ACAUAGCAUAUGAGGUGAANN	464
s	557	CACCUCAUAUGCUAUGUUA	185	CACCUCAUAUGCUAUGUUANN	465
as	575	UAACAUAGCAUAUGAGGUG	186	UAACAUAGCAUAUGAGGUGNN	466
s	56	CCUUGCUGGACUGGUAUUU	187	CCUUGCUGGACUGGUAUUUNN	467
as	74	AAAUACCAGUCCAGCAAGG	188	AAAUACCAGUCCAGCAAGGNN	468
s	563	AUAUGCUAUGUUAGAAGUC	189	AUAUGCUAUGUUAGAAGUCNN	469
as	581	GACUUCUAACAUAGCAUAU	190	GACUUCUAACAUAGCAUAUNN	470
s	564	UAUGCUAUGUUAGAAGUCC	191	UAUGCUAUGUUAGAAGUCCNN	471
as	582	GGACUUCUAACAUAGCAUA	192	GGACUUCUAACAUAGCAUANN	472
s	566	UGCUAUGUUAGAAGUCCAG	193	UGCUAUGUUAGAAGUCCAGNN	473
as	584	CUGGACUUCUAACAUAGCA	194	CUGGACUUCUAACAUAGCANN	474
s	57	CUUGCUGGACUGGUAUUUG	195	CUUGCUGGACUGGUAUUUGNN	475
as	75	CAAAUACCAGUCCAGCAAG	196	CAAAUACCAGUCCAGCAAGNN	476
s	578	AGUCCAGGCAGAGACAAUA	197	AGUCCAGGCAGAGACAAUANN	477
as	596	AUUGUCUCUGCCUGGACUTT	198	AUUGUCUCUGCCUGGACUTTNN	478
s	580	UCCAGGCAGAGACAAUAAA	199	UCCAGGCAGAGACAAUAAANN	479
as	598	UUUAUUGUCUCUGCCUGGA	200	UUUAUUGUCUCUGCCUGGANN	480
s	607	GUGAAAGGCACUUUUCAUU	201	GUGAAAGGCACUUUUCAUUNN	481
as	625	AAUGAAAAGUGCCUUUCAC	202	AAUGAAAAGUGCCUUUCACNN	482
s	62	UGGACUGGUAUUUGUGUCU	203	UGGACUGGUAUUUGUGUCUNN	483
as	80	AGACACAAAUACCAGUCCA	204	AGACACAAAUACCAGUCCANN	484
s	77	GUCUGAGGCUGGCCCUACG	205	GUCUGAGGCUGGCCCUACGNN	485
as	95	CGUAGGGCCAGCCUCAGAC	206	CGUAGGGCCAGCCUCAGACNN	486
s	79	CUGAGGCUGGCCCUACGGG	207	CUGAGGCUGGCCCUACGGGNN	487
as	97	CCCGUAGGGCCAGCCUCAG	208	CCCGUAGGGCCAGCCUCAGNN	488
s	81	GAGGCUGGCCCUACGGGCA	209	GAGGCUGGCCCUACGGGCANN	489
as	99	UGCCCGUAGGGCCAGCCUC	210	UGCCCGUAGGGCCAGCCUCNN	490
s	82	AGGCUGGCCCUACGGGCAC	211	AGGCUGGCCCUACGGGCACNN	491
as	100	GUGCCCGUAGGGCCAGCCU	212	GUGCCCGUAGGGCCAGCCUNN	492
s	84	GCUGGCCCUACGGGCACCG	213	GCUGGCCCUACGGGCACCGNN	493
as	102	CGGUGCCCGUAGGGCCAGC	214	CGGUGCCCGUAGGGCCAGCNN	494
s	85	CUGGCCCUACGGGCACCGG	215	CUGGCCCUACGGGCACCGGNN	495
as	103	CCGGUGCCCGUAGGGCCAG	216	CCGGUGCCCGUAGGGCCAGNN	496
s	87	GGCCCUACGGGCACCGGUG	217	GGCCCUACGGGCACCGGUGNN	497
as	105	CACCGGUGCCCGUAGGGCC	218	CACCGGUGCCCGUAGGGCCNN	498
s	9	CCACUCAUUCUUGGCAGGA	219	CCACUCAUUCUUGGCAGGANN	499
as	27	UCCUGCCAAGAAUGAGUGG	220	UCCUGCCAAGAAUGAGUGGNN	500
s	90	CCUACGGGCACCGGUGAAU	221	CCUACGGGCACCGGUGAAUNN	501
as	108	AUUCACCGGUGCCCGUAGG	222	AUUCACCGGUGCCCGUAGGNN	502
s	91	CUACGGGCACCGGUGAAUC	223	CUACGGGCACCGGUGAAUCNN	503
as	109	GAUUCACCGGUGCCCGUAG	224	GAUUCACCGGUGCCCGUAGNN	504
s	92	UACGGGCACCGGUGAAUCC	225	UACGGGCACCGGUGAAUCCNN	505

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
as	110	GGAUUCACCGGUGCCCGUA	226	GGAUUCACCGGUGCCCGUANN	506
s	93	ACGGGCACCGGUGAAUCCA	227	ACGGGCACCGGUGAAUCCANN	507
as	111	UGGAUUCACCGGUGCCCGU	228	UGGAUUCACCGGUGCCCGUNN	508
s	97	GCACCGGUGAAUCCAAGUG	229	GCACCGGUGAAUCCAAGUGNN	509
as	115	CACUUGGAUUCACCGGUGC	230	CACUUGGAUUCACCGGUGCNN	510
s	98	CACCGGUGAAUCCAAGUGU	231	CACCGGUGAAUCCAAGUGUNN	511
as	116	ACACUUGGAUUCACCGGUG	232	ACACUUGGAUUCACCGGUGNN	512
s	167	UGUGGCCAUGCAUGUGUUC	233	UGUGGCCAUGCAUGUGUUCNN	513
as	185	GAACACAUGCAUGGCCACA	234	GAACACAUGCAUGGCCACANN	514
s	168	GUGGCCAUGCAUGUGUUCA	235	GUGGCCAUGCAUGUGUUCANN	515
as	186	UGAACACAUGCAUGGCCAC	236	UGAACACAUGCAUGGCCACNN	516
s	171	GCCAUGCAUGUGUUCAGAA	237	GCCAUGCAUGUGUUCAGAANN	517
as	189	UUCUGAACACAUGCAUGGC	238	UUCUGAACACAUGCAUGGCNN	518
s	432	UAUUCCACCACGGCUGUCA	239	UAUUCCACCACGGCUGUCANN	519
as	449	UGACAGCCGUGGUGGAAUA	240	UGACAGCCGUGGUGGAAUANN	520
s	447	GUCAUCACCAAUCCCAAGG	241	GUCAUCACCAAUCCCAAGGNN	521
as	465	CCUUGGGAUUGGUGAUGAC	242	CCUUGGGAUUGGUGAUGACNN	522
s	115	GUCCUCUGAUGGUCAAAGU	243	GUCCUCUGAUGGUCAAAGUNN	523
as	133	ACUUUGACCAUCAGAGGAC	244	ACUUUGACCAUCAGAGGACNN	524
s	122	GAUGGUCAAAGUUCUAGAU	245	GAUGGUCAAAGUUCUAGAUNN	525
as	140	AUCUAGAACUUUGACCAUC	246	AUCUAGAACUUUGACCAUCNN	526
s	139	AUGCUGUCCGAGGCAGUCC	247	AUGCUGUCCGAGGCAGUCCNN	527
as	157	GGACUGCCUCGGACAGCAU	248	GGACUGCCUCGGACAGCAUNN	528
s	172	CCGUGCAUGUGUUCAGAAA	249	CCGUGCAUGUGUUCAGAAANN	529
as	190	UUUCUGAACACAUGCACGG	250	UUUCUGAACACAUGCACGGNN	530
s	238	AGUCUGGAGAGCUGCAUGG	251	AGUCUGGAGAGCUGCAUGGNN	531
as	256	CCAUGCAGCUCUCCAGACU	252	CCAUGCAGCUCUCCAGACUNN	532
s	252	CAUGGGCUCACAACUGAGG	253	CAUGGGCUCACAACUGAGGNN	533
as	270	CCUCAGUUGUGAGCCCAUG	254	CCUCAGUUGUGAGCCCAUGNN	534
s	33	UCUCAUCGUCUGCUCCUCC	255	UCUCAUCGUCUGCUCCUCCNN	535
as	51	GGAGGAGCAGACGAUGAGA	256	GGAGGAGCAGACGAUGAGANN	536
s	340	CCCCAUUCCAUGAGCAUGC	257	CCCCAUUCCAUGAGCAUGCNN	537
as	358	GCAUGCUCAUGGAAUGGGG	258	GCAUGCUCAUGGAAUGGGGNN	538
s	421	GCCCCUACUCCUAUUCCAC	259	GCCCCUACUCCUAUUCCACNN	539
as	439	GUGGAAUAGGAGUAGGGGC	260	GUGGAAUAGGAGUAGGGGCNN	540
s	431	CUAUUCCACCACGGCUGUC	261	CUAUUCCACCACGGCUGUCNN	541
as	449	GACAGCCGUGGUGGAAUAG	262	GACAGCCGUGGUGGAAUAGNN	542
s	440	CACGGCUGUCGUCACCAAU	263	CACGGCUGUCGUCACCAAUNN	543
as	458	AUUGGUGACGACAGCCGUG	264	AUUGGUGACGACAGCCGUGNN	544
s	496	AGGACGAGGGAUGGGAUUU	265	AGGACGAGGGAUGGGAUUUNN	545
as	514	AAAUCCCAUCCCUCGUCCU	266	AAAUCCCAUCCCUCGUCCUNN	546
s	556	UCACCUCAUAUGCUAUGUU	267	UCACCUCAUAUGCUAUGUUNN	547
as	574	AACAUAGCAUAUGAGGUGA	268	AACAUAGCAUAUGAGGUGANN	548
s	559	CCUCAUAUGCUAUGUUAGA	269	CCUCAUAUGCUAUGUUAGANN	549
as	577	UCUAACAUAGCAUAUGAGG	270	UCUAACAUAGCAUAUGAGGNN	550
s	570	AUGUUAGAAGUCCAGGCAG	271	AUGUUAGAAGUCCAGGCAGNN	551
as	588	CUGCCUGGACUUCUAACAU	272	CUGCCUGGACUUCUAACAUNN	552
s	78	UCUGAGGCUGGCCCUACGG	273	UCUGAGGCUGGCCCUACGGNN	553
as	96	CCGUAGGGCCAGCCUCAGA	274	CCGUAGGGCCAGCCUCAGANN	554

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
s	87	GGCCCUACGGGCACCGGUG	275	GGCCCUACGGGCACCGGUGNN	555
as	105	CACCGGUGCCCGUAGGGCC	276	CACCGGUGCCCGUAGGGCCNN	556
s	95	GGGCACCGGUGAAUCCAAG	277	GGGCACCGGUGAAUCCAAGNN	557
as	113	CUUGGAUUCACCGGUGCCC	278	CUUGGAUUCACCGGUGCCCNN	558
s	167	CCAUGCAUGUGUUCAGAAA	279	CCAUGCAUGUGUUCAGAAANN	559
as	185	UUUCUGAACACAUGCAUGG	280	UUUCUGAACACAUGCAUGGNN	560

Table 3B. Sense and antisense strand sequences of human TTR dsRNAs

Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_000371.2, SEQ ID NO:1329)

Strand	Position	Sequence with 3′deoxythimidine overhang (5′ to 3′)	SEQ ID NO:
s	100	CCGGUGAAUCCAAGUGUCCdTdT	561
as	118	GGACACUUGGAUUCACCGGdTdT	562
s	11	ACUCAUUCUUGGCAGGAUGdTdT	563
as	29	CAUCCUGCCAAGAAUGAGUdTdT	564
s	111	AAGUGUCCUCUGAUGGUCAdTdT	565
as	129	UGACCAUCAGAGGACACUUdTdT	566
s	13	UCAUUCUUGGCAGGAUGGCdTdT	567
as	31	GCCAUCCUGCCAAGAAUGAdTdT	568
s	130	AAGUUCUAGAUGCUGUCCGdTdT	569
as	148	CGGACAGCAUCUAGAACUUdTdT	570
s	132	GUUCUAGAUGCUGUCCGAGdTdT	571
as	150	CUCGGACAGCAUCUAGAACdTdT	572
s	135	CUAGAUGCUGUCCGAGGCAdTdT	573
as	153	UGCCUCGGACAGCAUCUAGdTdT	574
s	138	GAUGCUGUCCGAGGCAGUCdTdT	575
as	156	GACUGCCUCGGACAGCAUCdTdT	576
s	14	CAUUCUUGGCAGGAUGGCUdTdT	577
as	32	AGCCAUCCUGCCAAGAAUGdTdT	578
s	140	UGCUGUCCGAGGCAGUCCUdTdT	579
as	158	AGGACUGCCUCGGACAGCAdTdT	580
s	146	CCGAGGCAGUCCUGCCAUCdTdT	581
as	164	GAUGGCAGGACUGCCUCGGdTdT	582
s	152	CAGUCCUGCCAUCAAUGUGdTdT	583
as	170	CACAUUGAUGGCAGGACUGdTdT	584
s	164	CAAUGUGGCCGUGCAUGUGdTdT	585
as	182	CACAUGCACGGCCACAUUGdTdT	586
s	178	AUGUGUUCAGAAAGGCUGCdTdT	587
as	196	GCAGCCUUUCUGAACACAUdTdT	588
s	2	CAGAAGUCCACUCAUUCUUdTdT	589
as	20	AAGAAUGAGUGGACUUCUGdTdT	590
s	21	GGCAGGAUGGCUUCUCAUCdTdT	591
as	39	GAUGAGAAGCCAUCCUGCCdTdT	592
s	210	GAGCCAUUUGCCUCUGGGAdTdT	593
as	228	UCCCAGAGGCAAAUGGCUCdTdT	594
s	23	CAGGAUGGCUUCUCAUCGUdTdT	595
as	41	ACGAUGAGAAGCCAUCCUGdTdT	596
s	24	AGGAUGGCUUCUCAUCGUCdTdT	597
as	42	GACGAUGAGAAGCCAUCCUdTdT	598
s	245	AGAGCUGCAUGGGCUCACAdTdT	599
as	263	UGUGAGCCCAUGCAGCUCUdTdT	600
s	248	GCUGCAUGGGCUCACAACUdTdT	601

Strand	Position	Sequence with 3'deoxythimidine overhang (5' to 3')	SEQ ID NO:
as	266	AGUUGUGAGCCCAUGCAGCdTdT	602
s	25	GGAUGGCUUCUCAUCGUCUdTdT	603
as	43	AGACGAUGAGAAGCCAUCCdTdT	604
s	251	GCAUGGGCUCACAACUGAGdTdT	605
as	269	CUCAGUUGUGAGCCCAUGCdTdT	606
s	253	AUGGGCUCACAACUGAGGAdTdT	607
as	271	UCCUCAGUUGUGAGCCCAUdTdT	608
s	254	UGGGCUCACAACUGAGGAGdTdT	609
as	272	CUCCUCAGUUGUGAGCCCAdTdT	610
s	270	GAGGAAUUUGUAGAAGGGAdTdT	611
as	288	UCCCUUCUACAAAUUCCUCdTdT	612
s	276	UUUGUAGAAGGGAUAUACAdTdT	613
as	294	UGUAUAUCCCUUCUACAAAdTdT	614
s	277	UUGUAGAAGGGAUAUACAAdTdT	615
as	295	UUGUAUAUCCCUUCUACAAdTdT	616
s	278	UGUAGAAGGGAUAUACAAAdTdT	617
as	296	UUUGUAUAUCCCUUCUACAdTdT	618
s	281	AGAAGGGAUAUACAAAGUGdTdT	619
as	299	CACUUUGUAUAUCCCUUCUdTdT	620
s	295	AAGUGGAAAUAGACACCAAdTdT	621
as	313	UUGGUGUCUAUUUCCACUUdTdT	622
s	299	GGAAAUAGACACCAAAUCUdTdT	623
as	317	AGAUUUGGUGUCUAUUUCCdTdT	624
s	300	GAAAUAGACACCAAAUCUUdTdT	625
as	318	AAGAUUUGGUGUCUAUUUCdTdT	626
s	303	AUAGACACCAAAUCUUACUdTdT	627
as	321	AGUAAGAUUUGGUGUCUAUdTdT	628
s	304	UAGACACCAAAUCUUACUGdTdT	629
as	322	CAGUAAGAUUUGGUGUCUAdTdT	630
s	305	AGACACCAAAUCUUACUGGdTdT	631
as	323	CCAGUAAGAUUUGGUGUCUdTdT	632
s	317	UUACUGGAAGGCACUUGGCdTdT	633
as	335	GCCAAGUGCCUUCCAGUAAdTdT	634
s	32	UUCUCAUCGUCUGCUCCUCdTdT	635
as	50	GAGGAGCAGACGAUGAGAAdTdT	636
s	322	GGAAGGCACUUGGCAUCUCdTdT	637
as	340	GAGAUGCCAAGUGCCUUCCdTdT	638
s	326	GGCACUUGGCAUCUCCCCAdTdT	639
as	344	UGGGGAGAUGCCAAGUGCCdTdT	640
s	333	GGCAUCUCCCCAUUCCAUGdTdT	641
as	351	AUGGAAUGGGGAGAUGCCTTdTdT	642
s	334	GCAUCUCCCCAUUCCAUGAdTdT	643
as	352	UCAUGGAAUGGGGAGAUGCdTdT	644
s	335	CAUCUCCCCAUUCCAUGAGdTdT	645
as	353	CUCAUGGAAUGGGGAGAUGdTdT	646
s	336	AUCUCCCCAUUCCAUGAGCdTdT	647
as	354	GCUCAUGGAAUGGGGAGAUdTdT	648
s	338	CUCCCCAUUCCAUGAGCAUdTdT	649
as	356	AUGCUCAUGGAAUGGGGAGdTdT	650
s	341	CCCAUUCCAUGAGCAUGCAdTdT	651
as	359	UGCAUGCUCAUGGAAUGGGdTdT	652
s	347	CCAUGAGCAUGCAGAGGUGdTdT	653
as	365	CACCUCUGCAUGCUCAUGGdTdT	654
s	352	AGCAUGCAGAGGUGGUAUUdTdT	655
as	370	AAUACCACCUCUGCAUGCUdTdT	656
s	354	CAUGCAGAGGUGGUAUUCAdTdT	657
as	372	UGAAUACCACCUCUGCAUGdTdT	658

Strand	Position	Sequence with 3'deoxythimidine overhang (5' to 3')	SEQ ID NO:
s	355	AUGCAGAGGUGGUAUUCACdTdT	659
as	373	GUGAAUACCACCUCUGCAUdTdT	660
s	362	GGUGGUAUUCACAGCCAACdTdT	661
as	380	GUUGGCUGUGAAUACCACCdTdT	662
s	363	GUGGUAUUCACAGCCAACGdTdT	663
as	381	CGUUGGCUGUGAAUACCACdTdT	664
s	364	UGGUAUUCACAGCCAACGAdTdT	665
as	382	UCGUUGGCUGUGAAUACCAdTdT	666
s	365	GGUAUUCACAGCCAACGACdTdT	667
as	383	GUCGUUGGCUGUGAAUACCdTdT	668
s	366	GUAUUCACAGCCAACGACUdTdT	669
as	384	AGUCGUUGGCUGUGAAUACdTdT	670
s	367	UAUUCACAGCCAACGACUCdTdT	671
as	385	GAGUCGUUGGCUGUGAAUAdTdT	672
s	370	UCACAGCCAACGACUCCGGdTdT	673
as	388	CCGGAGUCGUUGGCUGUGAdTdT	674
s	390	CCCCGCCGCUACACCAUUGdTdT	675
as	408	CAAUGGUGUAGCGGCGGGGdTdT	676
s	4	GAAGUCCACUCAUUCUUGGdTdT	677
as	22	CCAAGAAUGAGUGGACUUCdTdT	678
s	412	CCCUGCUGAGCCCCUACUCdTdT	679
as	430	GAGUAGGGGCUCAGCAGGGdTdT	680
s	417	CUGAGCCCCUACUCCUAUUdTdT	681
as	435	AAUAGGAGUAGGGGCUCAGdTdT	682
s	418	UGAGCCCCUACUCCUAUUCdTdT	683
as	436	GAAUAGGAGUAGGGGCUCAdTdT	684
s	422	CCCCUACUCCUAUUCCACCdTdT	685
as	440	GGUGGAAUAGGAGUAGGGGdTdT	686
s	425	CUACUCCUAUUCCACCACGdTdT	687
as	443	CGUGGUGGAAUAGGAGUAGdTdT	688
s	426	UACUCCUAUUCCACCACGGdTdT	689
as	444	CCGUGGUGGAAUAGGAGUAdTdT	690
s	427	ACUCCUAUUCCACCACGGCdTdT	691
as	445	GCCGUGGUGGAAUAGGAGUdTdT	692
s	429	UCCUAUUCCACCACGGCUGdTdT	693
as	447	CAGCCGUGGUGGAAUAGGAdTdT	694
s	432	UAUUCCACCACGGCUGUCGdTdT	695
as	450	CGACAGCCGUGGUGGAAUAdTdT	696
s	433	AUUCCACCACGGCUGUCGUdTdT	697
as	451	ACGACAGCCGUGGUGGAAUdTdT	698
s	437	CACCACGGCUGUCGUCACCdTdT	699
as	455	GGUGACGACAGCCGUGGUGdTdT	700
s	438	ACCACGGCUGUCGUCACCAdTdT	701
as	456	UGGUGACGACAGCCGUGGUdTdT	702
s	439	CCACGGCUGUCGUCACCAAdTdT	703
as	457	UUGGUGACGACAGCCGUGGdTdT	704
s	441	ACGGCUGUCGUCACCAAUCdTdT	705
as	459	GAUUGGUGACGACAGCCGUdTdT	706
s	442	CGGCUGUCGUCACCAAUCCdTdT	707
as	460	GGAUUGGUGACGACAGCCGdTdT	708
s	449	CGUCACCAAUCCCAAGGAAdTdT	709
as	467	UUCCUUGGGAUUGGUGACGdTdT	710
s	455	CAAUCCCAAGGAAUGAGGGdTdT	711
as	473	CCCUCAUUCCUUGGGAUUGdTdT	712
s	491	CCUGAAGGACGAGGGAUGGdTdT	713
as	509	CCAUCCCUCGUCCUUCAGGdTdT	714
s	497	GGACGAGGGAUGGGAUUUCdTdT	715

Strand	Position	Sequence with 3′deoxythimidine overhang (5′ to 3′)	SEQ ID NO:
as	515	GAAAUCCCAUCCCUCGUCCdTdT	716
s	5	AAGUCCACUCAUUCUUGGCdTdT	717
as	23	GCCAAGAAUGAGUGGACUUdTdT	718
s	508	GGGAUUUCAUGUAACCAAGdTdT	719
as	526	CUUGGUUACAUGAAAUCCCdTdT	720
s	509	GGAUUUCAUGUAACCAAGAdTdT	721
as	527	UCUUGGUUACAUGAAAUCCdTdT	722
s	514	UCAUGUAACCAAGAGUAUUdTdT	723
as	532	AAUACUCUUGGUUACAUGAdTdT	724
s	516	AUGUAACCAAGAGUAUUCCdTdT	725
as	534	GGAAUACUCUUGGUUACAUdTdT	726
s	517	UGUAACCAAGAGUAUUCCAdTdT	727
as	535	UGGAAUACUCUUGGUUACAdTdT	728
s	518	GUAACCAAGAGUAUUCCAUdTdT	729
as	536	AUGGAAUACUCUUGGUUACdTdT	730
s	54	UGCCUUGCUGGACUGGUAUdTdT	731
as	72	AUACCAGUCCAGCAAGGCAdTdT	732
s	543	UAAAGCAGUGUUUUCACCUdTdT	733
as	561	AGGUGAAAACACUGCUUUAdTdT	734
s	55	GCCUUGCUGGACUGGUAUUdTdT	735
as	73	AAUACCAGUCCAGCAAGGCdTdT	736
s	551	UGUUUUCACCUCAUAUGCUdTdT	737
as	569	AGCAUAUGAGGUGAAAACAdTdT	738
s	552	GUUUUCACCUCAUAUGCUAdTdT	739
as	570	UAGCAUAUGAGGUGAAAACdTdT	740
s	553	UUUUCACCUCAUAUGCUAUdTdT	741
as	571	AUAGCAUAUGAGGUGAAAAdTdT	742
s	555	UUCACCUCAUAUGCUAUGUdTdT	743
as	573	ACAUAGCAUAUGAGGUGAAdTdT	744
s	557	CACCUCAUAUGCUAUGUUAdTdT	745
as	575	UAACAUAGCAUAUGAGGUGdTdT	746
s	56	CCUUGCUGGACUGGUAUUUdTdT	747
as	74	AAAUACCAGUCCAGCAAGGdTdT	748
s	563	AUAUGCUAUGUUAGAAGUCdTdT	749
as	581	GACUUCUAACAUAGCAUAUdTdT	750
s	564	UAUGCUAUGUUAGAAGUCCdTdT	751
as	582	GGACUUCUAACAUAGCAUAdTdT	752
s	566	UGCUAUGUUAGAAGUCCAGdTdT	753
as	584	CUGGACUUCUAACAUAGCAdTdT	754
s	57	CUUGCUGGACUGGUAUUUGdTdT	755
as	75	CAAAUACCAGUCCAGCAAGdTdT	756
s	578	AGUCCAGGCAGAGACAAUAdTdT	757
as	596	AUUGUCUCUGCCUGGACUTTdTdT	758
s	580	UCCAGGCAGAGACAAUAAAdTdT	759
as	598	UUUAUUGUCUCUGCCUGGAdTdT	760
s	607	GUGAAAGGCACUUUUCAUUdTdT	761
as	625	AAUGAAAAGUGCCUUUCACdTdT	762
s	62	UGGACUGGUAUUUGUGUCUdTdT	763
as	80	AGACACAAAUACCAGUCCAdTdT	764
s	77	GUCUGAGGCUGGCCCUACGdTdT	765
as	95	CGUAGGGCCAGCCUCAGACdTdT	766
s	79	CUGAGGCUGGCCCUACGGGdTdT	767
as	97	CCCGUAGGGCCAGCCUCAGdTdT	768
s	81	GAGGCUGGCCCUACGGGCAdTdT	769
as	99	UGCCCGUAGGGCCAGCCUCdTdT	770
s	82	AGGCUGGCCCUACGGGCACdTdT	771
as	100	GUGCCCGUAGGGCCAGCCUdTdT	772

Strand	Position	Sequence with 3′deoxythimidine overhang (5′ to 3′)	SEQ ID NO:
s	84	GCUGGCCCUACGGGCACCGdTdT	773
as	102	CGGUGCCCGUAGGGCCAGCdTdT	774
s	85	CUGGCCCUACGGGCACCGGdTdT	775
as	103	CCGGUGCCCGUAGGGCCAGdTdT	776
s	87	GGCCCUACGGGCACCGGUGdTdT	777
as	105	CACCGGUGCCCGUAGGGCCdTdT	778
s	9	CCACUCAUUCUUGGCAGGAdTdT	779
as	27	UCCUGCCAAGAAUGAGUGGdTdT	780
s	90	CCUACGGGCACCGGUGAAUdTdT	781
as	108	AUUCACCGGUGCCCGUAGGdTdT	782
s	91	CUACGGGCACCGGUGAAUCdTdT	783
as	109	GAUUCACCGGUGCCCGUAGdTdT	784
s	92	UACGGGCACCGGUGAAUCCdTdT	785
as	110	GGAUUCACCGGUGCCCGUAdTdT	786
s	93	ACGGGCACCGGUGAAUCCAdTdT	787
as	111	UGGAUUCACCGGUGCCCGUdTdT	788
s	97	GCACCGGUGAAUCCAAGUGdTdT	789
as	115	CACUUGGAUUCACCGGUGCdTdT	790
s	98	CACCGGUGAAUCCAAGUGUdTdT	791
as	116	ACACUUGGAUUCACCGGUGdTdT	792
s	167	UGUGGCCAUGCAUGUGUUCdTdT	793
as	185	GAACACAUGCAUGGCCACAdTdT	794
s	168	GUGGCCAUGCAUGUGUUCAdTdT	795
as	186	UGAACACAUGCAUGGCCACdTdT	796
s	171	GCCAUGCAUGUGUUCAGAAdTdT	797
as	189	UUCUGAACACAUGCAUGGCdTdT	798
s	432	UAUUCCACCACGGCUGUCAdTdT	799
as	449	UGACAGCCGUGGUGGAAUAdTdT	800
s	447	GUCAUCACCAAUCCCAAGGdTdT	801
as	465	CCUUGGGAUUGGUGAUGACdTdT	802
s	115	GUCCUCUGAUGGUCAAAGUdTdT	803
as	133	ACUUUGACCAUCAGAGGACdTdT	804
s	122	GAUGGUCAAAGUUCUAGAUdTdT	805
as	140	AUCUAGAACUUUGACCAUCdTdT	806
s	139	AUGCUGUCCGAGGCAGUCCdTdT	807
as	157	GGACUGCCUCGGACAGCAUdTdT	808
s	172	CCGUGCAUGUGUUCAGAAAdTdT	809
as	190	UUUCUGAACACAUGCACGGdTdT	810
s	238	AGUCUGGAGAGCUGCAUGGdTdT	811
as	256	CCAUGCAGCUCUCCAGACUdTdT	812
s	252	CAUGGGCUCACAACUGAGGdTdT	813
as	270	CCUCAGUUGUGAGCCCAUGdTdT	814
s	33	UCUCAUCGUCUGCUCCUCCdTdT	815
as	51	GGAGGAGCAGACGAUGAGAdTdT	816
s	340	CCCCAUUCCAUGAGCAUGCdTdT	817
as	358	GCAUGCUCAUGGAAUGGGGdTdT	818
s	421	GCCCCUACUCCUAUUCCACdTdT	819
as	439	GUGGAAUAGGAGUAGGGGCdTdT	820
s	431	CUAUUCCACCACGGCUGUCdTdT	821
as	449	GACAGCCGUGGUGGAAUAGdTdT	822
s	440	CACGGCUGUCGUCACCAAUdTdT	823
as	458	AUUGGUGACGACAGCCGUGdTdT	824
s	496	AGGACGAGGGAUGGGAUUUdTdT	825
as	514	AAAUCCCAUCCCUCGUCCUdTdT	826
s	556	UCACCUCAUAUGCUAUGUUdTdT	827
as	574	AACAUAGCAUAUGAGGUGAdTdT	828
s	559	CCUCAUAUGCUAUGUUAGAdTdT	829

Strand	Position	Sequence with 3'deoxythimidine overhang (5' to 3')	SEQ ID NO:
as	577	UCUAACAUAGCAUAUGAGGdTdT	830
s	570	AUGUUAGAAGUCCAGGCAGdTdT	831
as	588	CUGCCUGGACUUCUAACAUdTdT	832
s	78	UCUGAGGCUGGCCCUACGGdTdT	833
as	96	CCGUAGGGCCAGCCUCAGAdTdT	834
s	87	GGCCCUACGGGCACCGGUGdTdT	835
as	105	CACCGGUGCCCGUAGGGCCdTdT	836
s	95	GGGCACCGGUGAAUCCAAGdTdT	837
as	113	CUUGGAUUCACCGGUGCCCdTdT	838
s	167	CCAUGCAUGUGUUCAGAAAdTdT	839
as	185	UUUCUGAACACAUGCAUGGdTdT	840

Table 4. Chemically modified sense and antisense strand sequences of human TTR dsRNAs

See Table 2 for duplex #. Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_000371.2, SEQ ID NO:1329)

Strand	Oligo #	Position	Sequence(5' to 3')	SEQ ID NO:
s	A-32153	100	ccGGuGAAuccAAGuGuccdTdT	841
as	A-32154	118	GGAcACUUGGAUUcACCGGdTdT	842
s	A-32155	11	AcucAuucuuGGcAGGAuGdTdT	843
as	A-32156	29	cAUCCUGCcAAGAAUGAGUdTdT	844
s	A-32157	111	AAGuGuccucuGAuGGucAdTdT	845
as	A-32158	129	UGACcAUcAGAGGAcACUUdTdT	846
s	A-32163	13	ucAuucuuGGcAGGAuGGcdTdT	847
as	A-32164	31	GCcAUCCUGCcAAGAAUGAdTdT	848
s	A-32165	130	AAGuucuAGAuGcuGuccGdTdT	849
as	A-32166	148	CGGAcAGcAUCuAGAACUUdTdT	850
s	A-32167	132	GuucuAGAuGcuGuccGAGdTdT	851
as	A-32168	150	CUCGGAcAGcAUCuAGAACdTdT	852
s	A-32169	135	cuAGAuGcuGuccGAGGcAdTdT	853
as	A-32170	153	UGCCUCGGAcAGcAUCuAGdTdT	854
s	A-32171	138	GAuGcuGuccGAGGcAGucdTdT	855
as	A-32172	156	GACUGCCUCGGAcAGcAUCdTdT	856
s	A-32175	14	cAuucuuGGcAGGAuGGcudTdT	857
as	A-32176	32	AGCcAUCCUGCcAAGAAUGdTdT	858
s	A-32177	140	uGcuGuccGAGGcAGuccudTdT	859
as	A-32178	158	AGGACUGCCUCGGAcAGcAdTdT	860
s	A-32179	146	ccGAGGcAGuccuGccAucdTdT	861
as	A-32180	164	GAUGGcAGGACUGCCUCGGdTdT	862
s	A-32181	152	cAGuccuGccAucAAuGuGdTdT	863
as	A-32182	170	cAcAUUGAUGGcAGGACUGdTdT	864
s	A-32183	164	cAAuGuGGccGuGcAuGuGdTdT	865
as	A-32184	182	cAcAUGcACGGCcAcAUUGdTdT	866
s	A-32187	178	AuGuGuucAGAAAGGcuGcdTdT	867
as	A-32188	196	GcAGCCUUUCUGAAcAcAUdTdT	868
s	A-32189	2	cAGAAGuccAcucAuucuudTdT	869
as	A-32190	20	AAGAAUGAGUGGACUUCUGdTdT	870
s	A-32191	21	GGcAGGAuGGcuucucAucdTdT	871
as	A-32192	39	GAUGAGAAGCcAUCCUGCCdTdT	872
s	A-32193	210	GAGccAuuuGccucuGGGAdTdT	873
as	A-32194	228	UCCcAGAGGcAAAUGGCUCdTdT	874
s	A-32195	23	cAGGAuGGcuucucAucGudTdT	875
as	A-32196	41	ACGAUGAGAAGCcAUCCUGdTdT	876

Strand	Oligo #	Position	Sequence(5′ to 3′)	SEQ ID NO:
s	A-32199	24	AGGAuGGcuucucAucGucdTdT	877
as	A-32200	42	GACGAUGAGAAGCcAUCCUdTdT	878
s	A-32201	245	AGAGcuGcAuGGGcucAcAdTdT	879
as	A-32202	263	UGUGAGCCcAUGcAGCUCUdTdT	880
s	A-32203	248	GcuGcAuGGGcucAcAAcudTdT	881
as	A-32204	266	AGUUGUGAGCCcAUGcAGCdTdT	882
s	A-32205	25	GGAuGGcuucucAucGucudTdT	883
as	A-32206	43	AGACGAUGAGAAGCcAUCCdTdT	884
s	A-32207	251	GcAuGGGcucAcAAcuGAGdTdT	885
as	A-32208	269	CUcAGUUGUGAGCCcAUGCdTdT	886
s	A-32211	253	AuGGGcucAcAAcuGAGGAdTdT	887
as	A-32212	271	UCCUcAGUUGUGAGCCcAUdTdT	888
s	A-32213	254	uGGGcucAcAAcuGAGGAGdTdT	889
as	A-32214	272	CUCCUcAGUUGUGAGCCcAdTdT	890
s	A-32215	270	GAGGAAuuuGuAGAAGGGAdTdT	891
as	A-32216	288	UCCCUUCuAcAAAUUCCUCdTdT	892
s	A-32217	276	uuuGuAGAAGGGAuAuAcAdTdT	893
as	A-32218	294	UGuAuAUCCCUUCuAcAAAdTdT	894
s	A-32219	277	uuGuAGAAGGGAuAuAcAAdTdT	895
as	A-32220	295	UUGuAuAUCCCUUCuAcAAdTdT	896
s	A-32221	278	uGuAGAAGGGAuAuAcAAAdTdT	897
as	A-32222	296	UUUGuAuAUCCCUUCuAcAdTdT	898
s	A-32223	281	AGAAGGGAuAuAcAAAGuGdTdT	899
as	A-32224	299	cACUUUGuAuAUCCCUUCUdTdT	900
s	A-32225	295	AAGuGGAAAuAGAcAccAAdTdT	901
as	A-32226	313	UUGGUGUCuAUUUCcACUUdTdT	902
s	A-32227	299	GGAAAuAGAcAccAAAucudTdT	903
as	A-32228	317	AGAUUUGGUGUCuAUUUCCdTdT	904
s	A-32229	300	GAAAuAGAcAccAAAucuudTdT	905
as	A-32230	318	AAGAUUUGGUGUCuAUUUCdTdT	906
s	A-32231	303	AuAGAcAccAAAucuuAcudTdT	907
as	A-32232	321	AGuAAGAUUUGGUGUCuAUdTdT	908
s	A-32233	304	uAGAcAccAAAucuuAcuGdTdT	909
as	A-32234	322	cAGuAAGAUUUGGUGUCuAdTdT	910
s	A-32235	305	AGAcAccAAAucuuAcuGGdTdT	911
as	A-32236	323	CcAGuAAGAUUUGGUGUCUdTdT	912
s	A-32237	317	uuAcuGGAAGGcAcuuGGcdTdT	913
as	A-32238	335	GCcAAGUGCCUUCcAGuAAdTdT	914
s	A-32239	32	uucucAucGucuGcuccucdTdT	915
as	A-32240	50	GAGGAGcAGACGAUGAGAAdTdT	916
s	A-32241	322	GGAAGGcAcuuGGcAucucdTdT	917
as	A-32242	340	GAGAUGCcAAGUGCCUUCCdTdT	918
s	A-32243	326	GGcAcuuGGcAucucccAdTdT	919
as	A-32244	344	UGGGGAGAUGCcAAGUGCCdTdT	920
s	A-32247	333	GGcAucucccAuuccAuGdTdT	921
as	A-32248	351	cAUGGAAUGGGGAGAUGCCdTdT	922
s	A-32249	334	GcAucucccAuuccAuGAdTdT	923
as	A-32250	352	UcAUGGAAUGGGGAGAUGCdTdT	924
s	A-32251	335	cAucucccAuuccAuGAGdTdT	925
as	A-32252	353	CUcAUGGAAUGGGGAGAUGdTdT	926
s	A-32253	336	AucucccAuuccAuGAGcdTdT	927
as	A-32254	354	GCUcAUGGAAUGGGGAGAUdTdT	928
s	A-32255	338	cucccAuuccAuGAGcAudTdT	929
as	A-32256	356	AUGCUcAUGGAAUGGGGAGdTdT	930
s	A-32259	341	cccAuuccAuGAGcAuGcAdTdT	931
as	A-32260	359	UGcAUGCUcAUGGAAUGGGdTdT	932
s	A-32261	347	ccAuGAGcAuGcAGAGGuGdTdT	933
as	A-32262	365	cACCUCUGcAUGCUcAUGGdTdT	934

Strand	Oligo #	Position	Sequence(5′ to 3′)	SEQ ID NO:
s	A-32263	352	AGcAuGcAGAGGuGGuAuudTdT	935
as	A-32264	370	AAuACcACCUCUGcAUGCUdTdT	936
s	A-32265	354	cAuGcAGAGGuGGuAuucAdTdT	937
as	A-32266	372	UGAAuACcACCUCUGcAUGdTdT	938
s	A-32267	355	AuGcAGAGGuGGuAuucAcdTdT	939
as	A-32268	373	GUGAAuACcACCUCUGcAUdTdT	940
s	A-32269	362	GGuGGuAuucAcAGccAAcdTdT	941
as	A-32270	380	GUUGGCUGUGAAuACcACCdTdT	942
s	A-32271	363	GuGGuAuucAcAGccAAcGdTdT	943
as	A-32272	381	CGUUGGCUGUGAAuACcACdTdT	944
s	A-32273	364	uGGuAuucAcAGccAAcGAdTdT	945
as	A-32274	382	UCGUUGGCUGUGAAuACcAdTdT	946
s	A-32275	365	GGuAuucAcAGccAAcGAcdTdT	947
as	A-32276	383	GUCGUUGGCUGUGAAuACCdTdT	948
s	A-32277	366	GuAuucAcAGccAAcGAcudTdT	949
as	A-32278	384	AGUCGUUGGCUGUGAAuACdTdT	950
s	A-32279	367	uAuucAcAGccAAcGAcucdTdT	951
as	A-32280	385	GAGUCGUUGGCUGUGAAuAdTdT	952
s	A-32281	370	ucAcAGccAAcGAcuccGGdTdT	953
as	A-32282	388	CCGGAGUCGUUGGCUGUGAdTdT	954
s	A-32283	390	ccccGccGcuAcAccAuuGdTdT	955
as	A-32284	408	cAAUGGUGuAGCGGCGGGGdTdT	956
s	A-32285	4	GAAGuccAcucAuucuuGGdTdT	957
as	A-32286	22	CcAAGAAUGAGUGGACUUCdTdT	958
s	A-32287	412	cccuGcuGAGccccuAcucdTdT	959
as	A-32288	430	GAGuAGGGGCUcAGcAGGGdTdT	960
s	A-32289	417	cuGAGccccuAcuccuAuudTdT	961
as	A-32290	435	AAuAGGAGuAGGGGCUcAGdTdT	962
s	A-32291	418	uGAGccccuAcuccuAuucdTdT	963
as	A-32292	436	GAAuAGGAGuAGGGGCUcAdTdT	964
s	A-32295	422	ccccuAcuccuAuuccAccdTdT	965
as	A-32296	440	GGUGGAAuAGGAGuAGGGGdTdT	966
s	A-32297	425	cuAcuccuAuuccAccAcGdTdT	967
as	A-32298	443	CGUGGUGGAAuAGGAGuAGdTdT	968
s	A-32299	426	uAcuccuAuuccAccAcGGdTdT	969
as	A-32300	444	CCGUGGUGGAAuAGGAGuAdTdT	970
s	A-32301	427	AcuccuAuuccAccAcGGcdTdT	971
as	A-32302	445	GCCGUGGUGGAAuAGGAGUdTdT	972
s	A-32303	429	uccuAuuccAccAcGGcuGdTdT	973
as	A-32304	447	cAGCCGUGGUGGAAuAGGAdTdT	974
s	A-32307	432	uAuuccAccAcGGcuGucGdTdT	975
as	A-32308	450	CGAcAGCCGUGGUGGAAuAdTdT	976
s	A-32309	433	AuuccAccAcGGcuGucGudTdT	977
as	A-32310	451	ACGAcAGCCGUGGUGGAAUdTdT	978
s	A-32311	437	cAccAcGGcuGucGucAccdTdT	979
as	A-32312	455	GGUGACGAcAGCCGUGGUGdTdT	980
s	A-32313	438	AccAcGGcuGucGucAccAdTdT	981
as	A-32314	456	UGGUGACGAcAGCCGUGGUdTdT	982
s	A-32315	439	ccAcGGcuGucGucAccAAdTdT	983
as	A-32316	457	UUGGUGACGAcAGCCGUGGdTdT	984
s	A-32319	441	AcGGcuGucGucAccAAucdTdT	985
as	A-32320	459	GAUUGGUGACGAcAGCCGUdTdT	986
s	A-32321	442	cGGcuGucGucAccAAuccdTdT	987
as	A-32322	460	GGAUUGGUGACGAcAGCCGdTdT	988
s	A-32323	449	cGucAccAAucccAAGGAAdTdT	989
as	A-32324	467	UUCCUUGGGAUUGGUGACGdTdT	990
s	A-32325	455	cAAucccAAGGAAuGAGGGdTdT	991
as	A-32326	473	CCCUcAUUCCUUGGGAUUGdTdT	992

Strand	Oligo #	Position	Sequence(5′ to 3′)	SEQ ID NO:
s	A-32327	491	ccuGAAGGAcGAGGGAuGGdTdT	993
as	A-32328	509	CcAUCCCUCGUCCUUcAGGdTdT	994
s	A-32331	497	GGAcGAGGGAuGGGAuuucdTdT	995
as	A-32332	515	GAAAUCCcAUCCCUCGUCCdTdT	996
s	A-32333	5	AAGuccAcucAuucuuGGcdTdT	997
as	A-32334	23	GCcAAGAAUGAGUGGACUUdTdT	998
s	A-32335	508	GGGAuuucAuGuAAccAAGdTdT	999
as	A-32336	526	CUUGGUuAcAUGAAAUCCCdTdT	1000
s	A-32337	509	GGAuuucAuGuAAccAAGAdTdT	1001
as	A-32338	527	UCUUGGUuAcAUGAAAUCCdTdT	1002
s	A-32339	514	ucAuGuAAccAAGAGuAuudTdT	1003
as	A-32340	532	AAuACUCUUGGUuAcAUGAdTdT	1004
s	A-32341	516	AuGuAAccAAGAGuAuuccdTdT	1005
as	A-32342	534	GGAAuACUCUUGGUuAcAUdTdT	1006
s	A-32343	517	uGuAAccAAGAGuAuuccAdTdT	1007
as	A-32344	535	UGGAAuACUCUUGGUuAcAdTdT	1008
s	A-32345	518	GuAAccAAGAGuAuuccAudTdT	1009
as	A-32346	536	AUGGAAuACUCUUGGUuACdTdT	1010
s	A-32347	54	uGccuuGcuGGAcuGGuAudTdT	1011
as	A-32348	72	AuACcAGUCcAGcAAGGcAdTdT	1012
s	A-32349	543	uAAAGcAGuGuuuucAccudTdT	1013
as	A-32350	561	AGGUGAAAAcACUGCUUuAdTdT	1014
s	A-32351	55	GccuuGcuGGAcuGGuAuudTdT	1015
as	A-32352	73	AAuACcAGUCcAGcAAGGCdTdT	1016
s	A-32353	551	uGuuuucAccucAuAuGcudTdT	1017
as	A-32354	569	AGcAuAUGAGGUGAAAAcAdTdT	1018
s	A-32355	552	GuuuucAccucAuAuGcuAdTdT	1019
as	A-32356	570	uAGcAuAUGAGGUGAAAACdTdT	1020
s	A-32357	553	uuuucAccucAuAuGcuAudTdT	1021
as	A-32358	571	AuAGcAuAUGAGGUGAAAAdTdT	1022
s	A-32359	555	uucAccucAuAuGcuAuGudTdT	1023
as	A-32360	573	AcAuAGcAuAUGAGGUGAAdTdT	1024
s	A-32363	557	cAccucAuAuGcuAuGuuAdTdT	1025
as	A-32364	575	uAAcAuAGcAuAUGAGGUGdTdT	1026
s	A-32367	56	ccuuGcuGGAcuGGuAuuudTdT	1027
as	A-32368	74	AAAuACcAGUCcAGcAAGGdTdT	1028
s	A-32369	563	AuAuGcuAuGuuAGAAGucdTdT	1029
as	A-32370	581	GACUUCuAAcAuAGcAuAUdTdT	1030
s	A-32371	564	uAuGcuAuGuuAGAAGuccdTdT	1031
as	A-32372	582	GGACUUCuAAcAuAGcAuAdTdT	1032
s	A-32373	566	uGcuAuGuuAGAAGuccAGdTdT	1033
as	A-32374	584	CUGGACUUCuAAcAuAGcAdTdT	1034
s	A-32375	57	cuuGcuGGAcuGGuAuuuGdTdT	1035
as	A-32376	75	cAAAuACcAGUCcAGcAAGdTdT	1036
s	A-32379	578	AGuccAGGcAGAGAcAAuAdTdT	1037
as	A-32380	596	uAUUGUCUCUGCCUGGACUdTdT	1038
s	A-32381	580	uccAGGcAGAGAcAAuAAAdTdT	1039
as	A-32382	598	UUuAUUGUCUCUGCCUGGAdTdT	1040
s	A-32383	607	GuGAAAGGcAcuuuucAuudTdT	1041
as	A-32384	625	AAUGAAAAGUGCCUUUcACdTdT	1042
s	A-32385	62	uGGAcuGGuAuuuGuGucudTdT	1043
as	A-32386	80	AGAcAcAAAuACcAGUCcAdTdT	1044
s	A-32387	77	GucuGAGGcuGGcccuAcGdTdT	1045
as	A-32388	95	CGuAGGGCcAGCCUcAGACdTdT	1046
s	A-32391	79	cuGAGGcuGGcccuAcGGGdTdT	1047
as	A-32392	97	CCCGuAGGGCcAGCCUcAGdTdT	1048
s	A-32393	81	GAGGcuGGcccuAcGGGcAdTdT	1049
as	A-32394	99	UGCCCGuAGGGCcAGCCUCdTdT	1050

Strand	Oligo #	Position	Sequence(5′ to 3′)	SEQ ID NO:
s	A-32395	82	AGGcuGGcccuAcGGGcAcdTdT	1051
as	A-32396	100	GUGCCCGuAGGGCcAGCCUdTdT	1052
s	A-32397	84	GcuGGcccuAcGGGcAccGdTdT	1053
as	A-32398	102	CGGUGCCCGuAGGGCcAGCdTdT	1054
s	A-32399	85	cuGGcccuAcGGGcAccGGdTdT	1055
as	A-32400	103	CCGGUGCCCGuAGGGCcAGdTdT	1056
s	A-32401	87	GGcccuAcGGGcAccGGuGdTdT	1057
as	A-32402	105	cACCGGUGCCCGuAGGGCCdTdT	1058
s	A-32403	9	ccAcucAuucuuGGcAGGAdTdT	1059
as	A-32404	27	UCCUGCcAAGAAUGAGUGGdTdT	1060
s	A-32405	90	ccuAcGGGcAccGGuGAAudTdT	1061
as	A-32406	108	AUUcACCGGUGCCCGuAGGdTdT	1062
s	A-32407	91	cuAcGGGcAccGGuGAAucdTdT	1063
as	A-32408	109	GAUUcACCGGUGCCCGuAGdTdT	1064
s	A-32409	92	uAcGGGcAccGGuGAAuccdTdT	1065
as	A-32410	110	GGAUUcACCGGUGCCCGuAdTdT	1066
s	A-32411	93	AcGGGcAccGGuGAAuccAdTdT	1067
as	A-32412	111	UGGAUUcACCGGUGCCCGUdTdT	1068
s	A-32415	97	GcAccGGuGAAuccAAGuGdTdT	1069
as	A-32416	115	cACUUGGAUUcACCGGUGCdTdT	1070
s	A-32417	98	cAccGGuGAAuccAAGuGudTdT	1071
as	A-32418	116	AcACUUGGAUUcACCGGUGdTdT	1072
s	A-32419	167	uGuGGccAuGcAuGuGuucdTdT	1073
as	A-32420	185	GAAcAcAUGcAUGGCcAcAdTdT	1074
s	A-32421	168	GuGGccAuGcAuGuGuucAdTdT	1075
as	A-32422	186	UGAAcAcAUGcAUGGCcACdTdT	1076
s	A-32423	171	GccAuGcAuGuGuucAGAAdTdT	1077
as	A-32424	189	UUCUGAAcAcAUGcAUGGCdTdT	1078
s	A-32427	432	uAuuccAccAcGGcuGucAdTdT	1079
as	A-32428	449	UGAcAGCCGUGGUGGAAuAdTdT	1080
s	A-32429	447	GucAucAccAAucccAAGGdTdT	1081
as	A-32430	465	CCUUGGGAUUGGUGAUGACdTdT	1082
s	A-32159	115	GuccucuGAuGGucAAAGudTdT	1083
as	A-32160	133	ACUUUGACcAUcAGAGGACdTdT	1084
s	A-32161	122	GAuGGucAAAGuucuAGAudTdT	1085
as	A-32162	140	AUCuAGAACUUUGACcAUCdTdT	1086
s	A-32173	139	AuGcuGuccGAGGcAGuccdTdT	1087
as	A-32174	157	GGACUGCCUCGGAcAGcAUdTdT	1088
s	A-32185	172	ccGuGcAuGuGuucAGAAAdTdT	1089
as	A-32186	190	UUUCUGAAcAcAUGcACGGdTdT	1090
s	A-32197	238	AGucuGGAGAGcuGcAuGGdTdT	1091
as	A-32198	256	CcAUGcAGCUCUCcAGACUdTdT	1092
s	A-32209	252	cAuGGGcucAcAAcuGAGGdTdT	1093
as	A-32210	270	CCUcAGUUGUGAGCCcAUGdTdT	1094
s	A-32245	33	ucucAucGucuGcuccuccdTdT	1095
as	A-32246	51	GGAGGAGcAGACGAUGAGAdTdT	1096
s	A-32257	340	ccccAuuccAuGAGcAuGcdTdT	1097
as	A-32258	358	GcAUGCUcAUGGAAUGGGGdTdT	1098
s	A-32293	421	GccccuAcuccuAuuccAcdTdT	1099
as	A-32294	439	GUGGAAuAGGAGuAGGGGCdTdT	1100
s	A-32305	431	cuAuuccAccAcGGcuGucdTdT	1101
as	A-32306	449	GAcAGCCGUGGUGGAAuAGdTdT	1102
s	A-32317	440	cAcGGcuGucGucAccAAudTdT	1103
as	A-32318	458	AUUGGUGACGAcAGCCGUGdTdT	1104
s	A-32329	496	AGGAcGAGGGAuGGGAuuudTdT	1105
as	A-32330	514	AAAUCCcAUCCCUCGUCCUdTdT	1106
s	A-32361	556	ucAccucAuAuGcuAuGuudTdT	1107
as	A-32362	574	AAcAuAGcAuAUGAGGUGAdTdT	1108

Strand	Oligo #	Position	Sequence(5′ to 3′)	SEQ ID NO:
s	A-32365	559	ccucAuAuGcuAuGuuAGAdTdT	1109
as	A-32366	577	UCuAAcAuAGcAuAUGAGGdTdT	1110
s	A-32377	570	AuGuuAGAAGuccAGGcAGdTdT	1111
as	A-32378	588	CUGCCUGGACUUCuAAcAUdTdT	1112
s	A-32389	78	ucuGAGGcuGGcccuAcGGdTdT	1113
as	A-32390	96	CCGuAGGGCcAGCCUcAGAdTdT	1114
s	A-32401	87	GGcccuAcGGGcAccGGuGdTdT	1115
as	A-32402	105	cACCGGUGCCCGuAGGGCCdTdT	1116
s	A-32413	95	GGGcAccGGuGAAuccAAGdTdT	1117
as	A-32414	113	CUUGGAUUcACCGGUGCCCdTdT	1118
s	A-32425	167	ccAuGcAuGuGuucAGAAAdTdT	1119
as	A-32426	185	UUUCUGAAcAcAUGcAUGGdTdT	1120

Table 5: Identification numbers for rat TTR dsRNAs

See Table 7 for sequences.

Duplex #	Sense Oligo #	Antisense Oligo #
AD-18529	A-32745	A-32746
AD-18530	A-32747	A-32748
AD-18531	A-32749	A-32750
AD-18532	A-32751	A-32752
AD-18533	A-32753	A-32754
AD-18534	A-32755	A-32756
AD-18535	A-32757	A-32758
AD-18536	A-32759	A-32760
AD-18537	A-32761	A-32762
AD-18538	A-32763	A-32764
AD-18539	A-32159	A-32160
AD-18540	A-32765	A-32766
AD-18541	A-32767	A-32768
AD-18542	A-32769	A-32770
AD-18543	A-32771	A-32772
AD-18544	A-32773	A-32774
AD-18545	A-32775	A-32776
AD-18546	A-32777	A-32778
AD-18547	A-32779	A-32780
AD-18548	A-32781	A-32782
AD-18549	A-32783	A-32784
AD-18550	A-32785	A-32786
AD-18551	A-32787	A-32788
AD-18552	A-32791	A-32792
AD-18553	A-32793	A-32794
AD-18554	A-32795	A-32796

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Table 6A. Sense and antisense strand sequences for rat TTR dsRNAs

Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_012681.1, SEQ ID NO:1330)

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
s	115	GUCCUCUGAUGGUCAAAGU	1121	GUCCUCUGAUGGUCAAAGUNN	1173
as	133	ACUUUGACCAUCAGAGGAC	1122	ACUUUGACCAUCAGAGGACNN	1174
s	537	UUCUUGCUCUAUAAACCGU	1123	UUCUUGCUCUAUAAACCGUNN	1175
as	555	ACGGUUUAUAGAGCAAGAA	1124	ACGGUUUAUAGAGCAAGAANN	1176
s	543	CUCUAUAAACCGUGUUAGC	1125	CUCUAUAAACCGUGUUAGCNN	1177
as	561	GCUAACACGGUUUAUAGAG	1126	GCUAACACGGUUUAUAGAGNN	1178
s	392	UCGCCACUACACCAUCGCA	1127	UCGCCACUACACCAUCGCANN	1179
as	410	UGCGAUGGUGUAGUGGCGA	1128	UGCGAUGGUGUAGUGGCGANN	1180
s	538	UCUUGCUCUAUAAACCGUG	1129	UCUUGCUCUAUAAACCGUGNN	1181
as	556	CACGGUUUAUAGAGCAAGA	1130	CACGGUUUAUAGAGCAAGANN	1182
s	541	UGCUCUAUAAACCGUGUUA	1131	UGCUCUAUAAACCGUGUUANN	1183
as	559	UAACACGGUUUAUAGAGCA	1132	UAACACGGUUUAUAGAGCANN	1184
s	532	CAGUGUUCUUGCUCUAUAA	1133	CAGUGUUCUUGCUCUAUAANN	1185
as	550	UUAUAGAGCAAGAACACUG	1134	UUAUAGAGCAAGAACACUGNN	1186
s	542	GCUCUAUAAACCGUGUUAG	1135	GCUCUAUAAACCGUGUUAGNN	1187
as	560	CUAACACGGUUUAUAGAGC	1136	CUAACACGGUUUAUAGAGCNN	1188
s	134	CCUGGAUGCUGUCCGAGGC	1137	CCUGGAUGCUGUCCGAGGCNN	1189
as	152	GCCUCGGACAGCAUCCAGG	1138	GCCUCGGACAGCAUCCAGGNN	1190
s	119	UCUGAUGGUCAAAGUCCUG	1139	UCUGAUGGUCAAAGUCCUGNN	1191
as	137	CAGGACUUUGACCAUCAGA	1140	CAGGACUUUGACCAUCAGANN	1192
s	241	CUGGAGAGCUGCACGGGCU	1141	CUGGAGAGCUGCACGGGCUNN	1193
as	259	AGCCCGUGCAGCUCUCCAG	1142	AGCCCGUGCAGCUCUCCAGNN	1194
s	544	UCUAUAAACCGUGUUAGCA	1143	UCUAUAAACCGUGUUAGCANN	1195
as	562	UGCUAACACGGUUUAUAGA	1144	UGCUAACACGGUUUAUAGANN	1196
s	530	AACAGUGUUCUUGCUCUAU	1145	AACAGUGUUCUUGCUCUAUNN	1197
as	548	AUAGAGCAAGAACACUGUU	1146	AUAGAGCAAGAACACUGUUNN	1198
s	118	CUCUGAUGGUCAAAGUCCU	1147	CUCUGAUGGUCAAAGUCCUNN	1199
as	136	AGGACUUUGACCAUCAGAG	1148	AGGACUUUGACCAUCAGAGNN	1200
s	140	UGCUGUCCGAGGCAGCCCU	1149	UGCUGUCCGAGGCAGCCCUNN	1201
as	158	AGGGCUGCCUCGGACAGCA	1150	AGGGCUGCCUCGGACAGCANN	1202
s	239	GUCUGGAGAGCUGCACGGG	1151	GUCUGGAGAGCUGCACGGGNN	1203
as	257	CCCGUGCAGCUCUCCAGAC	1152	CCCGUGCAGCUCUCCAGACNN	1204
s	531	ACAGUGUUCUUGCUCUAUA	1153	ACAGUGUUCUUGCUCUAUANN	1205
as	549	UAUAGAGCAAGAACACUGU	1154	UAUAGAGCAAGAACACUGUNN	1206
s	117	CCUCUGAUGGUCAAAGUCC	1155	CCUCUGAUGGUCAAAGUCCNN	1207
as	135	GGACUUUGACCAUCAGAGG	1156	GGACUUUGACCAUCAGAGGNN	1208
s	131	AGUCCUGGAUGCUGUCCGA	1157	AGUCCUGGAUGCUGUCCGANN	1209
as	149	UCGGACAGCAUCCAGGACU	1158	UCGGACAGCAUCCAGGACUNN	1210
s	217	UUGCCUCUGGGAAGACCGC	1159	UUGCCUCUGGGAAGACCGCNN	1211
as	235	GCGGUCUUCCCAGAGGCAA	1160	GCGGUCUUCCCAGAGGCAANN	1212
s	242	UGGAGAGCUGCACGGGCUC	1161	UGGAGAGCUGCACGGGCUCNN	1213
as	260	GAGCCCGUGCAGCUCUCCA	1162	GAGCCCGUGCAGCUCUCCANN	1214
s	244	GAGAGCUGCACGGGCUCAC	1163	GAGAGCUGCACGGGCUCACNN	1215
as	262	GUGAGCCCGUGCAGCUCUC	1164	GUGAGCCCGUGCAGCUCUCNN	1216
s	246	GAGCUGCACGGGCUCACCA	1165	GAGCUGCACGGGCUCACCANN	1217
as	264	UGGUGAGCCCGUGCAGCUC	1166	UGGUGAGCCCGUGCAGCUCNN	1218
s	399	UACACCAUCGCAGCCCUGC	1167	UACACCAUCGCAGCCCUGCNN	1219
as	417	GCAGGGCUGCGAUGGUGUA	1168	GCAGGGCUGCGAUGGUGUANN	1220
s	132	GUCCUGGAUGCUGUCCGAG	1169	GUCCUGGAUGCUGUCCGAGNN	1221
as	150	CUCGGACAGCAUCCAGGAC	1170	CUCGGACAGCAUCCAGGACNN	1222

Strand	Position	Sequence (5′ to 3′)	SEQ ID NO:	Sequence with 3′ dinucleotide overhang (5′ to 3′)	SEQ ID NO:
s	245	AGAGCUGCACGGGCUCACC	1171	AGAGCUGCACGGGCUCACCNN	1223
as	263	GGUGAGCCCGUGCAGCUCU	1172	GGUGAGCCCGUGCAGCUCUNN	1224

Table 6B. Sense and antisense strand sequences for rat TTR dsRNAs

Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_012681.1, SEQ ID NO:1330)

Strand	Position	Sequence with 3′deoxythimidine overhang (5′ to 3′)	SEQ ID NO:
s	115	GUCCUCUGAUGGUCAAAGUdTdT	1225
as	133	ACUUUGACCAUCAGAGGACdTdT	1226
s	537	UUCUUGCUCUAUAAACCGUdTdT	1227
as	555	ACGGUUUAUAGAGCAAGAAdTdT	1228
s	543	CUCUAUAAACCGUGUUAGCdTdT	1229
as	561	GCUAACACGGUUUAUAGAGdTdT	1230
s	392	UCGCCACUACACCAUCGCAdTdT	1231
as	410	UGCGAUGGUGUAGUGGCGAdTdT	1232
s	538	UCUUGCUCUAUAAACCGUGdTdT	1233
as	556	CACGGUUUAUAGAGCAAGAdTdT	1234
s	541	UGCUCUAUAAACCGUGUUAdTdT	1235
as	559	UAACACGGUUUAUAGAGCAdTdT	1236
s	532	CAGUGUUCUUGCUCUAUAAdTdT	1237
as	550	UUAUAGAGCAAGAACACUGdTdT	1238
s	542	GCUCUAUAAACCGUGUUAGdTdT	1239
as	560	CUAACACGGUUUAUAGAGCdTdT	1240
s	134	CCUGGAUGCUGUCCGAGGCdTdT	1241
as	152	GCCUCGGACAGCAUCCAGGdTdT	1242
s	119	UCUGAUGGUCAAAGUCCUGdTdT	1243
as	137	CAGGACUUUGACCAUCAGAdTdT	1244
s	241	CUGGAGAGCUGCACGGGCUdTdT	1245
as	259	AGCCCGUGCAGCUCUCCAGdTdT	1246
s	544	UCUAUAAACCGUGUUAGCAdTdT	1247
as	562	UGCUAACACGGUUUAUAGAdTdT	1248
s	530	AACAGUGUUCUUGCUCUAUdTdT	1249
as	548	AUAGAGCAAGAACACUGUUdTdT	1250
s	118	CUCUGAUGGUCAAAGUCCUdTdT	1251
as	136	AGGACUUUGACCAUCAGAGdTdT	1252
s	140	UGCUGUCCGAGGCAGCCCUdTdT	1253
as	158	AGGGCUGCCUCGGACAGCAdTdT	1254
s	239	GUCUGGAGAGCUGCACGGGdTdT	1255
as	257	CCCGUGCAGCUCUCCAGACdTdT	1256
s	531	ACAGUGUUCUUGCUCUAUAdTdT	1257
as	549	UAUAGAGCAAGAACACUGUdTdT	1258
s	117	CCUCUGAUGGUCAAAGUCCdTdT	1259
as	135	GGACUUUGACCAUCAGAGGdTdT	1260
s	131	AGUCCUGGAUGCUGUCCGAdTdT	1261
as	149	UCGGACAGCAUCCAGGACUdTdT	1262
s	217	UUGCCUCUGGGAAGACCGCdTdT	1263
as	235	GCGGUCUUCCCAGAGGCAAdTdT	1264
s	242	UGGAGAGCUGCACGGGCUCdTdT	1265
as	260	GAGCCCGUGCAGCUCUCCAdTdT	1266
s	244	GAGAGCUGCACGGGCUCACdTdT	1267
as	262	GUGAGCCCGUGCAGCUCUCdTdT	1268
s	246	GAGCUGCACGGGCUCACCAdTdT	1269

Strand	Position	Sequence with 3'deoxythimidine overhang (5' to 3')	SEQ ID NO:
as	264	UGGUGAGCCCGUGCAGCUCdTdT	1270
s	399	UACACCAUCGCAGCCCUGCdTdT	1271
as	417	GCAGGGCUGCGAUGGUGUAdTdT	1272
s	132	GUCCUGGAUGCUGUCCGAGdTdT	1273
as	150	CUCGGACAGCAUCCAGGACdTdT	1274
s	245	AGAGCUGCACGGGCUCACCdTdT	1275
as	263	GGUGAGCCCGUGCAGCUCUdTdT	1276

Table 7. Chemically modified sense and antisense strand sequences for rat TTR dsRNAs

See Table 5 for duplex # (dsRNA name). Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_012681.1, SEQ ID NO:1330)

Strand	Oligo #	Position	Sequence (5' to 3')	SEQ ID NO:
s	A-32159	115	GuccucuGAuGGucAAAGudTdT	1277
as	A-32160	133	ACUUUGACcAUcAGAGGACdTdT	1278
s	A-32745	537	uucuuGcucuAuAAAccGudTdT	1279
as	A-32746	555	ACGGUUuAuAGAGcAAGAAdTdT	1280
s	A-32747	543	cucuAuAAAccGuGuuAGcdTdT	1281
as	A-32748	561	GCuAAcACGGUUuAuAGAGdTdT	1282
s	A-32749	392	ucGccAcuAcAccAucGcAdTdT	1283
as	A-32750	410	UGCGAUGGUGuAGUGGCGAdTdT	1284
s	A-32751	538	ucuuGcucuAuAAAccGuGdTdT	1285
as	A-32752	556	cACGGUUuAuAGAGcAAGAdTdT	1286
s	A-32753	541	uGcucuAuAAAccGuGuuAdTdT	1287
as	A-32754	559	uAAcACGGUUuAuAGAGcAdTdT	1288
s	A-32755	532	cAGuGuucuuGcucuAuAAdTdT	1289
as	A-32756	550	UuAuAGAGcAAGAAcACUGdTdT	1290
s	A-32757	542	GcucuAuAAAccGuGuuAGdTdT	1291
as	A-32758	560	CuAAcACGGUUuAuAGAGCdTdT	1292
s	A-32759	134	ccuGGAuGcuGuccGAGGcdTdT	1293
as	A-32760	152	GCCUCGGAcAGcAUCcAGGdTdT	1294
s	A-32761	119	ucuGAuGGucAAAGuccuGdTdT	1295
as	A-32762	137	cAGGACUUUGACcAUcAGAdTdT	1296
s	A-32763	241	cuGGAGAGcuGcAcGGGcudTdT	1297
as	A-32764	259	AGCCCGUGcAGCUCUCcAGdTdT	1298
s	A-32765	544	ucuAuAAAccGuGuuAGcAdTdT	1299
as	A-32766	562	UGCuAAcACGGUUuAuAGAdTdT	1300
s	A-32767	530	AAcAGuGuucuuGcucuAudTdT	1301
as	A-32768	548	AuAGAGcAAGAAcACUGUUdTdT	1302
s	A-32769	118	cucuGAuGGucAAAGuccudTdT	1303
as	A-32770	136	AGGACUUUGACcAUcAGAGdTdT	1304
s	A-32771	140	uGcuGuccGAGGcAGcccudTdT	1305
as	A-32772	158	AGGGCUGCCUCGGAcAGcAdTdT	1306
s	A-32773	239	GucuGGAGAGcuGcAcGGGdTdT	1307
as	A-32774	257	CCCGUGcAGCUCUCcAGACdTdT	1308
s	A-32775	531	AcAGuGuucuuGcucuAuAdTdT	1309
as	A-32776	549	uAuAGAGcAAGAAcACUGUdTdT	1310
s	A-32777	117	ccucuGAuGGucAAAGuccdTdT	1311
as	A-32778	135	GGACUUUGACcAUcAGAGGdTdT	1312
s	A-32779	131	AGuccuGGAuGcuGuccGAdTdT	1313
as	A-32780	149	UCGGAcAGcAUCcAGGACUdTdT	1314
s	A-32781	217	uuGccucuGGGAAGAccGcdTdT	1315
as	A-32782	235	GCGGUCUUCCcAGAGGcAAdTdT	1316
s	A-32783	242	uGGAGAGcuGcAcGGGcucdTdT	1317
as	A-32784	260	GAGCCCGUGcAGCUCUCcAdTdT	1318

Strand	Oligo #	Position	Sequence (5' to 3')	SEQ ID NO:
s	A-32785	244	GAGAGcuGcAcGGGcucAcdTdT	1319
as	A-32786	262	GUGAGCCCGUGcAGCUCUCdTdT	1320
s	A-32787	246	GAGcuGcAcGGGcucAccAdTdT	1321
as	A-32788	264	UGGUGAGCCCGUGcAGCUCdTdT	1322
s	A-32791	399	uAcAccAucGcAGcccuGcdTdT	1323
as	A-32792	417	GcAGGGCUGCGAUGGUGuAdTdT	1324
s	A-32793	132	GuccuGGAuGcuGuccGAGdTdT	1325
as	A-32794	150	CUCGGAcAGcAUCcAGGACdTdT	1326
s	A-32795	245	AGAGcuGcAcGGGcucAccdTdT	1327
as	A-32796	263	GGUGAGCCCGUGcAGCUCUdTdT	1328

Synthesis of TTR Sequences

TTR sequences were synthesized on MerMade 192 synthesizer at 1μmol scale. For all the sequences in the list, 'endolight' chemistry was applied as detailed below.

- All pyrimidines (cytosine and uridine) in the sense strand were replaced with corresponding 2'-O-Methyl bases (2' O-Methyl C and 2'-O-Methyl U)
- In the antisense strand, pyrimidines adjacent to (towards 5' position) ribo A nucleoside were replaced with their corresponding 2-O-Methyl nucleosides
- A two base dTdT extension at 3' end of both sense and antisense sequences was introduced
- The sequence file was converted to a text file to make it compatible for loading in the MerMade 192 synthesis software

The synthesis of TTR sequences used solid supported oligonucleotide synthesis using phosphoramidite chemistry. The synthesis of the above sequences was performed at 1um scale in 96 well plates. The amidite solutions were prepared at 0.1M concentration and ethyl thio tetrazole (0.6M in Acetonitrile) was used as activator.

The synthesized sequences were cleaved and deprotected in 96 well plates, using methylamine in the first step and triethylamine.3HF in the second step. The crude sequences thus obtained were precipitated using acetone: ethanol mix and the pellet were re-suspended in 0.5M sodium acetate buffer. Samples from each sequence were analyzed by LC-MS and the resulting mass data confirmed the identity of the sequences. A selected set of samples were also analyzed by IEX chromatography.

The next step in the process was purification. All sequences were purified on an AKTA explorer purification system using Source 15Q column. A single peak corresponding to the full length sequence was collected in the eluent and was subsequently analyzed for purity by ion exchange chromatography.

The purified sequences were desalted on a Sephadex G25 column using AKTA purifier. The desalted TTR sequences were analyzed for concentration and purity. The single strands were then annealed to form TTR-dsRNA.

Example 2B: *In vitro* screening of TTR siRNAs for mRNA suppression

Human TTR targeting dsRNAs (Table 2) were assayed for inhibition of endogenous TTR expression in HepG2 and Hep3B cells, using qPCR (real time PCR) and bDNA (branched DNA) assays to quantify TTR mRNA. Rodent TTR targeting dsRNA (Table 5) were synthesized and assayed for inhibition of endogenous TTR expression using bDNA assays in H.4.II.E cells. Results from single dose assays were used to select a subset of TTR dsRNA duplexes for dose response experiments to calculate IC50's. IC50 results were used to select TTR dsRNAs for further testing.

Cell culture and transfections:

The hepatocyte cell lines HepG2, Hep3B and H.4.II.E cells (ATCC, Manassas, VA) were grown to near confluence at 37°C in an atmosphere of 5% CO_2 in Dulbecco's modified Eagle's medium (ATCC) supplemented with 10% FBS, streptomycin, and glutamine (ATCC) before being released from the plate by trypsinization. H.4.II.E cells were also grown in Earle's minimal essential medium. Reverse transfection was carried out by adding 5 µl of Opti-MEM to 5 µl of siRNA duplexes per well into a 96-well plate along with 10 µl of Opti-MEM plus 0.2 µl of Lipofectamine RNAiMax per well (Invitrogen, Carlsbad CA. cat # 13778-150) and incubated at room temperature for 15 minutes. 80µl of complete growth media without antibiotics containing $4x10^4$ (HepG2), $2x10^4$ (Hep3B) or $2x10^4$ (H.4.II.E) cells were then added. Cells were incubated for 24 hours prior to RNA purification. Single dose experiments were performed at 10 nM final duplex concentration and dose response experiments were done with 10, 1, 0.5, 0.1,0.05, 0.01, 0.005, 0.001, 0.0005, 0.0001, 0.00005, 0.00001 nM.

Total RNA isolation using MagMAX-96 Total RNA Isolation Kit (Applied Biosystems, Foster City CA, part #: AM1830):

Cells were harvested and lysed in 140 µl of Lysis/Binding Solution then mixed for 1 minute at 850rpm using and Eppendorf Thermomixer (the mixing speed was the same throughout the process). Twenty micro liters of magnetic beads were added into cell-lysate and mixed for 5 minutes. Magnetic beads were captured using magnetic stand and the supernatant was removed without disturbing the beads. After removing supernatant, magnetic beads were washed with Wash Solution 1 (isopropanol added) and mixed for 1 minute. Beads were captured again and supernatant removed. Beads were then washed with 150µl Wash Solution 2 (Ethanol added), captured and supernatant was removed. 50µl of DNase mixture (MagMax turbo DNase Buffer and Turbo DNase) was then added to the beads and they were mixed for 10 to 15 minutes. After mixing, 100µl of RNA Rebinding Solution was added and mixed for 3 minutes. Supernatant was removed and magnetic beads were washed again with 150µl Wash

Solution 2 and mixed for 1 minute and supernatant was removed completely. The magnetic beads were mixed for 2 minutes to dry before RNA it was eluted with 50µl of water.

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

A master mix of 2µl 10X Buffer, 0.8µl 25X dNTPs, 2µl Random primers, 1µl Reverse Transcriptase, 1µl RNase inhibitor and 3.2µl of H2O per reaction were added into 10µl total RNA. cDNA was generated using a Bio-Rad C-1000 or S-1000 thermal cycler (Hercules, CA) through the following steps: 25°C 10 min, 37°C 120 min, 85°C 5 sec, 4°C hold.

Real time PCR:

2µl of cDNA was added to a master mix of 1µl 18S TaqMan Probe (Applied Biosystems Cat # 4319413E), 1µl TTR TaqMan probe (Applied Biosystems cat # HS00174914 M1) and 10µl TaqMan Universal PCR Master Mix (Applied Biosystems Cat #4324018) per well in a MicroAmp Optical 96 well plate (Applied Biosystems cat # 4326659). Real time PCR was done in an ABI 7000 Prism or an ABI 7900HT Real Time PCR system (Applied Biosystems) using the ΔΔ Ct(RQ) assay. All reactions were done in triplicate.

Real time data were analyzed using the ΔΔ Ct method and normalized to assays performed from cells transfected with 10nM BlockIT fluorescent Oligo (Invitrogen Cat # 2013) or 10nM AD-1955 (a control duplex that targets the non-mammalian luciferase gene) to calculate fold change.

Branched DNA assays- QuantiGene 1.0 (Panomics, Fremont, CA. cat #: QG0004)- Used to screen rodent specific duplexes

H.4.II.E cells (ATCC) were transfected with 10 nM siRNA. After removing media, H.4.II.E were lysed in 100ul of Diluted Lysis Mixture (a mixture of 1 volume of Lysis mixture, 2 volume of nuclease-free water and 10ul of Proteinase-K per ml for the final concentration of 20mg/ml) then incubated at 65 °C for 35 minutes. Then, 80µl of Working Probe Set (a mixture of TTR or GAPDH probe) and 20ul of cell-lysate were added into the Capture Plate. Capture Plates were incubated at 53 °C ±1 °C overnight (approximately 16-20hrs). Capture Plates were washed 3 times with 1X Wash Buffer (a mixture of nuclease-free water, Buffer Component 1 and Wash Buffer Component 2), then dried by centrifuging for 1 minute at 1000rpm. 100µl of Amplifier Working Reagent was added into the Capture Plate, which was then sealed and incubated for 1 hour at 46°C ±1°C. Wash and dry steps were repeated after 1 hour of incubation and 100µl of Label Solution Reagent was added. The plate was then washed, dried and 100µl Substrate (a mixture of Lithium Lauryl Sulfate and Substrate solution) was added. Capture

Plates were placed in the incubator for 30 minutes at 46 °C ±1 °C. Capture Plates were then removed from the incubator and incubated at room temperature for 30 minutes. Finally, the Capture Plates were read using the Victor Luminometer (Perkin Elmer, Waltham, MA).

Branched DNA assays- QuantiGene 2.0 (Panomics cat #: QS0011): Used to screen all other duplexes

After a 24 hour incubation at the dose or doses stated, media was removed and cells were lysed in 100ul Lysis Mixture (1 volume lysis mixture, 2 volumes nuclease-free water and 10µl of Proteinase-K/ml for a final concentration of 20mg/ml) then incubated at 65°C for 35 minutes. 20µl Working Probe Set (TTR probe for gene target and GAPDH for endogenous control) and 80µl of cell-lysate were then added to the Capture Plates. Capture Plates were incubated at 55°C ±1°C (approx. 16-20hrs). The next day, the Capture Plates were washed 3 times with 1X Wash Buffer (nuclease-free water, Buffer Component 1 and Wash Buffer Component 2), then dried by centrifuging for 1 minute at 240g. 100µl of pre-Amplifier Working Reagent was added to the Capture Plates, which were sealed with aluminum foil and incubated for 1 hour at 55°C ±1°C. Following a 1 hour incubation, the wash step was repeated, then 100µl Amplifier Working Reagent was added. After 1 hour, the wash and dry steps were repeated, and 100µl Label Probe was added. Capture plates were incubated 50°C ±1°C for 1 hour. The plates were then washed with 1X Wash Buffer and dried, and then 100µl Substrate was added to the Capture Plates. Capture Plates were read using the SpectraMax Luminometer (Molecular Devices, Sunnyvale, CA) following 5 to 15 minutes incubation.

bDNA data analysis:

bDNA data were analyzed by (i) subtracting the average background from each triplicate sample, (ii) averaging the resultant triplicate GAPDH (control probe) and TTR (experimental probe) values, and then (iii) taking the ratio: (experimental probe-background)/(control probe-background).

Results

A summary of the single dose and IC50 results for TTR-dsRNAs (TTR siRNAs) are presented below in Table 8. Single dose results are expressed as % TTR mRNA relative to control, assayed in HepG2 cells. IC50s were determined in HepG2 and/or Hep3B cells, as indicated.

Table 8. Single dose and IC50 results of *in vitro* screens of TTR siRNAs

ND: no data; * indicates result that represents average of two experiments.

	Single Dose at 10nM % relative to control		IC50 (nM)			
	HepG2		HepG2		Hep3B	
Duplex #	qPCR	bDNA	qPCR	bDNA	qPCR	bDNA
AD-18243	50.35	141.53	ND	ND	ND	ND
AD-18244	64.26	158.55	ND	ND	ND	ND
AD-18245	56.89	107.22	ND	ND	ND	ND
AD-18246	10.53	32.51*	0.265	0.086	ND	ND
AD-18247	125.56	69.57	ND	ND	ND	ND
AD-18248	127.78	66.97	ND	ND	ND	ND
AD-18249	48.77	48.76	ND	ND	ND	ND
AD-18250	96.94	86.42	ND	ND	ND	ND
AD-18251	170.41	129.15	ND	ND	ND	ND
AD-18252	73.52	81.90	ND	ND	ND	ND
AD-18253	25.25	61.25	ND	ND	ND	ND
AD-18254	95.13	103.96	ND	ND	ND	ND
AD-18255	119.46	ND	ND	ND	ND	ND
AD-18256	42.64	95.67	ND	ND	ND	ND
AD-18257	146.25	141.75	ND	ND	ND	ND
AD-18258	10.20	13.41*	0.007	0.005	0.004	0.005
AD-18259	9.30	20.91*	0.102	0.005	ND	ND
AD-18260	125.37	81.36	ND	ND	ND	ND
AD-18261	14.27	19.40*	0.210	ND	ND	ND
AD-18262	84.95	104.05	ND	ND	ND	ND
AD-18263	16.32	23.25*	0.110	ND	ND	ND
AD-18264	104.18	83.69	ND	ND	ND	ND
AD-18265	41.62	64.87	ND	ND	ND	ND
AD-18266	39.98	110.53	ND	ND	ND	ND
AD-18267	149.64	ND	ND	ND	ND	ND
AD-18268	152.93	174.04	ND	ND	ND	ND
AD-18269	37.27	92.28	ND	ND	ND	ND
AD-18270	99.44	164.75	ND	ND	ND	ND
AD-18271	18.89	28.33*	0.503	0.004	ND	ND
AD-18272	128.32	132.58	ND	ND	ND	ND
AD-18273	115.78	201.95	ND	ND	ND	ND
AD-18274	8.97	20.04*	0.009	0.176	0.036	0.012
AD-18275	4.09	22.25*	0.026	0.118	ND	ND
AD-18276	19.73	45.22*	0.198	0.677	ND	ND
AD-18277	10.55	26.31*	0.121	0.426	ND	ND
AD-18278	108.86	116.26	ND	ND	ND	ND
AD-18279	66.59	ND	ND	ND	ND	ND
AD-18280	103.26	170.52	ND	ND	ND	ND
AD-18281	87.98	123.88	ND	ND	ND	ND

	Single Dose at 10nM % relative to control		IC50 (nM)			
	HepG2		HepG2		Hep3B	
Duplex #	qPCR	bDNA	qPCR	bDNA	qPCR	bDNA
AD-18282	82.47	140.32	ND	ND	ND	ND
AD-18283	106.54	182.78	ND	ND	ND	ND
AD-18284	106.93	151.78	ND	ND	ND	ND
AD-18285	26.58	60.05*	ND	0.089	ND	ND
AD-18286	109.95	173.66	ND	ND	ND	ND
AD-18287	54.23	155.45	ND	ND	ND	ND
AD-18288	73.52	174.09	ND	ND	ND	ND
AD-18289	103.36	174.76	ND	ND	ND	ND
AD-18290	17.06	52.04*	1.253	0.181	ND	ND
AD-18291	7.71	169.29*	1.304	0.019	ND	ND
AD-18292	7.51	210.03*	0.604	0.005	ND	ND
AD-18293	3.61	62.53*	0.078	0.003	ND	ND
AD-18294	111.53	107.56	ND	ND	ND	ND
AD-18295	115.88	105.37	ND	ND	ND	ND
AD-18296	57.03	38.03	ND	ND	ND	ND
AD-18297	87.69	73.87	ND	ND	ND	ND
AD-18298	10.39	7.25*	0.455	0.008	ND	ND
AD-18299	18.79	18.06*	0.895	0.014	ND	ND
AD-18300	108.70	ND	ND	ND	ND	ND
AD-18301	114.22	70.50	ND	ND	ND	ND
AD-18302	116.19	122.40	ND	ND	ND	ND
AD-18303	124.89	ND	ND	ND	ND	ND
AD-18304	132.99	89.54	ND	ND	ND	ND
AD-18305	153.10	ND	ND	ND	ND	ND
AD-18306	159.22	ND	ND	ND	ND	ND
AD-18307	116.83	84.57	ND	ND	ND	ND
AD-18308	156.72	87.80	ND	ND	ND	ND
AD-18309	113.22	101.97	ND	ND	ND	ND
AD-18310	132.33	ND	ND	ND	ND	ND
AD-18311	161.68	92.92	ND	ND	ND	ND
AD-18312	103.01	71.17	ND	ND	ND	ND
AD-18313	120.65	53.26	ND	ND	ND	ND
AD-18314	116.33	ND	ND	ND	ND	ND
AD-18315	115.13	ND	ND	ND	ND	ND
AD-18316	118.73	122.34	ND	ND	ND	ND
AD-18317	114.03	121.10	ND	ND	ND	ND
AD-18318	80.85	122.57	ND	ND	ND	ND
AD-18319	119.14	148.87	ND	ND	ND	ND
AD-18320	22.86	55.43*	ND	0.023	0.403	ND
AD-18321	6.44	31.56*	0.001	0.033	ND	ND
AD-18322	54.21	100.46	ND	ND	ND	ND
AD-18323	6.37	28.71*	0.005	0.023	ND	ND

Duplex #	Single Dose at 10nM % relative to control		IC50 (nM)			
	HepG2		HepG2		Hep3B	
	qPCR	bDNA	qPCR	bDNA	qPCR	bDNA
AD-18324	2.53	15.98*	0.002	0.006	0.005	0.014
AD-18325	2.52	11.96*	0.001	0.016	ND	ND
AD-18326	18.34	43.16*	0.025	0.186	ND	ND
AD-18327	18.28	13.90*	0.044	0.215	ND	ND
AD-18328	4.53	26.04*	0.003	0.004	0.006	0.006
AD-18329	96.93	131.54	ND	ND	ND	ND
AD-18330	11.80	45.18*	0.0004	0.010	0.020	ND
AD-18331	117.77	163.07	ND	ND	ND	ND
AD-18332	11.53	35.09*	0.001	0.076	0.065	ND
AD-18333	12.24	46.94*	0.001	0.115	0.075	ND
AD-18334	16.27	55.28*	0.0004	0.181	1.071	ND
AD-18335	53.52	112.80	ND	ND	ND	ND
AD-18336	6.39	33.00*	0.001	0.112	0.081	ND
AD-18337	51.77	105.33	ND	ND	ND	ND
AD-18338	48.21	102.86	ND	ND	ND	ND
AD-18339	6.48	26.56*	0.004	0.002	0.018	0.029
AD-18340	4.53	30.76*	0.002	0.002	ND	ND
AD-18341	31.27	100.41	ND	ND	ND	ND
AD-18342	7.60	42.89*	ND	0.016	0.076	ND
AD-18343	3.42	17.45*	ND	0.001	ND	ND
AD-18344	75.08	134.31	ND	ND	ND	ND
AD-18345	13.62	42.75*	0.002	0.013	ND	ND
AD-18346	59.25	121.10	ND	ND	ND	ND
AD-18347	91.23	139.54	ND	ND	ND	ND
AD-18348	89.95	159.29	ND	ND	ND	ND
AD-18349	108.01	144.96	ND	ND	ND	ND
AD-18350	123.65	125.87	ND	ND	ND	ND
AD-18351	108.36	104.02	ND	ND	ND	ND
AD-18352	87.82	128.72	ND	ND	ND	ND
AD-18353	14.40	65.77	0.012	0.027	ND	ND
AD-18354	99.27	123.53	ND	ND	ND	ND
AD-18355	135.04	150.88	ND	ND	ND	ND
AD-18356	100.76	178.96	ND	ND	ND	ND
AD-18357	125.30	162.85	ND	ND	ND	ND
AD-18358	103.15	136.01	ND	ND	ND	ND
AD-18359	34.74	140.48	ND	ND	ND	ND
AD-18360	103.86	146.86	ND	ND	ND	ND
AD-18361	105.74	152.74	ND	ND	ND	ND
AD-18362	106.96	188.22	ND	ND	ND	ND
AD-18363	124.22	58.46	ND	ND	ND	ND
AD-18364	113.75	66.87	ND	ND	ND	ND
AD-18446	29.73	13.30	ND	ND	ND	ND

	Single Dose at 10nM % relative to control		IC50 (nM)			
	HepG2		HepG2		Hep3B	
Duplex #	qPCR	bDNA	qPCR	bDNA	qPCR	bDNA
AD-18447	109.74	53.63	ND	ND	ND	ND
AD-18448	22.96	8.81	ND	ND	ND	ND
AD-18449	112.59	50.11	ND	ND	ND	ND
AD-18450	89.41	34.89	ND	ND	ND	ND
AD-18451	74.35	23.88	ND	ND	ND	ND
AD-18452	125.25	54.86	ND	ND	ND	ND
AD-18453	126.98	56.31	ND	ND	ND	ND
AD-18454	113.88	52.48	ND	ND	ND	ND
AD-18455	163.00	48.89	ND	ND	ND	ND
AD-18456	15.70	10.52	ND	ND	ND	ND
AD-18457	12.86	8.22	ND	ND	ND	ND
AD-18458	13.00	7.00	ND	ND	ND	ND
AD-18459	14.41	10.72	ND	ND	ND	ND
AD-18460	121.16	74.87	ND	ND	ND	ND
AD-18461	100.53	71.87	ND	ND	ND	ND
AD-18462	47.75	29.35	ND	ND	ND	ND
AD-18463	58.98	44.79	ND	ND	ND	ND

The dose response data used to identify the IC50 for 5 TTR-dsRNAs (AD-18258, AD-18274, AD-18324, AD-18328, and AD-18339), are presented in detail below in Table 9. All 5 siRNAs were determined to have pM IC50s. The IC50 data for dsRNAs in Table 8 is a summary of the data presented in Table 9 below.

Table 9. Dose response data for 5 TTR-dsRNAs

		% inhibition relative to control AD-1955												
Duplex AD-18258		Dose of duplex (nM)												
Cell type	Detection method	10	1	0.5	0.1	0.05	0.01	0.005	0.001	0.0005	0.0001	0.00005	0.00001	IC50 (nM)
HepG2	qPCR	14.4	14.1	16.2	23.9	27.26	40.19	68.46	78.1	74.48	104.37	98.28	113.68	0.007
HepG2	bDNA	14.3	14.5	11.1	12.8	18.82	19.77	51.21	56.03	63.63	58.35	43.64	51.05	0.005
Hep3B	qPCR	11.9	8.62	12.4	16.4	28.35	30.49	58.36	54.57	81.26	89.43	81.85	101.87	0.004
Hep3B	bDNA	7.65	7.5	11.3	12.6	28.85	27.89	64.57	73.48	72.03	91.44	86.71	89.31	0.005

		% inhibition relative to control AD-1955												
Duplex AD-18274		Dose of duplex (nM)												
Cell type	Detection method	10	1	0.5	0.1	0.05	0.01	0.005	0.001	0.0005	0.0001	0.00005	0.00001	IC50 (nM)
HepG2	qPCR	6.68	8.45	11.7	24.2	42.08	49.89	56.95	62.99	64.47	54.92	67.39	72.67	0.009
HepG2	bDNA	27.5	69	25.2	34.2	73.03	103.4	121.57	97.31	154.93	156.7	Nd	152.25	0.176
Hep3B	qPCR	7.58	17	15.6	43.9	42.22	60.55	78.8	77.81	79.97	85.84	86.13	83.99	0.036
Hep3B	bDNA	3.77	4.92	7.51	15	35.21	51.66	72.45	70.12	78.31	77.52	90.72	83.01	0.012

		% inhibition relative to control AD-1955												
Duplex AD-18324		Dose of duplex (nM)												
Cell type	Detection method	10	1	0.5	0.1	0.05	0.01	0.005	0.001	0.0005	0.0001	0.00005	0.00001	IC50 (nM)
HepG2	qPCR	2.07	2.27	2.74	6.36	8.18	15.23	28.82	52.79	90.86	94.72	116.07	98.97	0.002
HepG2	bDNA	14.5	7.88	11.8	15.9	17.2	46.44	40.4	91.86	0	95.57	0	52.15	0.006
Hep3B	qPCR	2.07	3.48	5.76	16.2	18.73	44.54	49.77	68.88	63.48	76.61	74.7	77.83	0.005
Hep3B	bDNA	3.48	3.8	5.15	15.2	30.84	55.36	74.75	99.39	88.89	110.83	96.55	110.26	0.014

		% inhibition relative to control AD-1955												
Duplex AD-18328		Dose of duplex (nM)												
Cell type	Detection method	10	1	0.5	0.1	0.05	0.01	0.005	0.001	0.0005	0.0001	0.00005	0.00001	IC50 (nM)
HepG2	qPCR	5.85	3.97	3.32	5.62	8	16.75	55.01	39.76	122.41	102.37	114.02	124.09	0.003
HepG2	bDNA	12.3	10.7	10.7	11.9	20.06	25	69.52	57.29	112.28	98.14	142.26	148.92	0.004
Hep3B	qPCR	3.17	5.52	11.7	13.8	27.68	39.58	61.21	61.87	90.51	87.56	106.03	108.72	0.006
Hep3B	bDNA	3.08	3.66	4.19	7.25	21.05	22.1	73.74	63.19	105.55	96.27	105.97	96.46	0.006

		% inhibition relative to control AD-1955												
Duplex AD-18339		Dose of duplex (nM)												
Cell type	Detection method	10	1	0.5	0.1	0.05	0.01	0.005	0.001	0.0005	0.0001	0.00005	0.00001	IC50 (nM)
HepG2	qPCR	6.27	7.28	Nd	11	15.25	38.69	38.78	71.7	84.09	62.2	75.61	85.46	0.004
HepG2	bDNA	15.1	8.14	5.13	6.89	12.17	32.14	42.98	64.01	60.76	79.95	81.97	95.43	0.002
Hep3B	qPCR	8.3	9.47	13.2	34.5	44.54	77.38	81.04	81.41	93.95	81.04	75.61	78.28	0.018
Hep3B	bDNA	10.5	9.43	11.7	27.1	44.88	72.32	79.88	79.6	87.46	96.53	95.13	89.88	0.029

A summary of the single dose results for rodent specific TTR-dsRNAs (TTR siRNAs) are presented below in Table 10. Single dose results are expressed as % TTR mRNA relative to control, assayed in rat H.4.II.E cells, after transfection of rodent specific TTR siRNAs at 10 nM. These results show that some rodent specific TTR siRNAs are effective in suppressing endogenous rat TTR mRNA *in vitro*.

Table 10. Single dose results of *in vitro* screen of rodent specific TTR-dsRNAs (TTR siRNAs)

Duplex #	% Relative to control at 10 nM	Duplex #	% Relative to control at 10 nM
AD-18529	19.83	AD-18542	6.3
AD-18530	44.49	AD-18543	16.46
AD-18531	6.01	AD-18544	17.55
AD-18532	24.06	AD-18545	3.53
AD-18533	37.78	AD-18546	2.75
AD-18534	8.19	AD-18547	7.01
AD-18535	10.18	AD-18548	5.02
AD-18536	16.13	AD-18549	1.61
AD-18537	15.88	AD-18550	9.58
AD-18538	19.93	AD-18551	7.74
AD-18539	49.24	AD-18552	3.74
AD-18540	2.99	AD-18553	50.39
AD-18541	1.32	AD-18554	111.06

Example 3. *In vitro* assay of TTR siRNAs for induction of TNF-α and IFN-α secretion

To evaluate potential for immunostimulation, TTR siRNAs were assayed in vitro for induction of TNF-α and IFN-α secretion.

Human PBMC were isolated from freshly collected buffy coats obtained from healthy donors (Research Blood Components, Inc., Boston, MA) by a standard Ficoll-Hypaque density centrifugation. Freshly isolated cells ($1x10^5$/well/100μl) were seeded in 96-well plates and cultured in RPMI 1640 GlutaMax medium (Invitrogen) supplemented with 10% heat - inactivated fetal bovine serum and 1% antibiotic/antimycotic (Invitrogen).

siRNAs were transfected into PBMC using DOTAP transfection reagent (Roche Applied Science). The DOTAP was first diluted in Opti-MEM (Invitrogen) for 5 minutes before mixing with an equal volume of Opti-MEM containing the siRNA. siRNA/DOTAP complexes were incubated as specified by the manufacturer's instructions and subsequently added to PBMC (50μl/well) which were then cultured for 24 hours. Positive and negative control siRNAs were included in all assays. AD-5048 was used as a positive control siRNA. AD-5048 corresponds to a sequence that targets human Apolipoprotein B (Soutschek *et al.*, 2004) and elicits secretion of both IFN-α and TNF-α in this assay. AD-1955, which does not elicit IFN-α and TNF-α secretion in this assay, was used as a negative control siRNA. All siRNAs were used at a final concentration of 133 nM. The ratio of RNA to transfection reagent was16.5 pmoles per μg of DOTAP.

Cytokines were detected and quantified in culture supernatants with a commercially available ELISA kit for IFN-α (BMS216INST) and TNF-α (BMS223INST), both from Bender MedSystems (Vienna, Austria). TTR siRNA cytokine induction is expressed as percent IFN-α or TNF-α produced relative to the positive control siRNA AD-5048.

IFN-α and TNF-α stimulation results for a number of TTR siRNAs are presented in FIG. 1 (mean of quadruplicate wells ± SD) and below in Table 11 (percentage compared with AD-5048). None of the TTR siRNAs evaluated induced significant TNF-α or IFN-α secretion by cultured human PBMCs.

Table 11. IFN-α and TNF-α stimulation results for TTR siRNAs

Duplex #	IFN-α (% of AD-5048)	TNF-α (% of AD-5048)
AD-18246	0	4
AD-18258	0	0
AD-18259	0	0
AD-18261	0	0
AD-18263	0	0
AD-18271	0	0
AD-18274	2	1
AD-18275	0	0
AD-18276	0	0
AD-18277	0	0
AD-18285	0	0
AD-18290	0	0
AD-18291	0	0
AD-18292	0	0
AD-18293	0	0
AD-18298	0	0
AD-18299	0	0
AD-18320	0	0
AD-18321	0	0
AD-18323	0	0
AD-18324	0	0
AD-18325	0	0
AD-18326	0	0
AD-18327	0	0
AD-18328	0	0
AD-18330	0	0
AD-18332	1	0
AD-18333	0	1
AD-18334	0	1
AD-18336	1	0
AD-18339	0	0
AD-18340	0	0
AD-18342	0	0
AD-18343	0	0
AD-18345	0	0
AD-18353	0	0
AD-18448	0	0
AD-18456	0	0
AD-18457	0	0
AD-18458	0	0
AD-18459	0	0

The five lead TTR targeting dsRNAs (TTR siRNAs) were selected based on IC50s in the pM range in the human hepatocyte cell lines HepG2 and Hep3B, and the absence of immunostimulatory activity. Duplexes without any mismatches are more likely to achieve

significant knockdown of the target transcript than duplexes with mismatches between the oligo and the mRNA. To better enable interpretation of cross-species toxicology data and to have the broadest applicability to human patients, duplexes that have 100% identity in orthologous genes from rat, cynomolgus monkey and human, and that do not target regions with known polymorphisms are generally preferred. The five lead compounds were selected based on IC50 in hepatocyte cell lines in the pM range, the absence of immunostimulatory activity, specificity to the human TTR transcripts, and absence of known polymorphisms (mutations) in the region of the mRNA targeted by the duplex. In the case of TTR, no 19 base oligos were found with complete identity in human, rat and cynomolgus monkey. A summary of these data are presented in Table 12, which also includes information on known TTR mutations in the region targeted by the duplex and cross-species reactivity.

Table 12. Summary of data for five most potent TTR dsRNAs.

Duplex #	IC50 (qPCR): nM HepG2	IC50 (bDNA): nM HepG2	IFNa/TNFa	Mutations not covered	Cross-species reactivity
AD-18258	0.007	0.005	Negative	None (non-coding region)	Cyno: 1 mismatch @ position 14 A to G Rat: no homology at any position
AD-18274	0.009	0.176	Negative	Lys70Asn; Val71Ala; Ile73Val; Asp74His	Cyno: no mismatch Rat: no homology at any position
AD-18324	0.002	0.006	Negative	None (non-coding region)	Cyno: no mismatch Rat: no homology at any position
AD-18328	0.003	0.004	Negative	None (non-coding region)	Cyno: no mismatch Rat: 7 mismatches
AD-18339	0.004	0.002	Negative	None (non-coding region)	None

Example 4. *In vivo* reduction of liver TTR mRNA and plasma TTR protein by LNP01-18324, LNP01-18328 and LNP01-18246 in transgenic mice

Two TTR siRNAs, AD-18324 and AD-18328, were chosen for *in vivo* evaluation. These duplexes exhibited potent dose-dependent silencing *in vitro* in hepatocyte cell lines (*e.g.* HepG2). FIG. 2A and FIG. 2B show the dose responses in HepG2 cells after transfection with AD-18324 (FIG. 2A) or AD-18328 (FIG. 2B) where the doses are expressed in nM on the x-axis and the responses are expressed as fraction TTR mRNA remaining relative to control, on the y-axis. In HepG2 cells, the IC50s of AD-18324 and AD-18328 were determined to be 2 pM and 3

pM, respectively. The TTR target sites for both lead dsRNA candidates are in the 3' untranslated region of the TTR mRNA, in a region where there are no reported mutations in the literature.

The sequences of each strand of the two lead candidates are reproduced below from the Tables. Strand: s= sense; as= antisense; Position: position of 5' base on transcript NM_000371.2.

Duplex #	Strand	Oligo #	Position*	Sequence 5' to 3'	SEQ ID NO:
AD-18324	s	A-32337	509	GGAuuucAuGuAAccAAGAdTdT	1001
AD-18324	as	A-32338	527	UCUUGGUuAcAUGAAAUCCdTdT	1002
AD-18328	s	A-32345	518	GuAAccAAGAGuAuuccAudTdT	1009
AD-18328	as	A-32346	536	AUGGAAuACUCUUGGUuACdTdT	1010

In addition, a rodent cross-reactive TTR dsRNA, AD-18246, was chosen for further evaluation *in vivo*. AD-18246 targets a sequence beginning at position 88 of the open reading frame, where there are three mutations reported in the literature. A dose response curve for AD-18246 in HepG2 cells is shown in FIG. 3. AD-18246 is substantially less potent than AD-18324 and AD-18328; the IC50 of AD-18246 was determined to be 265 pM.

AD-18324, AD-18328, and AD-18246 were administered to transgenic mice after formulation in LNP01. 3-5 month old H129-mTTR-KO/iNOS-KO/hTTR transgenic mice (mouse transthyretin knock-out/ inducible nitric oxide synthase knock-out/human transthyretin transgenic) were intravenously (IV) administered 200 µl of LNP01-formulated transthyretin-specific siRNA (AD-18324, AD-18328, or AD-18246), LNP01-formulated control siRNA targeting the non-mammalian luciferase gene (AD-1955) or PBS via the tail vein at concentrations of 1.0 mg/kg, 3.0 mg/kg, or 6.0 mg/kg for siRNAs AD-18324 and AD-18328, 3.0 mg/kg for siRNA AD-18246, and 6.0 mg/kg for siRNA AD-1955. LNP01 is a lipidoid formulation comprised of ND98, Cholesterol, and PEG-Ceramide C16.

After approximately forty-hours, mice were anesthetized with 200 µl of ketamine, and then exsanguinated by severing the right caudal artery. Whole blood was isolated and plasma was isolated and stored at -80°C until assaying. Liver tissue was collected, flash-frozen and stored at -80°C until processing.

Efficacy of treatment was evaluated by (i) measurement of TTR mRNA in liver at 48 hours post-dose, and (ii) measurement of TTR protein in plasma at prebleed and at 48 hours post-dose. TTR liver mRNA levels were assayed utilizing the Branched DNA assays-QuantiGene 2.0 (Panomics cat #: QS0011). Briefly, mouse liver samples were ground and tissue

lysates were prepared. Liver lysis mixture (a mixture of 1 volume of lysis mixture, 2 volume of nuclease-free water and 10ul of Proteinase-K/ml for a final concentration of 20mg/ml) was incubated at 65 °C for 35 minutes. 20µl of Working Probe Set (TTR probe for gene target and GAPDH for endogenous control) and 80ul of tissue-lysate were then added into the Capture Plate. Capture Plates were incubated at 55 °C ±1 °C (aprx. 16-20hrs). The next day, the Capture Plate were washed 3 times with 1X Wash Buffer (nuclease-free water, Buffer Component 1 and Wash Buffer Component 2), then dried by centrifuging for 1 minute at 240g. 100ul of pre-Amplifier Working Reagent was added into the Capture Plate, which was sealed with aluminum foil and incubated for 1 hour at 55°C ±1°C. Following 1 hour incubation, the wash step was repeated, then 100µl of Amplifier Working Reagent was added. After 1 hour, the wash and dry steps were repeated, and 100µl of Label Probe was added. Capture plates were incubated 50 °C ±1 °C for 1 hour. The plate was then washed with 1X Wash Buffer, dried and 100µl Substrate was added into the Capture Plate. Capture Plates were read using the SpectraMax Luminometer following a 5 to 15 minute incubation. bDNA data were analyzed by subtracting the average background from each triplicate sample, averaging the resultant triplicate GAPDH (control probe) and TTR (experimental probe) values, and then computing the ratio: (experimental probe-background)/(control probe-background).

TTR plasma levels were assayed utilizing the commercially available kit "AssayMax Human Prealbumin ELISA Kit" (AssayPro, St. Charles, MO, Catalog # EP3010-1) according to manufacturer's guidelines. Briefly, mouse plasma was diluted 1:10,000 in 1X mix diluents and added to pre-coated plates along with kit standards, and incubated for 2 hours at room temperature followed by 5X washes with kit wash buffer. Fifty microliters of biotinylated prealbumin antibody was added to each well and incubated for 1 hr at room temperature, followed by 5X washes with wash buffer. Fifty microliters of streptavidin-peroxidase conjugate was added to each well and plates were incubated for 30 minutes at room temperature followed by washing as previously described. The reaction was developed by the addition of 50 µl/well of chromogen substrate and incubation for 10 minutes at room temperature with stopping of reaction by the addition of 50 µl/well of stop solution. Absorbance at 450 nm was read on a Versamax microplate reader (Molecular Devices, Sunnyvale, CA) and data were analyzed utilizing the Softmax 4.6 software package (Molecular Devices).

LNP01-18324 and LNP01-18328 were found to reduce liver TTR mRNA (FIG. 4A) and plasma TTR protein (FIG. 4B) levels in a dose-dependent manner with IV bolus administration. The mRNA ED50 of LNP01-18328 was determined to be ~1 mg/kg whereas the ED50 of LNP01-18324 was determined to be ~ 2 mg/kg. The effects of LNP01-18324 and LNP01-18328

were specific, because the control, LNP01-1955 at 6 mg/kg, did not significantly affect liver TTR mRNA levels, as compared with the PBS group. LNP01-18324 and LNP01-18328 reduced plasma TTR protein levels relative to the PBS group, with potencies that were similar to those on TTR mRNA levels. At 3 mg/kg, LNP01-18246 reduced liver TTR mRNA levels to a lessor extent than 3 mg/kg LNP01-18324 or LNP01-18328.

These results demonstrate that LNP01-18324 and LNP01-18328, administered by IV bolus, substantially reduce human TTR mRNA expressed by the transgenic mouse liver, which results in reduction of human TTR protein in the circulation.

Example 5. *In vivo* reduction of wild-type TTR mRNA in the non-human primate liver by SNALP-18324 and SNALP-18328

To evaluate the efficacy of TTR siRNAs AD-18324 and AD-18328 in non-human primates on liver TTR mRNA levels, the siRNAs were formulated in SNALP and administered by 15-minute IV infusion. Cynomolgus monkeys (*Macaca fascicularis*) (2 to 5 kg, 3 animals per group) were administered 15-minute IV infusions of SNALP-18324 (0.3, 1.0 or 3.0 mg/kg), SNALP-18328 (0.3, 1 or 3 mg/kg), or SNALP-1955 (3 mg/kg, with negative control siRNA AD-1955 which targets the non-mammalian gene luciferase). At forty-eight hours post-dosing, monkeys were anesthetized with sodium pentobarbital and exsanguinated. Liver tissue for TTR mRNA determination was collected, flash-frozen, and stored at -80°C until processing.

TTR mRNA levels in the liver were assayed utilizing a custom designed Branched DNA assay, utilizing the QuantiGene1.0 technology. Briefly, monkey liver samples were ground and tissue lysates were prepared. Liver lysis mixture (1 volume lysis mixture, 2 volume nuclease-free water, and 10µl of Proteinase-K/ml for a final concentration of 20mg/ml) was incubated at 65°C for 35 minutes. 20µl Working Probe Set (TTR probe for gene target and GAPDH for endogenous control) and 80µl tissue-lysate were then added into the Capture Plate. Capture Plates were incubated at 55°C ±1°C (approx. 16-20hrs). The next day, the Capture Plates were washed three times with 1X Wash Buffer (nuclease-free water, Buffer Component 1 and Wash Buffer Component 2), then dried by centrifuging for 1 minute at 240g. 100µl of pre-Amplifier Working Reagent was added into the Capture Plate, which was sealed with aluminum foil and incubated for 1 hour at 55°C ±1°C. Following a 1-hour incubation, the wash step was repeated, and then 100µl Amplifier Working Reagent was added. After 1 hour, the wash and dry steps were repeated, and 100µl Label Probe was added. Capture plates were incubated 50°C ±1°C for 1 hour. The plates were then washed with 1X Wash Buffer and dried, and then 100µl Substrate was added into the Capture Plate. Capture Plates were read using the SpectraMax Luminometer

following a 5 to 15 minute incubation. bDNA data were analyzed by (i) subtracting the average background from each triplicate sample, (ii) averaging the resultant GAPDH (control probe) and TTR (experimental probe) values, and then (iii) taking the ratio: (experimental probe-background)/(control probe-background).

The results are shown in FIG. 5. SNALP -18324 and SNALP -18328 reduced TTR mRNA levels in the liver in a dose-dependent manner, compared to the negative control SNALP-1955. The mRNA ED50s of SNALP-18328 and SNALP-18324 were determined to be ~0.3 and ~ 1 mg/kg, respectively.

These results demonstrate that SNALP-18324 and SNALP-18328 are effective in suppressing wild-type TTR mRNA in non-human primate liver when administered by IV infusion.

Example 6. *In vivo* reduction of mutant (V30M) TTR mRNA and protein by SNALP-18328 in the transgenic mouse

To evaluate the efficacy of TTR siRNA AD-18328 on mutant (V30M) TTR mRNA in the liver and mutant (V30M) TTR protein in the serum, AD-18328 was formulated in SNALP and administered by IV bolus to V30M hTTR transgenic mice. 8 to 12-week old V30M hTTR transgenic mice (5 animals/ group) were intravenously (IV) administered 200 µl SNALP-18328 (0.03, 0.3 or 3 mg/kg), SNALP-1955 (3 mg/kg, with negative control siRNA AD-1955 which targets the non-mammalian gene luciferase), or PBS. Mice used were the Mus musculus strain H129-hTTR KO from Institute of Molecular and Cellular Biology, Porto, Portugal. Briefly, hTTR H129 transgenic mice were crossed with a H129 endogenous TTR KO mice (null mice to generate the H129-hTTR transgenic mice, in a null mouse TTR background (Maeda, S., (2003), Use of genetically altered mice to study the role of serum amyloid P component in amyloid deposition. Amyloid Suppl. 1, 17-20.).

At 48 hrs post-injection, animals in all five treatment groups were given a lethal dose of ketamine/xylazine. Serum samples were collected and stored at -80°C until analysis. Liver tissue was collected, flash-frozen and stored at -80oC until processing.

For TTR mRNA quantitation, frozen liver tissue was ground into powder, and lysates were prepared. TTR mRNA levels relative to those of GAPDH mRNA were determined in the lysates by using a branched DNA assay (QuantiGene Reagent System, Panomics, Fremont, CA). Briefly, the QuantiGene assay (Genospectra) was used to quantify mRNA levels in tissue sample lysates according to the manufacturer's instructions. The mean level of TTR mRNA was normalized to the mean level of GAPDH mRNA for each sample. Group means of the

normalized values were then further normalized to the mean value for the PBS treated group, to obtain the relative level of TTR mRNA expression.

For TTR protein quantitation, serum was assayed using the AssayPro (St. Charles, MO) Assaymax PreAlbumin ELISA Kit according to the manufacturer's protocol.

The results are shown in FIG. 6A and FIG. 6B for liver mRNA and serum protein, respectively. SNALP-18328 treated V30M hTTR transgenic mice had a dose-dependent and significant decrease in liver TTR mRNA levels relative to the PBS control group, reaching a maximum reduction of 97% ($p < 0.001$) at 3 mg/kg SNALP-18328, and a 50% reduction (ED50) at ~ 0.15 mg/kg SNALP-18328. Serum TTR protein was also suppressed in a dose-dependent manner, with a maximum reduction of serum TTR protein of 99% ($p < 0.01$) (relative to pre-dose levels) at 3 mg/kg SNALP-18328, consistent with the reduction in TTR mRNA levels. SNALP-1955 at 3 mg/kg did not have a statistically significant effect on either TTR mRNA or protein levels, compared to PBS.

These results demonstrate that SNALP-18328, when administered IV, is active in suppressing mutant V30M TTR mRNA in the transgenic mouse liver, which results in reduction of mutant V30M TTR protein in the circulation.

Example 7. Durability of TTR mRNA and protein suppression by SNALP-18328 in the transgenic mouse

To evaluate the durability of TTR mRNA and protein suppression by SNALP-18328, AD-18328 was formulated in SNALP and administered by IV bolus to V30M hTTR transgenic mice. At various timepoints post-dose, liver TTR mRNA levels and serum TTR protein levels were quantified. 8- to 12-week old V30M hTTR transgenic mice (4 animals/ group) were intravenously (IV) administered 200 µl SNALP-18328 (1 mg/kg) or SNALP-1955 (1 mg/kg, with negative control siRNA AD-1955 which targets the non-mammalian gene luciferase). Mice used were Mus musculus strain H129-hTTR KO from Institute of Molecular and Cellular Biology, Porto, Portugal. Briefly, hTTR H129 transgenic mice were crossed with a H129 endogenous TTR KO mice (null mice to generate the H129-hTTR transgenic mice, in a null mouse TTR background (Maeda, S., (2003), Use of genetically altered mice to study the role of serum amyloid P component in amyloid deposition. Amyloid Suppl. 1, 17-20). Days 3, 8, 15, or 22 post-dose, animals in both treatment groups were given a lethal dose of ketamine/xylazine. Serum samples were collected and stored at -80°C until analysis. Liver tissue was collected, flash-frozen and stored at -80°C until processing.

For TTR mRNA quantitation, frozen liver tissue was ground into powder, and lysates were prepared. TTR mRNA levels relative to those of GAPDH mRNA were determined in the lysates by using a branched DNA assay (QuantiGene Reagent System, Panomics, Fremont, CA). Briefly, the QuantiGene assay (Genospectra) was used to quantify mRNA levels in tissue sample lysates according to the manufacturer's instructions. The mean level of TTR mRNA was normalized to the mean level of GAPDH mRNA for each sample. Group means of the normalized values were then further normalized to the mean value for the PBS treated group, to obtain the relative level of TTR mRNA expression.

For TTR protein quantitation, serum was assayed using the AssayPro (St. Charles, MO) Assaymax PreAlbumin ELISA Kit according to the manufacturer's protocol.

The results are shown in FIG. 7A and FIG. 7B for liver mRNA and serum protein, respectively. A single IV bolus administration of SNALP-18328 in the hTTR V30M transgenic mouse resulted in durable inhibition of TTR mRNA levels in the liver and TTR protein levels in the serum. Compared to the control group (1 mg/ml SNALP-1955), a single IV administration of SNALP-18328 at 1 mg/kg significantly reduced relative TTR mRNA levels on Days 3, 8, 15 and 22 post-dose by 96% ($p < 0.001$), 90% ($p < 0.001$), 82% ($p < 0.001$) and 73% ($p < 0.001$), respectively, and did not return to baseline levels at termination of the study (Day 22 post-dose). Protein levels also decreased with a maximum reduction of serum TTR of 97% ($p < 0.001$) (relative to SNALP-1955) at Day 3 post-dose. At Days 8, 15, and 22 post-dose, TTR protein levels were suppressed by 72% ($p < 0.05$), 32% ($p < 0.05$), and 40% ($p < 0.001$), respectively, relative to SNALP-1955.

These results demonstrate that a single IV administration of SNALP-18328 produces durable suppression of target liver mRNA and serum protein levels in the V30M hTTR transgenic mouse, with significant reductions of both liver TTR mRNA and serum TTR protein at 22 days post-dose.

Example 8. Durability of serum TTR protein suppression by SNALP-18328 in the non-human primate

To evaluate the durability of serum TTR protein suppression by SNALP-18328, AD-18328 was formulated in SNALP and administered by IV infusion to non-human primates. At various timepoints post-dose, serum TTR protein levels were quantified.

Cynomolgus monkeys (*Macaca fascicularis*) (n= 5 animals/group for SNALP-18328 groups and n = 3 animals/group for SNALP-1955 and PBS groups) were administered a 15-minute IV infusion of SNALP-18328 (0.3, 1 or 3 mg/kg), SNALP-1955 (3 mg/kg) with negative

control siRNA AD-1955 which targets the non-mammalian gene luciferase), or PBS. At Days 0, 1, 2, 3, 4, 5, 7, 10, and 14 of the dosing phase, serum samples were collected and stored at -80°C until analysis.

Western blot analysis was used to evaluate TTR protein levels in serum samples. Serum samples from each group were pooled and diluted 1:1 with Laemmli sample buffer (β-mercaptoethanol was added at a 1:20 dilution). The samples were heated at 95°C for 10 minutes. 12.5 µl of each sample was loaded in each lane of a 10-20% Criterion (Biorad, Hercules, CA) prep gel and separated by SDS-PAGE at 120V for 1.5 hrs, then transferred to a nitrocellulose membrane using a semi-dry system at 15V for 1 hour. The membrane was blocked overnight at 4°C in LiCOR (Lincoln, NE) blocking buffer diluted 1:1 with 1X PBS. The blot was probed first with primary antibodies (goat anti-TTR from Santa Cruz (Santa Cruz, CA) at a dilution of 1:1000 diluted in LiCOR blocking buffer/PBS on a rocker for 1 hr at room temperature. Blots were washed 4X with PBS + 0.2% Tween 20 (10 minutes per wash). The fluorescent labeled secondary antibodies (anti-goat 680nm from Invitrogen (Carlsbad, CA) were added at a dilution of 1:10,000 in LiCOR blocking buffer/PBS and the blot was incubated for 1 hour at room temperature. After incubation, blots were washed 4X with PBS + 0.2% Tween 20 followed by one wash with 1X PBS. The Li-COR's Odyssey Infrared Imaging System was used to detect the protein bands. TTR monomer migrates at 15 kDa.

The results are shown in FIG. 8. Serum TTR protein levels showed a dose-dependent reduction with 1 or 3 mg/kg SNALP-18328, as compared to pre-dose (Day 0) levels. The duration of suppression, following a single IV administration of SNALP-18328 is at least 14 days after 1 or 3 mg/kg SNALP-18328 treatment.

These results demonstrate that a single IV administration of SNALP-18328 produces durable suppression of TTR protein in the circulation in the non-human primate (*Macaca fascicularis*), with significant reduction of TTR protein at 14 days post-dose.

Example 9: *In vivo* reduction of mutant (V30M) TTR in peripheral tissues by SNALP-18328 in the transgenic mouse

To evaluate the efficacy of SNALP-18328 in reducing TTR in peripheral tissues, hTTR V30M/HSF-1 knock-out mice were evaluated with immunohistochemical staining for TTR. Two-month old hTTR V30M/HSF-1 knock-out mice (Maeda, S., (2003), Use of genetically altered mice to study the role of serum amyloid P component in amyloid deposition. *Amyloid* **Suppl. 1,** 17-20) were administered an IV bolus of 3 mg/kg SNALP-18328 (12 animals), 3 mg/kg SNALP-1955 (with negative control siRNA AD-1955 which targets the non-mammalian gene luciferase, 4 animals), or PBS (4 animals) once every two weeks for a total of four doses on

days 0, 14, 28, and 42. TTR liver mRNA levels and TTR-immunoreactivity in multiple peripheral tissues were evaluated at 8 weeks post-first dose on day 56.

Mice were anesthetised with 1 mg/kg medetomidine, and given a lethal dose of ketamine. Tissues and organs of interest were collected. For immunohistochemistry, esophagus (E), stomach (S), intestine (duodenum (I1) and colon (I4)), nerve (N) and dorsal root ganglia (D) were fixed in neutral buffered formalin and embedded in paraffin. For TTR detection, rabbit anti-human TTR primary antibody (1:1000, DAKO, Denmark), and anti-rabbit biotin-conjugated secondary antibody (1:20 Sigma, USA) were followed by extravidin labelling (1:20, Sigma, USA) in order to stain for the TTR protein. The reaction was developed with 3-amino-9-ethyl carbaxole, AEC (Sigma, USA). Semi-quantitative analysis of immunohistochemical slides was performed using Scion image quant program that measures the area occupied by the substrate reaction color and normalizes this value to the total image area. Mean values of % occupied area are displayed with the corresponding standard deviation. Each animal tissue was evaluated in four different areas. The presence of human TTR in parasympathetic ganglia of the stomach and intestine was studied by double immunofluorescent staining with rabbit anti-human TTR (1:1000, DAKO, Denmark) and mouse anti-PGP9.5 (1:40, Serotec, USA) as the primary antibodies; secondary antibodies were, respectively: anti-rabbit Alexa Fluor 488 (Molecular probes, UK)and goat anti-mouse Alexa Fluor 568 (Molecular probes, UK). Slides were mounted with vectashield (Vector) and visualized in a Zeiss Cell Observer System microscope (Carl Zeiss, Germany) equipped with filters for FITC and rhodamine.

The results are graphed in FIG. 9. In contrast with PBS and SNALP-1955 treated animals, SNALP-18328 treated animals had a significant reduction of TTR-immunoreactivity in all tissues examined (esophagus (E), stomach (S), intestine (duodenum (I1) and colon (I4)), nerve (N) and dorsal root ganglia (D).

These results demonstrate that SNALP-18328 administration to hTTR V30M/HSF-1 knock-out mice causes a significant reduction of TTR protein in peripheral tissues and organs, including esophagus, stomach, intestine (duodenum and colon), nerve, and dorsal root ganglion.

Example 10. *In vivo* reduction of wild-type TTR mRNA in the non-human primate liver by XTC-SNALP-18328

To evaluate the efficacy of the novel lipid nanoparticle formulation XTC-SNALP for delivery of siRNA in non-human primate, TTR siRNA AD-18328 was formulated in XTC-SNALP (XTC-SNALP-18328) and administered by 15-minute IV infusion, and liver TTR mRNA was quantified. Cynomolgus monkeys (*Macaca fascicularis*) were administered 15-minute IV infusions of XTC-SNALP-18328 (0.03, 0.1, 0.3 or 1 mg/kg) or XTC-SNALP-1955 (1

mg/kg, with negative control siRNA AD-1955 which targets the non-mammalian gene luciferase). At forty-eight hours post-dosing, monkeys were anesthetized with sodium pentobarbital and exsanguinated. Liver tissue for TTR mRNA determination was collected, flash-frozen, and stored at -80°C until processing. Methods used for TTR mRNA quantitation in liver tissue were similar to those described in Example 5 above.

The results are shown in FIG. 10. XTC-SNALP -18328 reduced TTR mRNA levels in the liver in a dose-dependent manner, compared to the negative control XTC-SNALP -1955. The mRNA ED50 was determined to be ~ 0.1 mg/kg XTC-SNALP -18328.

These results demonstrate that XTC-SNALP-18328 is effective in suppressing wild-type TTR mRNA in non-human primate liver when administered by IV infusion.

Example 11: *In vivo* reduction of wild-type TTR mRNA in the non-human primate liver by LNP09-18328 and LNP11-18328

To evaluate the efficacy of two novel lipid nanoparticle formulations, LNP09 and LNP11, for delivery of siRNA in non-human primate, TTR siRNA AD-18328 was formulated in LNP09 (LNP09-18328) or LNP11 (LNP11-18328), and administered by 15-minute IV infusion, and liver TTR mRNA and serum TTR protein levels were assayed. Cynomolgus monkeys (*Macaca fascicularis*) were administered 15-minute IV infusions of LNP09-18328 (0.03, 0.1, or 0.3 mg/kg), LNP11-18328 (0.03, 0.1, or 0.3 mg/kg), or PBS. Liver biopsy samples were collected at 48 hrs post-dosing, flash-frozen, and stored at -80°C until processing. Serum was collected before dosing (pre-bleed), and on Days 1, 2, 4, 7, 14, 21 and 28 post-dosing and stored at -80°C until processing. Methods used for TTR mRNA quantitation in liver tissue and serum TTR protein evaluation were similar to those described in Examples 5 and 8 above.

The results are shown in FIG. 11A for mRNA, and in FIG. 11B and FIG. 11C for protein. LNP09-18328 and LNP11-18328 treated animals showed a dose-dependent decrease in TTR mRNA levels in the liver, reaching a maximum reduction at 0.3 mg/kg of ~ 85% (LNP09-18328) and ~ 90% (LNP11-18328) mRNA relative to the PBS control. The mRNA ED50 was determined to be ~ 0.02 mg/kg for both LNP09-18328 and LNP11-18328. At Day 7 post-dosing, serum samples also exhibited a dose-dependent reduction of TTR protein for 0.1 and 0.3 mg/kg LNP09-18328 and LNP11-18328, compared to PBS control levels. FIG. 11C shows a decrease in TTR protein levels with a 0.3mg/kg dose of LNP09-18328 that persisted over at least 28 days post-dosing, as compared to the PBS control group and as compared with the pre-bleed samples.

These results demonstrate that LNP09-18328 and LNP11-18328 are effective in suppressing wild-type TTR mRNA in non-human primate liver and wild-type TTR protein in the circulation, when administered by IV infusion. Furthermore, the suppression with LN09-18328 is durable, persisting for at least 28 days following the IV infusion.

Example 12. Synthesis of TTR Tiled Sequences

A set of TTR duplexes ("tiled duplexes")were designed that targeted the TTR gene near the target region of AD-18328, which targets the human TTR gene starting at nucleotide 628 of NM_000371.3.

In the examples below, the numbering representing the position of the 5' base of an siRNA on the transcript is based on NM_000371.3 (FIG. 12; SEQ ID NO:1331). In the examples shown above, the numbering for siRNA targeting human siRNA was based on NM_000371.2 (FIG. 13A). NM_000371.3 extends the sequence of the 5' UTR by 110 bases compared to NM_000371.2, as shown in FIG. 14. Thus, as an example, the starting position of AD-18328 is 628 on NM_000371.3 and 518 on NM_000371.2 (FIG. 14).

TTR tiled sequences were synthesized on MerMade 192 synthesizer at 1umol scale. For all the sequences in the list, 'endolight' chemistry was applied as detailed below.

- All pyrimidines (cytosine and uridine) in the sense strand contained 2'-O-Methyl bases (2' O-Methyl C and 2'-O-Methyl U)
- In the antisense strand, pyrimidines adjacent to(towards 5' position) ribo A nucleoside were replaced with their corresponding 2-O-Methyl nucleosides
- A two base dTdT extension at 3' end of both sense and anti sense sequences was introduced
- The sequence file was converted to a text file to make it compatible for loading in the MerMade 192 synthesis software

Synthesis, Cleavage and deprotection:

The synthesis of TTR sequences used solid supported oligonucleotide synthesis using phosphoramidite chemistry. The synthesis of the sequences was performed at 1um scale in 96 well plates. The amidite solutions were prepared at 0.1M concentration and ethyl thio tetrazole (0.6M in Acetonitrile) was used as activator. The synthesized sequences were cleaved and deprotected in 96 well plates, using methylamine in the first step and fluoride reagent in the second step. The crude sequences were precipitated using acetone: ethanol (80:20) mix and the pellet were re-suspended in 0.2M sodium acetate buffer. Samples from each sequence were analyzed by LC-MS to confirm the identity, UV for quantification and a selected set of samples by IEX chromatography to determine purity.

Purification and desalting:

TTR tiled sequences were purified on AKTA explorer purification system using Source 15Q column. A column temperature of 65C was maintained during purification. Sample injection and collection was performed in 96 well (1.8mL -deep well) plates. A single peak corresponding to the full length sequence was collected in the eluent. The purified sequences were desalted on a Sephadex G25 column using AKTA purifier. The desalted TTR sequences were analyzed for concentration (by UV measurement at A260) and purity (by ion exchange HPLC). The single strands were then submitted for annealing.

TTR Single strands and duplexes:

A detailed list of TTR tiled duplexes and corresponding single strands (sense and antisense) are shown in the table below (Table 13).

Table 13: TTR tiled duplexes and corresponding single strands

Strand: s= sense; as= antisense; Position: position of 5' base on transcript (NM_000371.3, SEQ ID NO:1331).

Duplex #	Position	Oligo #	Strand	Sequence (5' to 3")	SEQ ID NO:
AD-18323	618	A-32335	S	GGGAuuucAuGuAAccAAGdTdT	1332
		A-32336	AS	CUUGGUuAcAUGAAAUCCCdTdT	1333
AD-18324	619	A-32337	S	GGAuuucAuGuAAccAAGAdTdT	1334
		A-32338	AS	UCUUGGUuAcAUGAAAUCCdTdT	1335
AD-23000	620	A-42927	S	GAuuucAuGuAAccAAGAGdTdT	1336
		A-42928	AS	CUCUUGGUuAcAUGAAAUCdTdT	1337
AD-23001	621	A-42929	S	AuuucAuGuAAccAAGAGudTdT	1338
		A-42930	AS	ACUCUUGGUuAcAUGAAAUdTdT	1339
AD-23002	622	A-42931	S	uuucAuGuAAccAAGAGuAdTdT	1340
		A-42932	AS	uACUCUUGGUuAcAUGAAAdTdT	1341
AD-23003	623	A-42933	S	uucAuGuAAccAAGAGuAudTdT	1342
		A-42934	AS	AuACUCUUGGUuAcAUGAAdTdT	1343
AD-18325	624	A-32339	S	ucAuGuAAccAAGAGuAuudTdT	1344
		A-32340	AS	AAuACUCUUGGUuAcAUGAdTdT	1345
AD-23004	625	A-42935	S	cAuGuAAccAAGAGuAuucdTdT	1346
		A-42936	AS	GAAuACUCUUGGUuAcAUGdTdT	1347
AD-18326	626	A-32341	S	AuGuAAccAAGAGuAuuccdTdT	1348
		A-32342	AS	GGAAuACUCUUGGUuAcAUdTdT	1349
AD-18327	627	A-32343	S	uGuAAccAAGAGuAuuccAdTdT	1350
		A-32344	AS	UGGAAuACUCUUGGUuAcAdTdT	1351
AD-23005	628	A-42937	S	uAAccAAGAGuAuuccAuudTdT	1352
		A-42938	AS	AAUGGAAuACUCUUGGUuAdTdT	1353
AD-23006	629	A-42939	S	AAccAAGAGuAuuccAuuudTdT	1354
		A-42940	AS	AAAUGGAAuACUCUUGGUUdTdT	1355
AD-23007	631	A-42941	S	AccAAGAGuAuuccAuuuudTdT	1356
		A-42942	AS	AAAAUGGAAuACUCUUGGUdTdT	1357
AD-23008	632	A-42943	S	ccAAGAGuAuuccAuuuuudTdT	1358

Duplex #	Position	Oligo #	Strand	Sequence (5' to 3")	SEQ ID NO:
		A-42944	AS	AAAAAUGGAAuACUCUUGGdTdT	1359
AD-23009	633	A-42945	S	cAAGAGuAuuccAuuuuuAdTdT	1360
		A-42946	AS	uAAAAAUGGAAuACUCUUGdTdT	1361
AD-23010	634	A-42947	S	AAGAGuAuuccAuuuuuAcdTdT	1362
		A-42948	AS	GuAAAAAUGGAAuACUCUUdTdT	1363
AD-23011	635	A-42949	S	AGAGuAuuccAuuuuuAcudTdT	1364
		A-42950	AS	AGuAAAAAUGGAAuACUCUdTdT	1365
AD-23012	636	A-42951	S	GAGuAuuccAuuuuuAcuAdTdT	1366
		A-42952	AS	uAGuAAAAAUGGAAuACUCdTdT	1367
AD-23013	637	A-42953	S	AGuAuuccAuuuuuAcuAAdTdT	1368
		A-42954	AS	UuAGuAAAAAUGGAAuACUdTdT	1369
AD-23014	638	A-42955	S	GuAuuccAuuuuuAcuAAAdTdT	1370
		A-42956	AS	UUuAGuAAAAAUGGAAuACdTdT	1371
AD-23015	639	A-42957	S	uAuuccAuuuuuAcuAAAGdTdT	1372
		A-42958	AS	CUUuAGuAAAAAUGGAAuAdTdT	1373
AD-23016	640	A-42959	S	AuuccAuuuuuAcuAAAGcdTdT	1374
		A-42960	AS	GCUUuAGuAAAAAUGGAAUdTdT	1375
AD-23017	641	A-42961	S	uuccAuuuuuAcuAAAGcAdTdT	1376
		A-42962	AS	UGCUUuAGuAAAAAUGGAAdTdT	1377
AD-23018	642	A-42963	S	uccAuuuuuAcuAAAGcAGdTdT	1378
		A-42964	AS	CUGCUUuAGuAAAAAUGGAdTdT	1379
AD-23019	643	A-42965	S	ccAuuuuuAcuAAAGcAGudTdT	1380
		A-42966	AS	ACUGCUUuAGuAAAAAUGGdTdT	1381
AD-23020	644	A-42967	S	cAuuuuuAcuAAAGcAGuGdTdT	1382
		A-42968	AS	cACUGCUUuAGuAAAAAUGdTdT	1383
AD-23021	645	A-42969	S	AuuuuuAcuAAAGcAGuGudTdT	1384
		A-42970	AS	AcACUGCUUuAGuAAAAAUdTdT	1385
AD-23022	646	A-42971	S	uuuuuAcuAAAGcAGuGuudTdT	1386
		A-42972	AS	AAcACUGCUUuAGuAAAAAdTdT	1387
AD-23023	647	A-42973	S	uuuuAcuAAAGcAGuGuuudTdT	1388
		A-42974	AS	AAAcACUGCUUuAGuAAAAdTdT	1389
AD-23024	648	A-42975	S	uuuAcuAAAGcAGuGuuuudTdT	1390
		A-42976	AS	AAAAcACUGCUUuAGuAAAdTdT	1391
AD-23025	649	A-42977	S	uuAcuAAAGcAGuGuuuucdTdT	1392
		A-42978	AS	GAAAAcACUGCUUuAGuAAdTdT	1393
AD-23026	650	A-42979	S	uAcuAAAGcAGuGuuuucAdTdT	1394
		A-42980	AS	UGAAAAcACUGCUUuAGuAdTdT	1395
AD-23027	651	A-42981	S	AcuAAAGcAGuGuuuucAcdTdT	1396
		A-42982	AS	GUGAAAAcACUGCUUuAGUdTdT	1397
AD-23028	652	A-42983	S	cuAAAGcAGuGuuuucAccdTdT	1398
		A-42984	AS	GGUGAAAAcACUGCUUuAGdTdT	1399
AD-18330	653	A-32349	S	uAAAGcAGuGuuuucAccudTdT	1400
		A-32350	AS	AGGUGAAAAcACUGCUUuAdTdT	1401
AD-23029	654	A-42985	S	AAAGcAGuGuuuucAccucdTdT	1402
		A-42986	AS	GAGGUGAAAAcACUGCUUUdTdT	1403
AD-23030	655	A-42987	S	AAGcAGuGuuuucAccucAdTdT	1404
		A-42988	AS	UGAGGUGAAAAcACUGCUUdTdT	1405
AD-23031	656	A-42989	S	AGcAGuGuuuucAccucAudTdT	1406
		A-42990	AS	AUGAGGUGAAAAcACUGCUdTdT	1407

Duplex #	Position	Oligo #	Strand	Sequence (5' to 3")	SEQ ID NO:
AD-18328	628	A-32345	S	GuAAccAAGAGuAuuccAudTdT	1408
		A-32346	AS	AUGGAAuACUCUUGGUuACdTdT	1409

Example 13. *In vitro* Screening of TTR Tiled siRNAs

Tiled TTR duplexes were assayed in Hep3B cells for inhibition of endogenous TTR expression using real time PCR assays.

Cell culture and transfection: 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 (EMEM, ATCC) supplemented with 10% FBS, streptomycin, and glutamine (ATCC) before being released from the plate by trypsinization. Reverse transfection was carried out by adding 5µl of Opti-MEM to 5µl of each siRNA in individual wells of a 96-well plate. To this 10µl of Opti-MEM plus 0.2µl of Lipofectamine RNAiMax was added per well (Invitrogen, Carlsbad CA. cat # 13778-150) and the mixture was incubated at room temperature for 15 minutes. 80µl of complete growth media described above, but without antibiotic containing 2.0 x10^4 Hep3B cells were then added. Cells were incubated for 24 hours prior to RNA purification. Experiments were performed at 0.1 or 10nM final duplex concentration.

Total RNA isolation using MagMAX-96 Total RNA Isolation Kit (Applied Biosystems, Foster City CA, part #: AM1830): Cells were harvested and lysed in 140µl of Lysis/Binding Solution then mixed for 1 minute at 850rpm using and Eppendorf Thermomixer (the mixing speed was the same throughout the process). Twenty micro liters of magnetic beads and Lysis/Binding Enhancer mixture were added into cell-lysate and mixed for 5 minutes. Magnetic beads were captured using magnetic stand and the supernatant was removed without disturbing the beads. After removing supernatant, magnetic beads were washed with Wash Solution 1 (isopropanol added) and mixed for 1 minute. Beads were capture again and supernatant removed. Beads were then washed with 150µl Wash Solution 2 (Ethanol added), captured and supernatant was removed. 50µl of DNase mixture (MagMax turbo DNase Buffer and Turbo DNase) was then added to the beads and they were mixed for 10 to 15 minutes. After mixing, 100µl of RNA Rebinding Solution was added and mixed for 3 minutes. Supernatant was removed and magnetic beads were washed again with 150µl Wash Solution 2 and mixed for 1 minute and supernatant was removed completely. The magnetic beads were mixed for 2 minutes to dry before RNA was eluted with 50µl of water.

cDNA synthesis using ABI High capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA, Cat #4368813): A master mix of 2µl 10X Buffer, 0.8µl 25X

dNTPs, 2μl Random primers, 1μl Reverse Transcriptase, 1μl RNase inhibitor and 3.2μl of H2O per reaction were added into 10μl total RNA. cDNA was generated using a Bio-Rad C-1000 or S-1000 thermal cycler (Hercules, CA) through the following steps: 25°C 10 min, 37°C 120 min, 85°C 5 sec, 4°C hold.

Real time PCR: 2 μl of cDNA were added to a master mix containing 0.5μl GAPDH TaqMan Probe (Applied Biosystems Cat # 4326317E), 0.5μl TTR TaqMan probe (Applied Biosystems cat #HS00174914 M1) and 10μl Roche Probes Master Mix (Roche Cat # 04887301001) per well in a LightCycler 480 384 well plate (Roche cat # 0472974001). Real time PCR was done in a LightCycler 480 Real Time PCR machine (Roche). Each duplex was tested in two independent transfections and each transfection was assayed in duplicate.

Real time data were analyzed using the ΔΔCt method. Each sample was normalized to GAPDH expression and knockdown was assessed relative to cells transfected with the non-targeting duplex AD-1955. Table 14 shows the knockdown of TTR using the siRNAs. Data are expressed as the percent of message remaining relative to cells targeted with AD-1955.

Many but not all tiled TTR-dsRNAs, targeting TTR near the target of AD-18328, reduced TTR mRNA by at least 70% when transfected into Hep3B cells at 0.1 nM.

Table 14: Inhibition of TTR by tiled dsRNA targeting TTR near target of AD-18328.

Duplex #	% message remaining 0.1nM	% SD 0.1nM	% message remaining 10nM	% SD 10nM
AD-18323	6.7	1.90	1.7	0.02
AD-18324	1.8	0.58	0.9	0.10
AD-23000	5.5	0.93	2.1	0.87
AD-23001	15.2	4.89	4.9	1.74
AD-23002	3.1	1.12	1.4	0.55
AD-23003	17.3	3.13	1.7	0.06
AD-18325	1.5	0.27	1.4	0.66
AD-23004	9.0	0.15	10.5	0.96
AD-18326	22.0	1.85	7.6	0.78
AD-18327	11.6	2.64	9.6	1.67
AD-18328	1.1	0.70	0.6	0.16
AD-23005	0.8	0.31	0.6	0.21
AD-23006	1.5	0.46	1.2	0.43
AD-23007	2.4	0.91	1.9	0.46
AD-23008	0.6	0.10	0.8	0.26
AD-23009	1.0	0.13	0.9	0.22
AD-23010	60.1	15.66	66.2	22.71
AD-23011	56.5	16.99	53.6	4.70
AD-23012	7.7	2.36	7.7	3.25

Duplex #	% message remaining 0.1nM	% SD 0.1nM	% message remaining 10nM	% SD 10nM
AD-23013	7.0	0.64	8.0	1.06
AD-23014	0.7	0.01	0.6	0.10
AD-23015	15.4	0.25	16.5	7.07
AD-23016	27.1	0.37	6.7	1.80
AD-23017	4.5	1.26	1.4	0.40
AD-23018	44.6	9.45	7.5	1.09
AD-23019	2.2	0.68	0.8	0.10
AD-23020	52.7	6.45	29.7	1.17
AD-23021	95.4	16.16	45.0	3.00
AD-23022	70.1	3.01	60.8	12.11
AD-23023	2.7	1.12	1.8	0.07
AD-23024	1.7	0.30	1.8	0.33
AD-23025	64.2	13.21	10.5	1.34
AD-23026	1.9	0.15	1.9	0.78
AD-23027	2.5	0.21	1.6	0.49
AD-23028	6.7	4.41	1.2	0.50
AD-18330	6.0	0.56	5.7	1.15
AD-23029	4.5	0.47	1.6	0.10
AD-23030	3.9	0.25	3.3	0.84
AD-23031	3.4	0.78	1.7	0.02

Example 14. Evaluation of Infusion Duration on Efficacy of a Single Intravenous Administration of SNALP-18534 in Sprague-Dawley Rats

Objectives

To determine the effect of infusion duration on efficacy of a single IV infusion of SNALP-18534 on liver TTR mRNA levels in Sprague-Dawley rats.

Table 15: Abbreviations and definitions used

SNALP-18534	Rodent transthyretin specific siRNA formulated in SNALP
SNALP-1955	Non-mammalian luciferase specific siRNA formulated in SNALP

The sequences of the sense and antisense strands of AD-18534 are reproduced below from the tables above:

Strand	Oligo #	Position	Sequence 5′ to 3′	SEQ ID NO:
s	A-32755	532	cAGuGuucuuGcucuAuAAdTdT	1289
as	A-32756	550	UuAuAGAGcAAGAAcACUGdTdT	1290

Study Materials

Test Article(s)

SNALP-18534 is comprised of an siRNA targeting rodent TTR mRNA (AD-18534), formulated in stable nucleic acid lipid particles (SNALP) for delivery to target tissues. The SNALP formulation (lipid particle) consists of a novel aminolipid (DLinDMA), a PEGylated lipid (mPEG2000-C-DMA), a neutral lipid (DPPC) and cholesterol. The ratio of lipid:nucleic acid in the SNALP formulation is approximately 5.8:1 (w:w). SNALP-1955 contains an siRNA targeting the non-mammalian luciferase mRNA, is formulated with the identical lipid particle as SNALP-18534, and serves as a non-pharmacologically active control. Dose levels are expressed as mg/kg based on the weight of siRNA content.

Study Design & Procedures

Animals and test article administration:

The study was comprised of 9 groups of Sprague-Dawley rats (4 males/ group). The animals were allowed to have at least a 2 day acclimation period before the study and all animals were 7 weeks old at the initiation of dosing. The dose administered was calculated based upon body weight data collected prior to dosing on Day 1. The test and control articles were administered as a single 15-minute, 1-hour, 2-hour, or 3-hour IV infusion via the tail vein using a 24G ¾" cannula sealed with a Baxter Injection Site septum connected via 27G Terumo butterfly needle to a Baxter AS40A Syringe Pump. The dose volume was 3 ml/kg, the infusion rate was 12 ml/kg/hr, and animals were freely moving in the cages during dosing. Rats were divided into nine treatment groups and administered a single IV infusion of SNALP-18534, SNALP-1955, or PBS as shown in Table 16:

Table 16: Test Animal Dosage Groups

Group	N	Test Article	Infusion Duration	Dose
A	4	PBS	15 minute	---
B	4	PBS	3 hour	---
C	4	SNALP -1955	1 hour	1 mg/kg
D	4	SNALP -1955	2 hour	1 mg/kg
E	4	SNALP -1955	3 hour	1 mg/kg
F	4	SNALP-18534	15 minute	1 mg/kg
G	4	SNALP-18534	1 hour	1 mg/kg
H	4	SNALP-18534	2 hour	1 mg/kg
I	4	SNALP-18534	3 hour	1 mg/kg

Tissue collection and RNA isolation:

On Day 0, animals were anesthetized by isofluorane inhalation and pre-dosing blood samples were collected into serum separator tubes by retro-orbital bleed. The blood samples were allowed to clot at room temperature for approximately 30 minutes prior to centrifugation at 4°C. Serum samples were then stored at -80°C until analysis was performed. On Day 3, animals in all nine treatment groups were given a lethal dose of ketamine/xylazine. Blood was collected via caudal vena cava into serum separation tubes, and then allowed to clot at room temperature for approximately 30 minutes prior to centrifugation at 4°C. Serum samples were stored at -80°C until analysis was performed. Liver tissue was harvested and snap frozen on dry ice. Frozen liver tissue was ground and tissue lysates were prepared for liver mRNA quantitation.

TTR mRNA Quantitation:

TTR mRNA levels relative to those of GAPDH mRNA were determined in the lysates by using a branched DNA assay (QuantiGene Reagent System, Panomics, Fremont, CA). Briefly, the QuantiGene assay (Genospectra) was used to quantify mRNA levels in tissue sample lysates according to the manufacturer's instructions. The mean level of TTR mRNA was normalized to the mean level of GAPDH mRNA for each sample.

To obtain the relative level of TTR mRNA expression, group mean values for SNALP-1955 and SNALP-18534 treated groups with 15-minute, 1 hour and 2 hour infusion durations were then normalized to the mean value for the PBS treated group with 15-minute infusion whereas group mean values for SNALP-1955 and SNALP-18534 treated groups with 3 hour infusion duration were then normalized to the mean value for the PBS treated group with 3 hour infusion duration.

Results

As shown in FIG. 16, a single IV infusion of 1 mg/kg SNALP-18534 with different infusion durations of 15 minutes to 3 hours results in comparable inhibition of liver TTR mRNA levels measured two days after dosing. A single IV infusion of 1 mg/kg SNALP-18534 also showed durable TTR downregulation over 29 days following a single 15 minute IV infusion, as compared to SNALP-1955 control (data not shown). Compared to the PBS-treated group, a single 15-minute, 1-hour, 2-hour, or 3-hour IV infusion of SNALP-18534 at 1 mg/kg significantly reduced relative TTR mRNA expression levels by 94% ($p<0.001$), 94% ($p < 0.001$), 92% ($p < 0.001$) and 93% ($p < 0.001$), respectively. Specificity of SNALP-18534 activity is demonstrated by lack of significant target inhibition by SNALP-1955 administration via 1-hour, 2-hour, or 3-hour IV infusion at the same dose level.

Conclusions

This study demonstrates that varying the infusion duration from 15 minutes to up to 3 hours does not affect the efficacy of a single IV administration of 1 mg/kg SNALP-18534 in rats, as assessed by reduction of TTR mRNA levels in the liver.

Example 15. *In vivo* reduction of wild-type TTR mRNA in the rat liver by LNP07-18534 and LNP08-18534

To evaluate the efficacy of 2 novel lipid nanoparticle formulations, LNP07 and LNP08, for delivery of siRNA in the rat, the rodent-specific TTR siRNA, AD-18534, was formulated in LNP07 (LNP07-18534) or LNP08 (LNP08-18534), and administered by 15-minute IV infusion, and liver TTR mRNA was quantified. Sprague-Dawley rats (4 animals per group) were administered 15-minute IV infusions of LNP07-18534 (0.03, 0.1, 0.3 or 1 mg/kg), LNP08-18534 (0.01, 0.03 or 0.1 mg/kg), or LNP07-1955 (1 mg/kg) or LNP08-1955 (0.1 mg/kg) containing the negative control siRNA AD-1955 which targets the non-mammalian gene luciferase. Forty-eight hours later, animals were euthanized and liver tissue was collected, flash-frozen and stored at -80°C until processing.

For TTR mRNA quantitation, frozen liver tissue was ground into powder, and lysates were prepared. TTR mRNA levels relative to those of GAPDH mRNA were determined in the lysates by using a branched DNA assay (QuantiGene Reagent System, Panomics, Fremont, CA). Briefly, the QuantiGene assay (Genospectra) was used to quantify mRNA levels in tissue sample lysates according to the manufacturer's instructions. The mean level of TTR mRNA was normalized to the mean level of GAPDH mRNA for each sample. Group means of the normalized values were then further normalized to the mean value for the PBS treated group, to obtain the relative level of TTR mRNA expression.

The results are shown in FIG. 17. LNP07-18534 reduced TTR mRNA levels in the liver in a dose-dependent manner, with 94% suppression of TTR mRNA at 1 mg/kg. The effect was specific, since the negative control LNP07-1955 at 1 mg/kg did not significantly affect TTR mRNA levels compared to the PBS control. The mRNA ED50 was determined to be ~ 0.05 mg/kg LNP07-18534. LNP08-18534 reduced TTR mRNA levels in the liver in a dose-dependent manner, with 86% suppression of TTR mRNA at 0.1 mg/kg. The effect was specific, since the negative control LNP08-1955 at 0.1 mg/kg did not significantly affect TTR mRNA levels compared to the PBS control. The mRNA ED50 was determined to be ~ 0.02 mg/kg LNP08-18534.

These results demonstrate that LNP07-18534 and LNP08-18534 are effective in suppressing wild-type TTR mRNA in the rat liver when administered by IV infusion, and that LNP07 and LNP08 are effective formulations for delivering siRNA to the liver.

Example 16: Reduction of TTR liver mRNA by a single intravenous administration of LNP09-18534 or LNP11-18534 in Sprague-Dawley Rats

Objective:

To evaluate the efficacy of two novel lipid nanoparticle (LNP) formulations for delivery of the rodent TTR-specific siRNA, AD-18534 in the Sprague-Dawley rat for reducing endogenous (wild type) liver TTR mRNA levels. Rats were intravenously dosed via a 15 minute infusion with either 0.01, 0.03, 0.1, or 0.3 mg/kg LNP09-18534, LNP11-18534, or phosphate buffered saline (PBS) and TTR liver mRNA levels were assayed at 48 hrs post-treatment.

Material and Methods:

LNP09 formulation: (XTC/DSPC/Chol/PEG_{2000}-C14) = 50/10/38.5/1.5 mol%; Lipid:siRNA ~ 11:1. LNP11 formulation: (MC3/DSPC/Chol/PEG_{2000}-C14) = 50/10/38.5/1.5 mol%; Lipid:siRNA ~ 11.1

Tissue collection and RNA isolation: On Day 3, animals in all treatment groups were given a lethal dose of ketamine/xylazine. Blood was collected via caudal vena cava into serum separation tubes, and then allowed to clot at room temperature for approximately 30 minutes prior to centrifugation at 4°C. Serum samples were stored at -80°C until for future analysis. Liver tissues were harvested and snap frozen on dry ice. Frozen liver tissue was ground and tissue lysates were prepared for liver mRNA quantitation.

TTR mRNA Quantitation: TTR mRNA levels relative to those of GAPDH mRNA were determined in the lysates by using a branched DNA assay (QuantiGene Reagent System, Panomics, Fremont, CA). Briefly, the QuantiGene assay (Genospectra) was used to quantify mRNA levels in tissue sample lysates according to the manufacturer's instructions. The mean level of TTR mRNA was normalized to the mean level of GAPDH mRNA for each sample. Group mean values were then normalized to the mean value for the PBS treated group, to obtain the relative level of TTR mRNA expression.

Results:

As shown in FIG. 18, in contrast with PBS treated animals, LNP09-18534 and LNP11-18534 treated animals had a significant dose-dependent decrease in TTR mRNA levels in the liver, reaching maximum reduction of ~ 90% mRNA reduction for both LNP09 and LNP11

formulated groups, relative to PBC control group at 0.3 mg/kg, and a dose achieving 50% reduction (ED_{50}) of < 0.03 mg/kg for LNP11-18534 and < 0.1 mg/kg for LNP09-18534.

Conclusions

This study demonstrates that a single 15 minute IV infusion of LNP09-18534 or LNP11-18534 in Sprague-Dawley rats results in a dose-dependent reduction of liver TTR mRNA. These data demonstrate the efficacy of LNP09-18328 and LNP11-18328 in reducing endogenously expressed (wild type) TTR mRNA with ED50 levels of <0.03 and <0.1 mg/kg for LNP11-18534 and LNP09-18534, respectively.

Example 17: Inhibition of TTR in humans

A human subject is treated with a dsRNA targeted to a TTR gene to inhibit expression of the TTR gene to treat a condition.

A subject in need of treatment is selected or identified. The subject can have a liver disorder, transthyretin amyloidosis, and/or a transplanted liver.

The identification of the subject can occur in a clinical setting, or elsewhere, e.g., in the subject's home through the subject's own use of a self-testing kit.

At time zero, a suitable first dose of an anti-TTR siRNA is administered to the subject. The dsRNA is formulated as described herein. After a period of time following the first dose, e.g., 7 days, 14 days, and 21 days, the subject's condition is evaluated, e.g., by measuring liver function. This measurement can be accompanied by a measurement of TTR expression in said subject, and/or the products of the successful siRNA-targeting of TTR mRNA. Other relevant criteria can also be measured. The number and strength of doses are adjusted according to the subject's needs.

After treatment, the subject's tumor growth rate is lowered relative to the rate existing prior to the treatment, or relative to the rate measured in a similarly afflicted but untreated subject.

CLAIMS

1. A double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR), wherein said dsRNA comprises a sense strand and an antisense strand, the antisense strand comprising a region complementary to a part of a mRNA encoding transthyretin (TTR), wherein said region of complementarity is 19 nucleotides in length, the antisense strand comprises SEQ ID NO:170, and each strand of the dsRNA is 19, 20, 21, 22, 23, or 24 nucleotides in length; and wherein the dsRNA is formulated in a lipid formulation comprising a cationic lipid, a non-cationic lipid, and a lipid that prevents aggregation of a particle.

2. The dsRNA of claim 1, wherein said cationic lipid is (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino) butanoate (MC3).

3. The dsRNA of claim 1, wherein said non-cationic lipid is distearoylphosphatidylcholine (DSPC).

4. The dsRNA of claim 1, wherein said lipid that prevents aggregation of the particle is a polyethyleneglycol (PEG)-lipid.

5. The dsRNA of any one of claims 1 to 4, wherein the lipid formulation further comprises cholesterol.

6. The dsRNA of claim 1, wherein the lipid formulation comprises MC3, DSPC, cholesterol and PEG_{2000}-C14.

7. The dsRNA of claim 1, wherein the lipid formulation comprises MC3/DSPC/cholesterol/PEG_{2000}-C14 in a ratio of about 50/10/38.5/1.5 mol%.

8. The dsRNA of any one of claims 1 to 7, wherein

   (a) the sense strand consists of SEQ ID NO:449 and the antisense strand consists of SEQ ID NO:450;

(b) the sense strand consists of SEQ ID NO:729 and the antisense strand consists of SEQ ID NO:730; or

(c) the sense strand consists of SEQ ID NO:1009 and the antisense strand consists of SEQ ID NO:1010.

9. The dsRNA of any one of claims 1 to 7, wherein the sense strand comprises SEQ ID NO:169.

10. The dsRNA of any one of claims 1 to 7, wherein said dsRNA comprises at least one modified nucleotide, wherein preferably at least one of said modified nucleotides is chosen from the group of: a 2'-O-methyl modified nucleotide, a nucleotide comprising a 5'-phosphorothioate group, a terminal nucleotide linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group, a 2'-deoxy-2'-fluoro modified nucleotide, a 2'-deoxy-modified nucleotide, a locked nucleotide, an abasic nucleotide, 2'-amino-modified nucleotide, 2'-alkyl-modified nucleotide, morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide.

11. The dsRNA of any one of claims 1 to 7, wherein said dsRNA comprises at least one modified nucleotide, wherein said nucleotide is a 2'-O-methyl modified nucleotide.

12. The dsRNA of any one of claims 1 to 11, wherein the dsRNA is conjugated to a ligand.

13. A pharmaceutical composition for inhibiting expression of a TTR gene comprising the dsRNA of claims 1 to 12 and a pharmaceutically acceptable carrier.

14. A method of inhibiting TTR expression in a cell, the method comprising:

(a) contacting the cell with the dsRNA of claims 1 to 12; and

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

provided that any method of treatment of the human or animal body by therapy is

excluded.

15. A dsRNA of claims 1 to 12 for use in treating in a human a disorder mediated by TTR expression, wherein

(a) the human has transthyretin amyloidosis; and/or

(b) the human has a liver disorder

wherein said transthyretin amyloidosis is preferably selected from familial amyloidotic polyneuropathy (FAP), familial amyloidotic cardiomyopathy (FAC), leptomeningeal/CNS amyloidosis, senile systemic amyloidosis (SSA) and senile cardiac amyloidosis (SCA).

16. The dsRNA for use of claim 15, wherein said dsRNA is to be administered to the human at about 0.01, 0.1, 0.2, 0.3, 0.4, 0.5, 0.543, 0.59, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 2.5, or 5.0 mg/kg.

17. The dsRNA for use of claim 15 or 16, wherein the human is to be additionally receiving a therapeutic for treating a TTR amyloidosis, the therapeutic selected from the group consisting of diuretics, angiotensin converting enzyme inhibitors, angiotensin receptor blockers, dialysis, or a liver transplant.

18. The dsRNA for use of any one of claims 15 to 17, wherein the dsRNA is to be administered to the human at not more than 1, 2, 3, or 4 week intervals.

19. The dsRNA for use of any one of claims 15 to 18, wherein said dsRNA is to be administered intravenously or by intravenous infusion over 15 minutes time.

20. A use of a dsRNA of claims 1 to 12 in the manufacture of a medicament for the treatment of a human disorder mediated by TTR expression selected from transthyretin amyloidosis; and/or

the human has a liver disorder;

wherein said transthyretin amyloidosis is preferably selected from familial amyloidotic polyneuropathy (FAP), familial amyloidotic cardiomyopathy (FAC),

leptomeningeal/CNS amyloidosis, senile systemic amyloidosis (SSA) and senile cardiac amyloidosis (SCA).

21. The use of claim 20, wherein said dsRNA is to be administered to the human at about 0.01, 0.1, 0.2, 0.3, 0.4, 0.5, 0.543, 0.59, 0.6, 0.7, 0.8, 0.9, 1.0, 1.1, 1.2, 1.3, 1.4, 2.5, or 5.0 mg/kg.

22. The use of claim 20 or 21, wherein the human is additionally receiving a therapeutic method for treating a TTR amyloidosis, the therapeutic method selected from the group consisting of diuretics, angiotensin converting enzyme inhibitors, angiotensin receptor blockers, dialysis, or a liver transplant.

23. The use of any one of claims 20 to 22, wherein the dsRNA is to be administered to the human at not more than 1, 2, 3, or 4 week intervals.

24. The use of any one of claims 20 to 22, wherein the dsRNA is to be administered every 3 weeks.

25. The use of any one of claims 20 to 23, wherein said dsRNA is to be administered intravenously or by intravenous infusion over 15 minutes time.

26. An *in vitro* method of inhibiting TTR expression in a cell, the method comprising:
(a) contacting the cell with a composition comprising a double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR) and a lipid formulation, wherein the dsRNA comprises a sense strand and an antisense strand comprising a region complementary to an mRNA encoding transthyretin (TTR), wherein the region of complementarity comprises SEQ ID NO:170 and each strand is 19, 20, 21, 22, 23, or 24 nucleotides in length, the lipid formulation comprising the lipid (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3); and
(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of a TTR gene, thereby inhibiting expression of the TTR gene

in the cell.

27 An *in vitro* method of inhibiting TTR expression in a cell, the method comprising:
(a) contacting the cell with a composition comprising a double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR) and a lipid formulation, wherein the dsRNA comprises a sense strand and an antisense strand comprising a region complementary to an mRNA encoding transthyretin (TTR), wherein the region of complementarity comprises SEQ ID NO:170, the lipid formulation comprising the lipid (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino)butanoate (MC3), wherein each strand is 21 nucleotides in length; and
(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of a TTR gene, thereby inhibiting expression of the TTR gene in the cell.

28. An *in vitro* method of inhibiting TTR expression in a cell, the method comprising:
(a) contacting the cell with a double-stranded ribonucleic acid (dsRNA) for inhibiting expression of transthyretin (TTR), wherein the dsRNA comprises a sense strand and an antisense strand, the antisense strand comprising a region complementary to an mRNA encoding transthyretin (TTR), wherein the region of complementarity comprises SEQ ID NO:170 and each strand of the dsRNA is 19, 20, 21, 22, 23, or 24 nucleotides in length; and
(b) maintaining the cell produced in step (a) for a time sufficient to obtain degradation of the mRNA transcript of a TTR gene, thereby inhibiting expression of the TTR gene in the cell.

29. The method of claim 28, wherein the region of complementarity consists of SEQ ID NO:170.

30. The method of claim 28, wherein
(a) the sense strand consists of SEQ ID NO:449 and the antisense strand consists of SEQ ID NO:450;
(b) the sense strand consists of SEQ ID NO:729 and the antisense strand consists of

SEQ ID NO:730; or

(c) the sense strand consists of SEQ ID NO:1009 and the antisense strand consists of SEQ ID NO:1010 and the dsRNA is formulated in a lipid formulation.

31. The method of claim 28, wherein each strand is 21 nucleotides in length.

32. The method of claim 28, wherein the dsRNA comprises at least one modified nucleotide.

33. The method of claim 28, wherein the dsRNA comprises at least one modified nucleotide chosen from the group of: a 2′-O-methyl modified nucleotide, a nucleotide comprising a 5′-phosphorothioate group, a terminal nucleotide linked to a cholesteryl derivative or dodecanoic acid bisdecylamide group, a 2′-deoxy-2′-fluoro modified nucleotide, a 2′-deoxy-modified nucleotide, a locked nucleotide, an abasic nucleotide, 2′-amino-modified nucleotide, 2′-alkyl-modified nucleotide, morpholino nucleotide, a phosphoramidate, and a non-natural base comprising nucleotide.

34. The method of claim 28, wherein the dsRNA comprises at least one 2′-O-methyl modified nucleotide.

35. The method of claim 28, wherein the dsRNA is conjugated to a ligand.

36. The method of claim 28 or 31, wherein the dsRNA is formulated in a lipid formulation.

37. The method of claim 28 or 31, wherein the dsRNA is formulated in a lipid formulation comprising MC3.

38. The method of claim 28, wherein contacting the cell with the dsRNA results in at least one of the following:

a) about 95% inhibition of TTR mRNA expression as measured by a real time PCR assay, wherein the cell is a HepG2 cell or a Hep3B cell, and the dsRNA concentration

is 10 nM;

b) about 74% inhibition of TTR mRNA expression as measured by a branched DNA assay, wherein the cell is a HepG2 cell or a Hep3B cell and the dsRNA concentration is 10 nM;

c) the dsRNA has an IC50 of less than 10 pM in a HepG2 cell and the dsRNA concentration is 10 nM;

d) the dsRNA has an ED50 of about 1 mg/kg;

e) the dsRNA reduces TTR expression by 98.9% as measured by real-time PCR in a Hep3B cell and the dsRNA concentration is 0.1 nM;

f) the dsRNA reduces TTR expression by 99.4% as measured by real-time PCR in a Hep3B cell and the dsRNA concentration is 10 nM.

39. The method of claim 28, wherein the sense strand consists of SEQ ID NO:1009 and the antisense strand consists of SEQ ID NO:1010 and the dsRNA is lipid formulated in a formulation comprising MC3.