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(54) **Title:** NUCLEIC ACIDS FOR INHIBITING EXPRESSION OF *LPA* IN A CELL

(57) **Abstract:** The present invention relates to products and compositions and their uses. In particular the invention relates to nucleic acid products that interfere with the *LPA* gene expression or inhibit its expression, preferably for use as treatment, prevention or reduction of risk of suffering cardiovascular disease such as coronary heart disease or aortic stenosis or stroke or any other disorder, pathology or syndrome linked to elevated levels of Lp(a) particles.

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Nucleic acids for inhibiting expression of *LPA* in a cell

Field of the invention

The present invention relates to products and compositions and their uses. In particular the invention relates to nucleic acid products that interfere with the *LPA* gene expression or inhibit its expression. Such therapeutic Lp(a) lowering therapy serves to prevent and reduce the risk of suffering stroke, atherosclerosis, thrombosis and cardiovascular diseases such as coronary heart disease and aortic stenosis or any other disorder, pathology or syndrome linked to elevated levels of Lp(a) particles.

Background

Double stranded RNAs (dsRNA) able to complementarily bind expressed mRNA have been shown to be able to block gene expression (Fire et al., 1998, Nature. 1998 Feb 19;391(6669):806-11 and Elbashir et al., 2001, Nature. 2001 May 24;411(6836):494-8) by a mechanism that has been termed RNA interference (RNAi). Short dsRNAs direct gene specific, post transcriptional silencing in many organisms, including vertebrates, and have become a useful tool for studying gene function. RNAi is mediated by the RNA induced silencing complex (RISC), a sequence specific, multi component nuclease that degrades messenger RNAs homologous to the silencing trigger loaded into the RISC complex. Interfering RNA (termed herein iRNA) such as siRNAs, antisense RNAs, and micro RNAs are oligonucleotides that prevent the formation of proteins by gene silencing i.e. inhibiting gene translation of the protein through degradation of mRNA molecules. Gene silencing agents are becoming increasingly important for therapeutic applications in medicine.

According to Watts and Corey in the Journal of Pathology (2012; Vol 226, p 365 379) there are algorithms that can be used to design nucleic acid silencing triggers, but all of these have severe limitations. It may take various experimental methods to identify potent iRNAs, as algorithms do not take into account factors such as tertiary structure of the target mRNA or the involvement of RNA binding proteins. Therefore, the discovery of a potent nucleic acid silencing trigger with minimal off target effects is a complex process. For the pharmaceutical development of these highly charged molecules it is necessary that they can be synthesised economically, distributed to target tissues, enter cells and function within acceptable limits of toxicity.

Lp(a) particles are heterogeneous low-density lipoprotein particles expressed predominantly in the liver (Witztum and Ginsberg, J Lipid Res. 2016 Mar;57(3):336-9). They are composed of Apolipoprotein(a) (Apo(a) or Lp(a) encoded by the *LPA* gene) linked to an LDL-like particle via the ApoB poly-peptide. Genetically defined high Lp(a) particle serum levels are unaffected by diet and exercise and are associated to increased risk to suffer from cardiovascular disease through the associated atherosclerotic potential (Alonso et al., Journal of the American College of Cardiology Vol. 63, No. 19, 2014). In terms of diagnostics and preventive medicine the patient's serum level of Lp(a) particles is a highly prevalent, independent, genetic risk factor for coronary heart disease and aortic stenosis (Saeedi and Frohlich Clinical Diabetes and Endocrinology (2016) 2:7). There is no current approved specific Lp(a) particle reduction therapy beyond indirect standard general LDL-lowering measures. Accordingly, methods for effective treatment, prevention and reduction of risk of suffering from disorders such as and associated with stroke, atherosclerosis, thrombosis and cardiovascular diseases such as coronary heart disease, aortic stenosis and other yet unidentified associated disorders, pathologies or syndromes are currently needed. The present invention addresses this unmet medical need.

Summary of the invention

One aspect of the invention relates to a nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of a RNA transcribed from the *LPA* gene, wherein said first strand comprises a nucleotide sequence selected from the following sequences: SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43,
wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to positions 11-13 of the first strand are modified with a 2' fluoro modification.

The invention also provides a composition comprising the nucleic acid or conjugated nucleic acid of any aspect of the invention, and optionally a physiologically acceptable excipient.

One aspect relates to a nucleic acid that is capable of inhibiting expression of *LPA* for use as a medicament.

Also provided is a nucleic acid or conjugated nucleic acid according to any aspect of the

invention for use in the treatment of a disease, disorder or syndrome and/or in the manufacture of a medicament for treating a disease, disorder, or syndrome.

The invention provides a method of treating or preventing a disease, disorder or syndrome comprising administration of a composition comprising a nucleic acid or conjugated nucleic acid according to any aspect of the invention to an individual in need of treatment. The nucleic acid or conjugated nucleic acid may be administered to the subject subcutaneously, intravenously or using any other application routes such as oral, rectal or intraperitoneal.

A method of making the nucleic acid or conjugated nucleic acid according to the invention is also included.

The nucleic acid or the composition comprising the nucleic acid or conjugated nucleic acid of the invention may be used in the treatment of a disease, disorder or syndrome. The treatment may be to prevent and reduce risk to suffer from stroke, atherosclerosis, thrombosis or cardiovascular diseases such as coronary heart disease or aortic stenosis and any other disease or pathology associated to elevated levels of Lp(a)-containing particles.

Detailed Description of the Invention

The present invention relates to a nucleic acid which is double stranded and directed to an expressed RNA transcript of *LPA* and compositions thereof. These nucleic acids or conjugated nucleic acids can be used in the treatment and prevention of a variety of diseases, disorders and syndromes where reduced expression of *LPA* gene product is desirable.

One aspect relates to a nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of a RNA transcribed from the *LPA* gene, wherein said first strand comprises, or preferably consists of, a nucleotide sequence selected from the following sequences: SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43,
wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to positions 11-13 of the first strand are modified with a 2' fluoro modification.

One aspect relates to a nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises a first strand and a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of a RNA transcribed from the *LPA* gene, wherein said first strand comprises, or preferably consists of, a nucleotide sequence selected from the following sequences: SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43,
wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to positions 11-13 of the first strand are modified with a 2' fluoro modification.

Such nucleic acids are able to efficiently reduce the expression of *LPA* in a cell and are very stable. The nucleic acid of the invention is preferably capable of inhibiting expression of *LPA* in a cell to a similar, such as the same, or a higher degree than the same nucleic acids with a different modification pattern in comparable conditions. More specifically, the nucleic acid of the invention is preferably capable of inhibiting expression of *LPA* in a cell by 80, 90, 100, 105, 110 or more percent as compared to the same nucleic acid with a different modification pattern in comparable conditions.

One aspect relates to a nucleic acid wherein all nucleotides of the nucleic acid are modified at the 2' position of the sugar.

One aspect relates to a nucleic acid wherein the nucleic acid is modified preferably along the entire length of the first strand with alternating 2' O-methyl modifications and 2' fluoro modifications.

One aspect relates to a nucleic acid wherein the remaining modifications of the second strand are naturally occurring modifications, preferably 2' O-methyl. In other words, nucleotides on the second strand which correspond to positions 11-13 of the first strand are modified with a 2' fluoro modification and all other nucleotides of the second strand are modified with a naturally occurring modification, which is preferably 2' O-methyl.

The second strand may comprise a nucleotide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 38, 40, 42, or 44.

The nucleic acid may: a) be blunt ended at both ends; b) have an overhang at one end and a blunt end at the other; or c) have an overhang at both ends. The nucleic acid is preferably blunt ended at both ends.

These nucleic acids among others have the advantage of being active in various species that are relevant for pre-clinical and clinical development and/or of having few relevant off-target effects as well as being stable *in vivo* and having a long duration of action. They also comprise comprises relatively few non-naturally occurring modified nucleotides but are nonetheless able to efficiently inhibit the target gene for long periods of time. The specific modification pattern with few non-naturally occurring modified nucleotides (2'F modified nucleotides) also makes them easier to synthesise.

The nucleic acid may comprise a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 9, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 10; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 5, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 6; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 1, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 2; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO:3, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 4; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 7, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 8; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 11, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 12; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 13, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 14; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 15, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 16; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 17, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 18; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 19, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 20; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 21, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 22; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO:23, and optionally a second strand that

comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 24; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO:25, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 26; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 27, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 28; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 29, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 30; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 31, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 32; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 33, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 34; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 35, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 36; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 37, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 38; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 39, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 40; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 41, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 42; or a first strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 43, and optionally a second strand that comprises or preferably consists of a nucleotide sequence of SEQ ID NO: 44.

The nucleic acid wherein said first strand comprises, and preferably consists of, the nucleotide sequence of SEQ ID NO: 9 and optionally, wherein said second strand comprises, and preferably consists of, the nucleotide sequence of SEQ ID NO. 10.

The *LPA* gene comprises highly repetitive sequences. First strand nucleic acids with very similar sequences can therefore have perfect sequence complementarity to very different target regions of the mRNA.

One aspect is a nucleic acid for inhibiting expression of *LPA* in a cell, wherein the nucleic acid comprises at least one duplex region that comprises: a first strand; and a second strand, wherein said second strand is at least partially complementary to the first strand,

wherein said first strand comprises a sequence of at least 15, preferably at least 16, more preferably at least 17, yet more preferably at least 18 and most preferably at least 19 nucleotides of any one of the reference sequences SEQ ID NO: 9, 5, 1, 3, 7, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43, and wherein the number of single nucleotide mismatches and/or deletions and/or insertions in the first strand sequence relative to the portion of the reference sequence that is comprised in the first strand sequence is at most three, preferably at most two, more preferably at most one and most preferably zero. The sequence may however be modified by a number of modifications that do not change the identity of the nucleotide. For examples, modifications of the backbone of the nucleic acid do not change the identity of the nucleotide because the base itself remains the same as in the reference sequence.

In one aspect, the first strand of the nucleic acid comprises a sequence of at least 18 nucleotides of any one of the reference sequences, preferably of any one of the reference sequences SEQ ID NO: 9 and 5, and wherein the number of single-nucleotide mismatches and/or deletions and/or insertions in the first strand sequence relative to the portion of the reference sequence that is comprised in the first strand sequence is at most one, and preferably zero.

In one aspect, the first strand of the nucleic acid comprises a sequence of at least 19 nucleotides of any of the reference sequences SEQ ID NO: 9 and 5.

When reference is made herein to a reference sequence comprising or consisting of unmodified nucleotides, this reference is not limited to the sequence with unmodified nucleotides. The same reference also encompasses the same nucleotide sequence in which one, several, such as two, three, four, five, six, seven or more, including all, nucleotides are modified by modifications such as 2'-OMe, 2'-F, a ligand, a linker, a 3' end or 5' end modification or any other modification. It also refers to sequences in which two or more nucleotides are linked to each other by the natural phosphodiester linkage or by any other linkage such as a phosphorothioate or a phosphorodithioate linkage.

A double-stranded nucleic acid is a nucleic acid in which the first strand and the second strand hybridise to each other over at least part of their lengths and are therefore capable of forming a duplex region under physiological conditions, such as in PBS at 37°C at a concentration of 1 μM of each strand. The first and second strand are preferably able to hybridise to each other and therefore to form a duplex region over a region of at least 15 nucleotides, preferably 16, 17, 18 or 19 nucleotides. This duplex region comprises

nucleotide base parings between the two strands, preferably based on Watson-Crick base pairing and/or wobble base pairing (such as GU base pairing). All the nucleotides of the two strands within a duplex region do not have to base pair to each other to form a duplex region. A certain number of mismatches, deletions or insertions between the nucleotide sequences of the two strands are acceptable. Overhangs on either end of the first or second strand or unpaired nucleotides at either end of the double-stranded nucleic acid are also possible. The double stranded nucleic acid is preferably a stable double stranded nucleic acid under physiological conditions and preferably has a melting temperature (Tm) of 45°C or more, preferably 50°C or more, and more preferably 55°C or more for example in PBS at a concentration 1 μM of each first strand and the second strand are preferably capable of forming a duplex region (ie are complementary to each other) over i) at least a portion of their lengths, preferably over at least 15 nucleotides of both of their lengths, ii) over the entire length of the first strand, iii) over the entire length of the second strand and/or iv) over the entire length of both the first and the second strand. Strands being complementary to each other over a certain length means that the strands are able to base pair to each other, either via Watson-Crick or wobble base pairing, over that length. Each nucleotide of the length does not necessarily have to be able to base pair with its counterpart in the other strand over the entire given length as long as a stable double-stranded nucleotide under physiological conditions can be formed. This is however preferred.

A certain number of mismatches, deletions or insertions between the first (antisense) strand and the target sequence, or between the first strand and the second (sense) strand can be tolerated in the context of siRNA and even have the potential in certain cases to increase activity.

By nucleic acid it is meant a nucleic acid comprising two strands comprising nucleotides, that is able to interfere with gene expression. Inhibition may be complete or partial and results in down regulation of gene expression in a targeted manner. The nucleic acid comprises two separate polynucleotide strands; the first strand, which may also be a guide strand; and a second strand, which may also be a passenger strand. The first strand and the second strand may be part of the same polynucleotide molecule that is self-complementary which 'folds' back to form a double stranded molecule. The nucleic acid may be an siRNA molecule.

The nucleic acid may comprise ribonucleotides, modified ribonucleotides, deoxynucleotides, deoxyribonucleotides, or nucleotide analogues non-nucleotides that are able to mimic nucleotides such that they may 'pair' with the corresponding base on the target sequence or complementary strand. The nucleic acid may further comprise a

double-stranded nucleic acid portion or duplex region formed by all or a portion of the first strand (also known in the art as a guide strand) and all or a portion of the second strand (also known in the art as a passenger strand). The duplex region is defined as beginning with the first base pair formed between the first strand and the second strand and ending with the last base pair formed between the first strand and the second strand, inclusive.

By duplex region it is meant the region in two complementary or substantially complementary oligonucleotides that form base pairs with one another, either by Watson-Crick base pairing or any other manner that allows for a duplex between oligonucleotide strands that are complementary or substantially complementary. For example, an oligonucleotide strand having 21 nucleotide units can base pair with another oligonucleotide of 21 nucleotide units, yet only 19 nucleotides on each strand are complementary or substantially complementary, such that the "duplex region" consists of 19 base pairs. The remaining base pairs may exist as 5′ and 3′ overhangs, or as single stranded regions. Further, within the duplex region, 100% complementarity is not required; substantial complementarity is allowable within a duplex region. Substantial complementarity refers to complementarity between the strands such that they are capable of annealing under biological conditions. Techniques to empirically determine if two strands are capable of annealing under biological conditions are well known in the art. Alternatively, two strands can be synthesised and added together under biological conditions to determine if they anneal to one another.

The portion of the first strand and second strand that form at least one duplex region may be fully complementary or be at least partially complementary to each other.

Depending on the length of a nucleic acid, a perfect match in terms of base complementarity between the first strand and the second strand is not necessarily required. However, the first and second strands must be able to hybridise under physiological conditions.

The complementarity between the first strand and second strand in the at least one duplex region may be perfect in that there are no nucleotide mismatches or additional/deleted nucleotides in either strand. Alternatively, the complementarity may not be perfect. The complementarity may be from about 70% to about 100%. More specifically, the complementarity may be at least 70%, 75%, 80%, 85%, 90% or 95% and intermediate values.

In the context of this invention, "a portion of" as for example in "one duplex region that comprises at least a portion of a first strand" should be understood to mean that the duplex region comprises at least 10, preferably at least 12, more preferably at least 14, yet more preferably at least 16, even more preferably at least 18 and most preferably all of the nucleotides of a given reference strand sequence. The portion of the reference sequence in the duplex region is at least 70%, preferably at least 80%, more preferably at least 90%, yet more preferably at least 95% and most preferably 100% identical to the corresponding portion of the reference sequence. Alternatively, the number of single nucleotide mismatches relative to the portion of the reference sequence is at most three, preferably at most two, more preferably at most one and most preferably zero.

The first strand and the second strand may each comprise a region of complementarity which comprises at least 15 contiguous nucleotides differing by no more than 3 nucleotides from any one of the sequences listed in Table 1.

Use of a nucleic acid according to the present invention involves the formation of a duplex region between all or a portion of the first strand and a portion of a target nucleic acid. The portion of the target nucleic acid that forms a duplex region with the first strand, defined as beginning with the first base pair formed between the first strand and the target sequence and ending with the last base pair formed between the first strand and the target sequence, inclusive, is the target nucleic acid sequence or simply, target sequence. The duplex region formed between the first strand and the second strand need not be the same as the duplex region formed between the first strand and the target sequence. That is, the second strand may have a sequence different from the target sequence; however, the first strand must be able to form a duplex structure with both the second strand and the target sequence, at least under physiological conditions.

The complementarity between the first strand and the target sequence may be perfect (no nucleotide mismatches or additional/deleted nucleotides in either nucleic acid).

The complementarity between the first strand and the target sequence may not be perfect. The complementarity may be from about 70% to about 100%. More specifically, the complementarity may be at least 70%, 80%, 85%, 90% or 95% and intermediate values.

The identity between the first strand and the complementary sequence of the target sequence may range from about 75% to about 100%. More specifically, the

complementarity may be at least 75%, 80%, 85%, 90% or 95% and intermediate values, provided a nucleic acid is capable of reducing or inhibiting the expression of *LPA*.

A nucleic acid having less than 100% complementarity between the first strand and the target sequence may be able to reduce the expression of *LPA* to the same level as a nucleic acid having perfect complementarity between the first strand and target sequence. Alternatively, it may be able to reduce expression of *LPA* to a level that is 15% - 100% of the level of reduction achieved by the nucleic acid with perfect complementarity.

In one aspect, the nucleic acid comprises a first nucleic acid strand and a second nucleic acid strand, wherein the first strand is capable of hybridising under physiological conditions to a nucleic acid of sequence SEQ ID NO: 10, 6, 2, 4, 8, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, or 44;
wherein the second strand is capable of hybridising under physiological conditions to the first strand to form a duplex region; and
wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to positions 11-13 of the first strand are modified with a 2' fluoro modification.

Nucleic acids that are capable of hybridising under physiological conditions are nucleic acids that are capable of forming base pairs, preferably Watson-Crick or wobble base-pairs, between at least a portion of the opposed nucleotides in the strands so as to form at least a duplex region. Such a double-stranded nucleic acid is preferably a stable double-stranded nucleic acid under physiological conditions (for example in PBS at 37°C at a concentration of 1 μM of each strand), meaning that under such conditions, the two strands stay hybridised to each other. The Tm of the double-stranded nucleotide is preferably 45°C or more, preferably 50°C or more and more preferably 55°C or more.

One aspect relates to a nucleic acid for inhibiting expression of *LPA*, wherein the nucleic acid comprises a first sequence of at least 15, preferably at least 16, more preferably at least 17, yet more preferably at least 18 and most preferably all nucleotides differing by no more than 3 nucleotides, preferably no more than 2 nucleotides, more preferably no more than 1 nucleotide and most preferably not differing by any nucleotide from any of the sequences of Table 1, the first sequence being able to hybridise to a target gene transcript (such as an mRNA) under physiological conditions. Preferably the nucleic acid further comprises a second sequence of at least 15, preferably at least 16, more preferably at least 17, yet more preferably at least 18 and most preferably all nucleotides differing by no more

than 3 nucleotides, preferably no more than 2 nucleotides, more preferably no more than 1 nucleotide and most preferably not differing by any nucleotide from any of the sequences of Table 1, the second sequence being able to hybridise to the first sequence under physiological conditions and preferably the nucleic acid being an siRNA that is capable of inhibiting *LPA* expression via the RNAi pathway.

The nucleic acids described herein may be capable of inhibiting the expression of *LPA*. Inhibition may be complete, i.e. 0% remaining expression compared of the expression level of *LPA* in the absence of the nucleic acid of the invention. Inhibition of *LPA* expression may be partial, i.e. it may be 15%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95% or intermediate values of *LPA* expression in the absence of a nucleic acid of the invention. The level of inhibition may be measured by comparing a treated sample with an untreated sample or with a sample treated with a control such as for example a siRNA that does not target *LPA*. Inhibition may be measured by measuring *LPA* mRNA and/or protein levels or levels of a biomarker or indicator that correlates with *LPA* presence or activity. It may be measured in cells that may have been treated *in vitro* with a nucleic acid described herein. Alternatively, or in addition, inhibition may be measured in cells, such as hepatocytes, or tissue, such as liver tissue, or an organ, such as the liver, or in a body fluid such as blood, serum, lymph or any other body part that has been taken from a subject previously treated with a nucleic acid disclosed herein. Preferably inhibition of *LPA* expression is determined by comparing the *LPA* mRNA level measured in *LPA* -expressing cells after 24 or 48 hours *in vitro* treatment under ideal conditions (see the examples for appropriate concentrations and conditions) with a nucleic acid disclosed herein to the *LPA* mRNA level measured in the same cells that were untreated or mock treated or treated with a control nucleic acid.

As used herein, the term “inhibit”, “down-regulate”, or “reduce” with respect to gene expression means the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits (e.g., mRNA), or activity of one or more proteins or protein subunits, is reduced below that observed in the absence of the nucleic acid or conjugated nucleic acid of the invention or in reference to an siRNA molecule with no known homology to human transcripts (herein termed non-silencing control). Such control may be conjugated and modified in an analogous manner to the molecule of the invention and delivered into the target cell by the same route; for example the expression may be reduced to 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 15%, or to intermediate values, or less than that observed in the absence of the nucleic acid or conjugated nucleic acid or in the presence of a non-silencing control.

The nucleic acid may comprise a first strand and a second strand that are each from 19-25 nucleotides in length. The first strand and the second strand may be of different lengths.

The first strand and/or the second strand may each be from 17-35, preferably 18-30, more preferably 19-25 and most preferably 19 nucleotides in length and at least one duplex region may be from 10-25 nucleotides, preferably 18-23 nucleotides in length. The duplex may comprise two separate strands or it may comprise a single strand which comprises the first strand and the second strand.

The first strand may be 17-25 nucleotides in length, preferably it may be 18-24 nucleotides in length, it may be 18, 19, 20, 21, 22, 23 or 24 nucleotides in length. Most preferably, the first strand is 19 nucleotides in length. The second strand may independently be 17-25 nucleotides in length, preferably it may be 18-24 nucleotides in length, it may be 18, 19, 20, 21, 22, 23 or 24 nucleotides in length. More preferably, the second strand is 18 or 19 nucleotides in length, and most preferably it is 18 nucleotides in length.

The nucleic acid may be 15-25 nucleotide pairs in length. The nucleic acid may be 17-23 nucleotide pairs in length. The nucleic acid may be 17-25 nucleotide pairs in length. The nucleic acid may be 23-24 nucleotide pairs in length. The nucleic acid may be 19-21 nucleotide pairs in length. The nucleic acid may be 21-23 nucleotide pairs in length.

The nucleic acid may comprise a duplex region that consists of 19-25 nucleotide base pairs. The duplex region may consist of 17, 18, 19, 20, 21, 22, 23, 24 or 25 base pairs, which may be contiguous. Preferably, the duplex region consists of 19 base pairs.

Preferably, the nucleic acid mediates RNA interference.

In one embodiment, the nucleic acid for inhibiting expression of *LPA* in a cell, comprises at least one duplex region that comprises a first strand and a second strand that is at least partially complementary to the first strand, wherein said first strand comprises a sequence of at least 15, preferably at least 16, more preferably at least 17, yet more preferably at least 18 and most preferably at least 19 nucleotides with a sequence identity of at least 70%, preferably at least 80%, more preferably at least 90%, yet more preferably at least 95% and most preferably 100% of any of sequences SEQ ID NOs: 9, 5, 1, 3, 7, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43.

In a further aspect the nucleic acid or conjugated nucleic acid as described may reduce the expression of *LPA* by at least 15% compared to the expression observed in the absence of the nucleic acid or conjugated nucleic acid. All preferred features of any of the previous aspects also apply to this aspect. In particular, the expression of *LPA* may be reduced to at least the following given % or less than 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 15% or less, and intermediate values, than that observed in the absence of the nucleic acid or conjugated nucleic acid or in the presence of a non-silencing control.

The nucleic acid may have an overhang at one end and a blunt end at the other. The nucleic acid may have an overhang at both ends. The nucleic acid may be blunt ended at both ends. The nucleic acid may be blunt ended at the end with the 5'-end of the first strand and the 3'-end of the second strand or at the 3'-end of the first strand and the 5'-end of the second strand.

An "overhang" as used herein has its normal and customary meaning in the art, i.e. a single stranded portion of a nucleic acid that extends beyond the terminal nucleotide of a complementary strand in a double strand nucleic acid. The term "blunt end" includes double stranded nucleic acid whereby both strands terminate at the same position, regardless of whether the terminal nucleotide(s) are base-paired. The terminal nucleotide of a first strand and a second strand at a blunt end may be base paired. The terminal nucleotide of a first strand and a second strand at a blunt end may not be paired. The terminal two nucleotides of a first strand and a second strand at a blunt end may be base-paired. The terminal two nucleotides of a first strand and a second strand at a blunt end may not be paired.

The nucleic acid may comprise an overhang at a 3'- or 5'-end. The nucleic acid may have a 3'-overhang on the first strand. The nucleic acid may have a 3'-overhang on the second strand. The nucleic acid may have a 5'-overhang on the first strand. The nucleic acid may have a 5'-overhang on the second strand. The nucleic acid may have an overhang at both the 5'-end and 3'-end of the first strand. The nucleic acid may have an overhang at both the 5'-end and 3'-end of the second strand. The nucleic acid may have a 5' overhang on the first strand and a 3' overhang on the second strand. The nucleic acid may have a 3' overhang on the first strand and a 5' overhang on the second strand. The nucleic acid may have a 3' overhang on the first strand and a 3' overhang on the second strand. The nucleic acid may have a 5' overhang on the first strand and a 5' overhang on the second strand.

An overhang at the 3'-end or 5' end of the second strand or the first strand may be selected from consisting of 1, 2, 3, 4 and 5 nucleotides in length. Optionally, an overhang may consist of 1 or 2 nucleotides, which may or may not be modified.

Preferably, the nucleic acid is an siRNA. siRNAs are short interfering or short silencing RNAs that are able to inhibit the expression of a target gene through the RNA interference (RNAi) pathway. Inhibition occurs through targeted degradation of mRNA transcripts of the target gene after transcription. The siRNA forms part of the RISC complex. The RISC complex specifically targets the target RNA by sequence complementarity of the first (antisense) strand with the target sequence.

Preferably, the nucleic acid mediates RNA interference (RNAi). The nucleic acid, or at least the first strand of the nucleic acid, is therefore preferably able to be incorporated into the RISC complex. As a result, the nucleic acid, or at least the first strand of the nucleic acid, is therefore able to guide the RISC complex to a specific target RNA with which the nucleic acid, or at least the first strand of the nucleic acid, is at least partially complementary. The RISC complex then specifically cleaves this target RNA and as a result leads to inhibition of the expression of the gene from which the RNA stems.

Nucleic acid modifications

Unmodified polynucleotides, particularly ribonucleotides, may be prone to degradation by cellular nucleases, and, as such, modifications/ modified nucleotides may be included in the nucleic acid of the invention. Such modifications may help to stabilise the nucleic acid by making them more resistant against nucleases. This improved resistance allows nucleic acids to be active in mediating RNA interference for longer time periods and is especially desirable when the nucleic acids are to be used for treatment.

Modifications of the nucleic acid of the present invention generally provide a powerful tool in overcoming potential limitations including, but not limited to, *in vitro* and *in vivo* stability and bioavailability inherent to native RNA molecules. The nucleic acid according to the invention may be modified by chemical modifications. Modified nucleic acid can also minimise the possibility of inducing interferon activity in humans. Modification can further enhance the functional delivery of a nucleic acid to a target cell. The modified nucleic acid of the present invention may comprise one or more chemically modified ribonucleotides of either or both of the first strand or the second strand. A ribonucleotide may comprise a

chemical modification of the base, sugar or phosphate moieties. The ribonucleic acid may be modified by substitution or insertion with analogues of nucleic acids or bases.

Preferably, at least one nucleotide of the first and/or second strand of the nucleic acid is a modified nucleotide, preferably a non-naturally occurring nucleotide such as preferably a 2'-F modified nucleotide.

One or more nucleotides of a nucleic acid of the present invention may be modified. The nucleic acid may comprise at least one modified nucleotide. The modified nucleotide may be in the first strand. The modified nucleotide may be in the second strand. The modified nucleotide may be in the duplex region. The modified nucleotide may be outside the duplex region, i.e., in a single stranded region. The modified nucleotide may be on the first strand and may be outside the duplex region. The modified nucleotide may be on the second strand and may be outside the duplex region. The 3'-terminal nucleotide of the first strand may be a modified nucleotide. The 3'-terminal nucleotide of the second strand may be a modified nucleotide. The 5'-terminal nucleotide of the first strand may be a modified nucleotide. The 5'-terminal nucleotide of the second strand may be a modified nucleotide.

A nucleic acid of the invention may have 1 modified nucleotide or a nucleic acid of the invention may have about 2-4 modified nucleotides, or a nucleic acid may have about 4-6 modified nucleotides, about 6-8 modified nucleotides, about 8-10 modified nucleotides, about 10-12 modified nucleotides, about 12-14 modified nucleotides, about 14-16 modified nucleotides about 16-18 modified nucleotides, about 18-20 modified nucleotides, about 20-22 modified nucleotides, about 22-24 modified nucleotides, 24-26 modified nucleotides or about 26-28 modified nucleotides or all of the nucleotides may be modified. In each case the nucleic acid comprising said modified nucleotides retains at least 50% of its activity as compared to the same nucleic acid but without said modified nucleotides or vice versa. The nucleic acid may retain 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% and intermediate values of its activity as compared to the same nucleic acid but without said modified nucleotides, or may have more than 100% of the activity of the same nucleic acid without said modified nucleotides.

The modified nucleotide may be a purine or a pyrimidine. At least half of the purines may be modified. At least half of the pyrimidines may be modified. All of the purines may be modified. All of the pyrimidines may be modified. The modified nucleotides may be selected from the group consisting of a 3'-terminal deoxy-thymine (dT) nucleotide, a 2'-O-methyl modified nucleotide, a 2' modified nucleotide, a 2'-deoxy-modified nucleotide, a locked

nucleotide, an abasic nucleotide, a 2'-amino-modified nucleotide, a 2'-alkyl-modified nucleotide, a morpholino nucleotide, a phosphoramidate, a non-natural base comprising nucleotide, a nucleotide comprising a 5'-phosphorothioate group, a nucleotide comprising a 5' phosphate or 5' phosphate mimic and a terminal nucleotide linked to a cholesteryl derivative or a dodecanoic acid bisdecylamide group.

The nucleic acid may comprise a nucleotide comprising a modified nucleotide, wherein the base is selected from 2-aminoadenosine, 2,6-diaminopurine,inosine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidine (e.g., 5-methylcytidine), 5-alkyluridine (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine), 6-azapyrimidine, 6-alkylpyrimidine (e.g. 6-methyluridine), propyne, quesosine, 2-thiouridine, 4-thiouridine, wybutosine, wybutoxosine, 4-acetylcytidine, 5-(carboxyhydroxymethyl)uridine, 5'-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluridine, beta-D-galactosylqueosine, 1-methyladenosine, 1-methylinosine, 2,2-dimethylguanosine, 3-methylcytidine, 2-methyladenosine, 2-methylguanosine, N6-methyladenosine, 7-methylguanosine, 5-methoxyaminomethyl-2-thiouridine, 5-methylaminomethyluridine, 5-methylcarbonylmethyluridine, 5-methyloxyuridine, 5-methyl-2-thiouridine, 2-methylthio-N6-isopentenyladenosine, beta-D-mannosylqueosine, uridine-5-oxyacetic acid and 2-thiocytidine.

Nucleic acids discussed herein include unmodified RNA as well as RNA which has been modified, e.g., to improve efficacy, and polymers of nucleoside surrogates. Unmodified RNA refers to a molecule in which the components of the nucleic acid, namely sugars, bases, and phosphate moieties, are the same or essentially the same as that which occur in nature, for example as occur naturally in the human body. Modified nucleotide as used herein refers to a nucleotide in which one or more of the components of the nucleotides, namely sugars, bases, and phosphate moieties, are different from those which occur in nature. While they are referred to as modified nucleotides they will of course, because of the modification, the term also includes molecules which are not nucleotides, for example a polynucleotide molecule in which the ribophosphate backbone is replaced with a non-ribophosphate construct that allows hybridisation between strands i.e. the modified nucleotides mimic the ribophosphate backbone.

Many of the modifications described below that occur within a nucleic acid will be repeated within a polynucleotide molecule, such as a modification of a base, or a phosphate moiety, or a non-linking O of a phosphate moiety. In some cases the modification will occur at all of

the possible positions/nucleotides in the polynucleotide but in many cases it will not. A modification may only occur at a 3′ or 5′ terminal position, may only occur in a terminal regions, such as at a position on a terminal nucleotide or in the last 2, 3, 4, 5, or 10 nucleotides of a strand. A modification may occur in a double strand region, a single strand region, or in both. A modification may occur only in the double strand region of a nucleic acid of the invention or may only occur in a single strand region of a nucleic acid of the invention. A phosphorothioate modification at a non-linking O position may only occur at one or both termini, may only occur in a terminal region, e.g., at a position on a terminal nucleotide or in the last 2, 3, 4 or 5 nucleotides of a strand, or may occur in duplex and/or in single strand regions, particularly at termini. The 5′ end or 3′ ends may be phosphorylated.

Stability of a nucleic acid of the invention may be increased by including particular bases in overhangs, or to include modified nucleotides, in single strand overhangs, e.g., in a 5′ or 3′ overhang, or in both. Purine nucleotides may be included in overhangs. All or some of the bases in a 3′ or 5′ overhang may be modified. Modifications can include the use of modifications at the 2′ OH group of the ribose sugar, the use of deoxyribonucleotides, instead of ribonucleotides, and modifications in the phosphate group, such as phosphorothioate modifications. Overhangs need not be homologous with the target sequence.

Nucleases can hydrolyse nucleic acid phosphodiester bonds. However, chemical modifications to nucleic acids can confer improved properties, and, can render oligoribonucleotides more stable to nucleases.

Modified nucleic acids, as used herein, can include one or more of:

(i) alteration, e.g., replacement, of one or both of the non-linking phosphate oxygens and/or of one or more of the linking phosphate oxygens (referred to as linking even if at the 5′ and 3′ terminus of the nucleic acid of the invention);
(ii) alteration, e.g., replacement, of a constituent of the ribose sugar, e.g., of the 2′ hydroxyl on the ribose sugar;
(iii) replacement of the phosphate moiety with “dephospho” linkers;
(iv) modification or replacement of a naturally occurring base;
(v) replacement or modification of the ribose-phosphate backbone;
(vi) modification of the 3′ end or 5′ end of the RNA, e.g., removal, modification or replacement of a terminal phosphate group or conjugation of a moiety, e.g., a fluorescently labelled moiety, to either the 3′ or 5′ end of RNA.

The terms replacement, modification, alteration, indicate a difference from a naturally occurring molecule.

Specific modifications are discussed in more detail below.

Examples of modified phosphate groups include phosphorothioate, phosphoroselenates, borano phosphates, borano phosphate esters, hydrogen phosphonates, phosphoroamidates, alkyl or aryl phosphonates and phosphotriesters. Phosphorodithioates have both non-linking oxygens replaced by sulphur. One, each or both non-linking oxygens in the phosphate group can be independently any one of S, Se, B, C, H, N, or OR (R is alkyl or aryl).

The phosphate linker can also be modified by replacement of a linking oxygen with nitrogen (bridged phosphoroamidates), sulfur (bridged phosphorothioates) and carbon (bridged methylenephosphonates). The replacement can occur at a terminal oxygen. Replacement of the non-linking oxygens with nitrogen is possible.

A modified nucleotide can include modification of the sugar groups. The 2′ hydroxyl group (OH) can be modified or replaced with a number of different “oxy” or “deoxy” substituents.

Examples of “oxy”-2′ hydroxyl group modifications include alkoxy or aryloxy (OR, e.g., R=H, alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or sugar); polyethyleneglycols (PEG), O(CH2CH2O)nCH2CH2OR; “locked” nucleic acids (LNA) in which the 2′ hydroxyl is connected, e.g., by a methylene bridge, to the 4′ carbon of the same ribose sugar; O-AMINE (AMINE=NH2; alkylamino, dialkylamino, heterocyclyl, arylamino, diaryl amino, heteroaryl amino, or diheteroaryl amino, ethylene diamine, polyamino) and aminoalkoxy, O(CH2)nAMINE, (e.g., AMINE=NH2; alkylamino, dialkylamino, heterocyclyl, arylamino, diaryl amino, heteroaryl amino, or diheteroaryl amino, ethylene diamine, polyamino).

“Deoxy” modifications include hydrogen, halogen, amino (e.g., NH2; alkylamino, dialkylamino, heterocyclyl, arylamino, diaryl amino, heteroaryl amino, diheteroaryl amino, or amino acid); NH(CH2CH2NH)nCH2CH2-AMINE (AMINE=NH2; alkylamino, dialkylamino, heterocyclyl, arylamino, diaryl amino, heteroaryl amino, or diheteroaryl amino), —NHC(O)R (R=alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or sugar), cyano; mercapto; alkyl-thio-alkyl; thioalkoxy; and alkyl, cycloalkyl, aryl, alkenyl and alkynyl, which may be optionally substituted with e.g., an amino functionality. Other substitutents of certain embodiments include 2′-methoxyethyl, 2′-OCH3, 2′-O-allyl, 2′-C-allyl, and 2′-fluoro.

The sugar group can also contain one or more carbons that possess the opposite stereochemical configuration than that of the corresponding carbon in ribose. Thus, a modified nucleotide may contain a sugar such as arabinose.

Modified nucleotides can also include "abasic" sugars, which lack a nucleobase at C—1′. These abasic sugars can further contain modifications at one or more of the constituent sugar atoms.

The 2′ modifications may be used in combination with one or more phosphate linker modifications (e.g., phosphorothioate).

The phosphate groups can individually be replaced by non-phosphorus containing connectors.

Examples of moieties which can replace the phosphate group include siloxane, carbonate, carboxymethyl, carbamate, amide, thioether, ethylene oxide linker, sulfonate, sulfonamide, thioformacetal, formacetal, oxime, methyleneimino, methylenemethylimino, methylenehydrazo, methylenedimethylhydrazo and methyleneoxymethylimino. In certain embodiments, replacements may include the methylenecarbonylamino and methylenemethylimino groups.

The phosphate linker and ribose sugar may be replaced by nuclease resistant nucleotides.

Examples include the morpholino, cyclobutyl, pyrrolidine and peptide nucleic acid (PNA) nucleoside surrogates. In certain embodiments, PNA surrogates may be used.

The 3′ and 5′ ends of an oligonucleotide can be modified. Such modifications can be at the 3′ end or the 5′ end or both ends of the molecule. They can include modification or replacement of an entire terminal phosphate or of one or more of the atoms of the phosphate group. For example, the 3′ and 5′ ends of an oligonucleotide can be conjugated to other functional molecular entities such as labelling moieties, e.g., fluorophores (e.g., pyrene, TAMRA, fluorescein, Cy3 or Cy5 dyes) or protecting groups (based e.g., on sulfur, silicon, boron or ester). The functional molecular entities can be attached to the sugar through a phosphate group and/or a linker. The terminal atom of the linker can connect to or replace the linking atom of the phosphate group or the C-3′ or C-5′ O, N, S or C group of the sugar. Alternatively, the linker can connect to or replace the terminal atom of a nucleotide surrogate (e.g., PNAs). These spacers or linkers can include e.g., —$(CH_2)_n$—, —$(CH_2)_n$N—, —

$(CH_2)_nO$—, —$(CH_2)_nS$—, — $(CH_2CH_2O)_nCH_2CH_2O$— (e.g., n=3 or 6), abasic sugars, amide, carboxy, amine, oxyamine, oxyimine, thioether, disulfide, thiourea, sulfonamide, or morpholino, or biotin and fluorescein reagents. The 3′ end can be an —OH group.

Other examples of terminal modifications include dyes, intercalating agents (e.g., acridines), cross-linkers (e.g., psoralene, mitomycin C), porphyrins (TPPC4, texaphyrin, Sapphyrin), polycyclic aromatic hydrocarbons (e.g., phenazine, dihydrophenazine), artificial endonucleases, EDTA, lipophilic carriers (e.g., cholesterol, cholic acid, adamantane acetic acid, 1-pyrene butyric acid, dihydrotestosterone, 1,3-Bis-O(hexadecyl)glycerol, geranyloxyhexyl group, hexadecylglycerol, borneol, menthol, 1,3-propanediol, heptadecyl group, palmitic acid, myristic acid, O3-(oleoyl)lithocholic acid, O3-(oleoyl)cholenic acid, dimethoxytrityl, or phenoxazine) and peptide conjugates (e.g., antennapedia peptide, Tat peptide), alkylating agents, phosphate, amino, mercapto, PEG (e.g., PEG-40K), MPEG, [MPEG]2, polyamino, alkyl, substituted alkyl, radiolabeled markers, enzymes, haptens (e.g., biotin), transport/absorption facilitators (e.g., aspirin, vitamin E, folic acid), synthetic ribonucleases (e.g., imidazole, bisimidazole, histamine, imidazole clusters, acridine-imidazole conjugates, Eu3+ complexes of tetraazamacrocycles).

Terminal modifications can be added for a number of reasons, including to modulate activity or to modulate resistance to degradation. Terminal modifications useful for modulating activity include modification of the 5′ end with phosphate or phosphate analogues. Nucleic acids of the invention, on the first or second strand, may be 5′ phosphorylated or include a phosphoryl analogue at the 5′ prime terminus. 5′-phosphate modifications include those which are compatible with RISC mediated gene silencing. Suitable modifications include: 5′-monophosphate ($(HO)_2(O)P$—O-5′); 5′-diphosphate ($(HO)_2(O)P$—O—P(HO)(O)—O-5′); 5′-triphosphate ($(HO)_2(O)P$—O—(HO)(O)P—O—P(HO)(O)—O-5′); 5′-guanosine cap (7-methylated or non-methylated) (7m-G-O-5′-(HO)(O)P—O—(HO)(O)P—O—P(HO)(O)—O-5′); 5′-adenosine cap (Appp), and any modified or unmodified nucleotide cap structure (N—O-5′-(HO)(O)P—O—(HO)(O)P—O—P(HO)(O)—O-5′); 5′-monothiophosphate (phosphorothioate; $(HO)_2(S)P$—O-5′); 5′-monodithiophosphate (phosphorodithioate; (HO)(HS)(S)P—O-5′), 5′-phosphorothiolate ((HO)2(O)P—S-5′); any additional combination of oxygen/sulfur replaced monophosphate, diphosphate and triphosphates (e.g., 5′-alpha-thiotriphosphate, 5′-gamma-thiotriphosphate, etc.), 5′-phosphoramidates ((HO)2(O)P—NH-5′, (HO)(NH2)(O)P—O-5′), 5′-alkylphosphonates (R=alkyl=methyl, ethyl, isopropyl, propyl, etc., e.g., RP(OH)(O)—O-5′-, $(OH)_2(O)P$-5′-CH_2-), 5′vinylphosphonate, 5′-alkyletherphosphonates (R=alkylether=methoxymethyl ($MeOCH_2$-), ethoxymethyl, etc., e.g., RP(OH)(O)—O-5′-).

Terminal modifications can also be useful for monitoring distribution, and in such cases the groups to be added may include fluorophores, e.g., fluorescein or an Alexa dye. Terminal modifications can also be useful for enhancing uptake, useful modifications for this include cholesterol. Terminal modifications can also be useful for cross-linking an RNA agent to another moiety.

Adenine, guanine, cytosine and uracil are the most common bases found in RNA. These bases can be modified or replaced to provide RNAs having improved properties. E.g., nuclease resistant oligoribonucleotides can be prepared with these bases or with synthetic and natural nucleobases (e.g., inosine, thymine, xanthine, hypoxanthine, nubularine, isoguanisine, or tubercidine) and any one of the above modifications. Alternatively, substituted or modified analogues of any of the above bases and "universal bases" can be employed. Examples include 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 5-halouracil, 5-(2-aminopropyl)uracil, 5-amino allyl uracil, 8-halo, amino, thiol, thioalkyl, hydroxyl and other 8-substituted adenines and guanines, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylguanine, 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine, dihydrouracil, 3-deaza-5-azacytosine, 2-aminopurine, 5-alkyluracil, 7-alkylguanine, 5-alkyl cytosine, 7-deazaadenine, N6,N6-dimethyladenine, 2,6-diaminopurine, 5-amino-allyl-uracil, N3-methyluracil, substituted 1,2,4-triazoles, 2-pyridinone, 5-nitroindole, 3-nitropyrrole, 5-methoxyuracil, uracil-5-oxyacetic acid, 5-methoxycarbonylmethyluracil, 5-methyl-2-thiouracil, 5-methoxycarbonylmethyl-2-thiouracil, 5-methylaminomethyl-2-thiouracil, 3-(3-amino-3-carboxypropyl)uracil, 3-methylcytosine, 5-methylcytosine, N<4>-acetyl cytosine, 2-thiocytosine, N6-methyladenine, N6-isopentyladenine, 2-methylthio-N6-isopentenyladenine, N-methylguanines, or O-alkylated bases.

As used herein, the terms "non-pairing nucleotide analogue" means a nucleotide analogue which includes a non-base pairing moiety including but not limited to: 6 des amino adenosine (Nebularine), 4-Me-indole, 3-nitropyrrole, 5-nitroindole, Ds, Pa, N3-Me ribo U, N3-Me riboT, N3-Me dC, N3-Me-dT, N1-Me-dG, N1-Me-dA, N3-ethyl-dC, N3-Me dC. In some embodiments the non-base pairing nucleotide analogue is a ribonucleotide. In other embodiments it is a deoxyribonucleotide.

As used herein, the term, "terminal functional group" includes without limitation a halogen, alcohol, amine, carboxylic, ester, amide, aldehyde, ketone, ether groups.

Certain moieties may be linked to the 5' terminus of the first strand or the second strand. These include abasic ribose moiety, abasic deoxyribose moiety, modifications abasic ribose and abasic deoxyribose moieties including 2' O alkyl modifications; inverted abasic ribose and abasic deoxyribose moieties and modifications thereof, C6-imino-Pi; a mirror nucleotide including L-DNA and L-RNA; 5'OMe nucleotide; and nucleotide analogues including 4',5'-methylene nucleotide; 1-(β-D-erythrofuranosyl)nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 12-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; alpha-nucleotide; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted abasic moiety; 1,4-butanediol phosphate; 5'-amino; and bridging or non-bridging methylphosphonate and 5'-mercapto moieties.

The nucleic acid of the present invention may comprise an abasic nucleotide. The term "abasic" as used herein, refers to moieties lacking a base or having other chemical groups in place of a base at the 1' position, for example a 3',3'-linked or 5',5'-linked deoxyabasic ribose derivative.

The nucleic acid may comprise one or more nucleotides on the second and/or first strands that are modified. Alternating nucleotides may be modified, to form modified nucleotides.

Alternating as described herein means to occur one after another in a regular way. In other words, alternating means to occur in turn repeatedly. For example, if one nucleotide is modified, the next contiguous nucleotide is not modified and the following contiguous nucleotide is modified and so on. One nucleotide may be modified with a first modification, the next contiguous nucleotide may be modified with a second modification and the following contiguous nucleotide is modified with the first modification and so on, where the first and second modifications are different.

One or more of the odd numbered nucleotides of the first strand of the nucleic acid of the invention may be modified wherein the first strand is numbered 5' to 3', the 5'-most nucleotide being nucleotide number 1 of the first strand. The term "odd numbered" as described herein means a number not divisible by two. Examples of odd numbers are 1, 3, 5, 7, 9, 11 and so on. One or more of the even numbered nucleotides of the first strand of

the nucleic acid of the invention may be modified, wherein the first strand is numbered 5' to 3'. The term "even numbered" as described herein means a number which is evenly divisible by two. Examples of even numbers are 2, 4, 6, 8, 10, 12, 14 and so on. One or more of the odd numbered nucleotides of the second strand of the nucleic acid of the invention may be modified wherein the second strand is numbered 3' to 5', the 3'-most nucleotide being nucleotide number 1 of the second strand. One or more of the even numbered nucleotides of the second strand of the nucleic acid of the invention may be modified, wherein the second strand is numbered 3' to 5'.

One or more nucleotides on the first and/or second strand may be modified, to form modified nucleotides. One or more of the odd numbered nucleotides of the first strand may be modified. One or more of the even numbered nucleotides of the first strand may be modified by at least a second modification, wherein the at least second modification is different from the modification on the one or more odd nucleotides. At least one of the one or more modified even numbered nucleotides may be adjacent to at least one of the one or more modified odd numbered nucleotides.

A plurality of odd numbered nucleotides in the first strand may be modified in the nucleic acid of the invention. A plurality of even numbered nucleotides in the first strand may be modified by a second modification. The first strand may comprise adjacent nucleotides that are modified by a common modification. The first strand may also comprise adjacent nucleotides that are modified by a second different modification.

One or more of the odd numbered nucleotides of the second strand may be modified by a modification that is different to the modification of the odd numbered nucleotides on the first strand and/or one or more of the even numbered nucleotides of the second strand may be modified by the same modification of the odd numbered nucleotides of the first strand. At least one of the one or more modified even numbered nucleotides of the second strand may be adjacent to the one or more modified odd numbered nucleotides. A plurality of odd numbered nucleotides of the second strand may be modified by a common modification and/or a plurality of even numbered nucleotides may be modified by the same modification that is present on the first stand odd numbered nucleotides. A plurality of odd numbered nucleotides on the second strand may be modified by a second modification, wherein the second modification is different from the modification of the first strand odd numbered nucleotides.

The second strand may comprise adjacent nucleotides that are modified by a common

modification, which may be a second modification that is different from the modification of the odd numbered nucleotides of the first strand.

In the nucleic acid of the invention, each of the odd numbered nucleotides in the first strand and each of the even numbered nucleotides in the second strand may be modified with a common modification and, each of the even numbered nucleotides may be modified in the first strand with a second modification and each of the odd numbered nucleotides may be modified in the second strand with a second different modification.

The nucleic acid of the invention may have the modified nucleotides of the first strand shifted by at least one nucleotide relative to the unmodified or differently modified nucleotides of the second strand.

One or more or each of the odd numbered nucleotides may be modified in the first strand and one or more or each of the even numbered nucleotides may be modified in the second strand. One or more or each of the alternating nucleotides on either or both strands may be modified by a second modification. One or more or each of the even numbered nucleotides may be modified in the first strand and one or more or each of the even numbered nucleotides may be modified in the second strand. One or more or each of the alternating nucleotides on either or both strands may be modified by a second modification. One or more or each of the odd numbered nucleotides may be modified in the first strand and one or more of the odd numbered nucleotides may be modified in the second strand by a common modification. One or more or each of the alternating nucleotides on either or both strands may be modified by a second modification. One or more or each of the even numbered nucleotides may be modified in the first strand and one or more or each of the odd numbered nucleotides may be modified in the second strand by a common modification. One or more or each of the alternating nucleotides on either or both strands may be modified by a second modification.

The nucleic acid of the invention may comprise single or double stranded constructs that comprise at least two regions of alternating modifications in one or both of the strands. These alternating regions can comprise up to about 12 nucleotides but preferably comprise from about 3 to about 10 nucleotides. The regions of alternating nucleotides may be located at the termini of one or both strands of the nucleic acid of the invention. The nucleic acid may comprise from 4 to about 10 nucleotides of alternating nucleotides at each termini (3' and 5') and these regions may be separated by from about 5 to about 12 contiguous unmodified or differently or commonly modified nucleotides.

The odd numbered nucleotides of the first strand may be modified and the even numbered nucleotides may be modified with a second modification. The second strand may comprise adjacent nucleotides that are modified with a common modification, which may be the same as the modification of the odd numbered nucleotides of the first strand. One or more nucleotides of second strand may also be modified with the second modification. One or more nucleotides with the second modification may be adjacent to each other and to nucleotides having a modification that is the same as the modification of the odd numbered nucleotides of the first strand. The first strand may also comprise phosphorothioate linkages between the two nucleotides at the 3' end and at the 5' end. The second strand may comprise a phosphorothioate linkage between the two nucleotides at 5' end. The second strand may also be conjugated to a ligand at the 5' end.

The nucleic acid of the invention may comprise a first strand comprising adjacent nucleotides that are modified with a common modification. One or more of such nucleotides may be adjacent to one or more nucleotides which may be modified with a second modification. One or more nucleotides with the second modification may be adjacent. The second strand may comprise adjacent nucleotides that are modified with a common modification, which may be the same as one of the modifications of one or more nucleotides of the first strand. One or more nucleotides of second strand may also be modified with the second modification. One or more nucleotides with the second modification may be adjacent. The first strand may also comprise phosphorothioate linkages between the two nucleotides at the 5' end and at the 3' end. The second strand may comprise a phosphorothioate linkage between the two nucleotides at the 3' end. The second strand may also be conjugated to a ligand at the 5' end.

The nucleotides numbered from 5' to 3' on the first strand and 3' to 5' on the second strand, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 and 25 may be modified by a modification on the first strand. The nucleotides numbered 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 and 24 may be modified by a second modification on the first strand. The nucleotides numbered 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 may be modified by a modification on the second strand. The nucleotides numbered 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 and 24 may be modified by a second modification on the second strand. Nucleotides are numbered for the sake of the nucleic acid of the present invention from 5' to 3' on the first strand and 3' to 5' on the second strand

The nucleotides numbered 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 and 24 may be modified by a modification on the first strand. The nucleotides numbered 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 may be modified by a second modification on the first strand. The nucleotides numbered 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 may be modified by a modification on the second strand. The nucleotides numbered 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 and 24 may be modified by a second modification on the second strand.

Clearly, if the first and/or the second strand are shorter than 25 nucleotides in length, such as 19 nucleotides in length, there are no nucleotides numbered 20, 21, 22, 23, 24 and 25 to be modified. The skilled person understands the description above to apply to shorter strands, accordingly.

One or more modified nucleotides on the first strand may be paired with modified nucleotides on the second strand having a common modification. One or more modified nucleotides on the first strand may be paired with modified nucleotides on the second strand having a different modification. One or more modified nucleotides on the first strand may be paired with unmodified nucleotides on the second strand. One or more modified nucleotides on the second strand may be paired with unmodified nucleotides on the first strand. In other words, the alternating nucleotides can be aligned on the two strands such as, for example, all the modifications in the alternating regions of the second strand are paired with identical modifications in the first strand or alternatively the modifications can be offset by one nucleotide with the common modifications in the alternating regions of one strand pairing with dissimilar modifications (i.e. a second or further modification) in the other strand. Another option is to have dissimilar modifications in each of the strands.

The modifications on the first strand may be shifted by one nucleotide relative to the modified nucleotides on the second strand, such that common modified nucleotides are not paired with each other.

The modification and/or modifications may each and individually be selected from the group consisting of 3'-terminal deoxy-thymine, 2'-O-methyl, a 2'-deoxy-modification, a 2'-amino-modification, a 2'-alkyl-modification, a morpholino modification, a phosphoramidate modification, 5'-phosphorothioate group modification, a 5' phosphate or 5' phosphate mimic modification and a cholesteryl derivative or a dodecanoic acid bisdecylamide group modification and/or the modified nucleotide may be any one of a locked nucleotide, an abasic nucleotide or a non-natural base comprising nucleotide.

At least one modification may be 2'-O-methyl and/or at least one modification may be 2'-F. Further modifications as described herein may be present on the first and/or second strand.

Throughout the description of the invention, "same or common modification" means the same modification to any nucleotide, be that A, G, C or U modified with a group such as a methyl group or a fluoro group. Is it not taken to mean the same addition on the same nucleotide. For example, 2'F-dU, 2'F-dA, 2'F-dC, 2'F-dG are all considered to be the same or common modification, as are 2'-OMe-rU, 2'-OMe-rA; 2'-OMe-rC; 2'-OMe-rG. A 2-'F modification is a different modification to a 2'-OMe modification.

Some representative modified nucleic acid sequences of the present invention are shown in the examples. These examples are meant to be representative and not limiting.

Preferably, the nucleic acid may comprise a modification and a second or further modification which are each and individually selected from the group comprising 2'-O-methyl modification and 2'-F modification. The nucleic acid may comprise a modification that is 2'-O-methyl (2'-OMe) that may be a first modification, and a second modification that is 2'-F. The nucleic acid of the invention may also include a phosphorothioate modification and/or a deoxy modification which may be present in or between the terminal 2 or 3 nucleotides of each or any end of each or both strands.

The invention provides as a further aspect, a nucleic acid for inhibiting expression of *LPA* in a cell, comprising a nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43, wherein the nucleotides of first strand are modified by a first modification on the odd numbered nucleotides, and modified by a second modification on the even numbered nucleotides, and nucleotides of the second strand are modified by a third modification on the even numbered nucleotides and modified by a fourth modification the odd numbered nucleotides, wherein at least the first modification is different to the second modification and the third modification is different to the fourth modification. The third and first modifications may be the same or different, the second and fourth modifications may be the same or different. The first and second modifications may be different to each other and the third and fourth modifications may be different to each other.

The second strand may comprise a nucleotide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, or 44. The nucleotides of the first strand may be modified by a first modification on the odd numbered nucleotides, and modified with a second modification on the even numbered nucleotides, and the second

strand may be modified on the odd numbered nucleotides with the second modification and modified with the first modification on the even numbered nucleotides. The first modification may be 2'OMe and the second modification may be 2' F. The first strand may comprise the nucleotide sequence of SEQ ID NO: 5 or SEQ ID NO: 9 and/or the second strand may comprise the nucleotide sequence of SEQ ID NO: 6, or SEQ ID NO:10. The modifications may be those as set out in Table 1.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotide on the second strand which corresponds to position 13 of the first strand is not modified with a 2' O-methyl modification.

A nucleotide on the second strand that "corresponds to" a position on the first strand is suitably the nucleotide that base pairs with that nucleotide on the first strand.

In one aspect the nucleotide on the second strand which corresponds to position 13 of the first strand is the nucleotide that forms a base pair with position 13 of the first strand.

In one aspect the nucleotide on the second strand which corresponds to position 11 of the first strand is the nucleotide that forms a base pair with position 11 of the first strand.

In one aspect the nucleotide on the second strand which corresponds to position 12 of the first strand is the nucleotide that forms a base pair with position 12 of the first strand.

This nomenclature may be applied to other positions of the second strand. For example, in a 19-mer nucleic acid which is double stranded and blunt ended, position 13 of the first strand would pair with position 7 of the second strand. Position 11 of the first strand would pair with position 9 of the second strand. This nomenclature may be applied to other positions of the second strand.

The nucleotide that corresponds to position 13 of the first strand is suitably position 13 of the second strand, counting from the 3' of the second strand, starting from the first nucleotide of the double stranded region. Likewise position 11 of the second strand is suitably the 11^{th} nucleotide from the 3' of the second strand, starting from the first nucleotide of the double stranded region. This nomenclature may be applied to other positions of the second strand.

In one aspect, in the case of a partially complementary first and second strand, the nucleotide on the second strand that "corresponds to" a position on the first strand may not necessarily form a base pair if that position is the position in which there is a mismatch, but the principle of the nomenclature still applies.

Preferred is a first and second strand that are fully complementary over the duplex region (ignoring any overhang regions) and there are no mismatches within the double stranded region of the nucleic acid.

Also preferred are:

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotide on the second strand which corresponds to position 11 of the first strand is not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotides on the second strand which corresponds to position 11 and 13 of the first strand are not modified with a 2' O-methyl modification.

In one aspect the nucleotide on the second strand which corresponds to position 12 of the first strand is not modified with a 2' O-methyl modification. This limitation on the nucleic acid may be seen with any other limitation described herein.

Therefore another aspect of the invention is a nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotides on the second strand which corresponds to position 11-13 of the first strand are not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotides on the second strand which correspond to position 11, or 13, or 11 and 13, or 11-13 of the first strand are modified with a 2' fluoro modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on

the second strand which correspond to position 11, or 13, or 11 and 13, or 11-13 of the first strand are not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to position 11, or 13, or 11 and 13, or preferably 11-13 of the first strand are modified with a 2' fluoro modification. Preferably in this embodiment, all even numbered nucleotide of the first strand are modified with a 2' fluoro modification and all odd numbered nucleotides of the first strand are modified with a 2' O-methyl modification. In addition, the nucleotides on the second strand other than those which correspond to position 11, or 13, or 11 and 13, or preferably 11-13 of the first strand are modified with a 2' O-methyl modification. One advantage of such a nucleic is that it comprises relatively few non-naturally occurring modified nucleotides but is nonetheless able to efficiently inhibit the target gene for long periods of time. Such a nucleic acid is easier to synthesise than corresponding nucleic acids with more non-naturally occurring (2'F modified) nucleotides.

A nucleic acid as disclosed herein wherein greater than 50% of the nucleotides of the first and/or second strand comprise a 2' O-methyl modification, such as greater than 55%, 60%, 65%, 70%, 75%, 80%, or 85%, or more, of the first and/or second strand comprise a 2' O-methyl modification, preferably measured as a percentage of the total nucleotides of both the first and second strands.

A nucleic acid as disclosed herein wherein greater than 50% of the nucleotides of the first and/or second strand comprise a naturally occurring RNA modification, such as wherein greater than 55%, 60%, 65%, 70%, 75%, 80%, or 85% or more of the first and/or second strands comprise such a modification, preferably measured as a percentage of the total nucleotides of both the first and second strands. Suitable naturally occurring modifications include, as well as 2 O' methyl, other 2' sugar modifications, in particular a 2' H modification resulting in a DNA nucleotide.

A nucleic acid as disclosed herein comprising no more than 20%, such as no more than 15% such as no more than 10%, of nucleotides which have 2' modifications that are not 2' O methyl modifications on the first and/or second strand, preferably as a percentage of the total nucleotides of both the first and second strands.

A nucleic acid as disclosed herein comprising no more than 20%, (such as no more than 15% or no more than 10%) of 2' fluoro modifications on the first and/or second strand, preferably as a percentage of the total nucleotides of both strands.

A nucleic acid as disclosed herein, wherein all nucleotides are modified with a 2' O-methyl modification except positions 2 and 14 from the 5' end of the first strand and the nucleotides on the second strand which correspond to position 11, or 13, or 11 and 13, or preferably 11-13 of the first strand. Preferably the nucleotides that are not modified with 2' O-methyl are modified with fluoro at the 2' position.

Preferred is a nucleic acid as disclosed herein wherein all nucleotides of the nucleic acid are modified at the 2' position of the sugar. Preferably these nucleotides are modified with a 2'- fluoro modification where the modification is not a 2' O-Methyl modification.

Nucleic acids of the invention may comprise one or more nucleotides modified at the 2' position with a 2' H, and therefore having a DNA nucleotide within the nucleic acid. Nucleic acids of the invention may comprise DNA nucleotides at positions 2 and/or 14 of the first strand counting from the 5' end of the first strand. Nucleic acids may comprise DNA nucleotides on the second strand which correspond to position 11, or 13, or 11 and 13, or 11-13 of the first strand.

In one aspect there is no more than one DNA per nucleic acid of the invention.

Nucleic acids of the invention may comprise one or more LNA nucleotides. Nucleic acids of the invention may comprise LNA nucleotides at positions 2 and/or 14 of the first strand counting from the 5' end of the first strand. Nucleic acids may comprise LNA on the second strand which correspond to position 11, or 13, or 11 and 13, or 11-13 of the first strand.

In one aspect the nucleic acid is modified on the first strand, preferably along the entire strand, with alternating 2' O-methyl modifications and 2' fluoro modifications, and positions 2 and 14 (starting from the 5' end) are modified with 2' fluoro. Preferably the second strand is modified with 2' fluoro modifications at nucleotides on the second strand which correspond to position 11, or 13, or 11 and 13, or preferably 11-13 of the first strand. Preferably the second strand is modified with 2' fluoro modifications at positions 11-13 counting from the 3' end starting at the first position of the complementary (double stranded) region, and the remaining modifications are naturally occurring modifications, preferably 2'

O-methyl. In this case at least, the nucleic acid preferably has a blunt end at least at the end that comprises the 5' end of the first strand.

A nucleotide of the second strand that is in a position corresponding for example to an even-numbered nucleotide of the first strand is a nucleotide of the second strand that is base-paired to an even-numbered nucleotide of the first strand.

In one aspect of the nucleic acid, the nucleotide/nucleotides of the second strand in a position corresponding to nucleotide 11 or nucleotide 13 or nucleotides 11 and 13 or preferably nucleotides 11-13 of the first strand is/are modified by a fourth modification. Preferably, all the nucleotides of the second strand other than the nucleotide/nucleotides in a position corresponding to nucleotide 11 or nucleotide 13 or nucleotides 11 and 13 or preferably nucleotides 11-13 of the first strand is/are modified by a third modification. Preferably in the same nucleic acid nucleotides 2 and 14 or preferably all the even numbered nucleotides of the first strand are modified with a first modification. In addition, or alternatively, the odd-numbered nucleotides of the first strand are modified with a second modification. The fourth modification is preferably different from the second modification and preferably different from the third modification and the fourth modification is preferably the same as the first modification. The first and the fourth modification are preferably a 2'-OMe modification and the second and third modification are preferably a 2'-F modification. The nucleotides on the first strand are numbered consecutively starting with nucleotide number 1 at the 5' end of the first strand.

In one aspect of the nucleic acid, all the even-numbered nucleotides of the first strand are modified by a first modification, all the odd-numbered nucleotides of the first strand are modified by a second modification, all the nucleotides of the second strand in positions corresponding to nucleotides 11-13 of the first strand are modified by a fourth modification, all the nucleotides of the second strand other than the nucleotides corresponding to nucleotides 11-13 of the first strand are modified by a third modification, wherein the first and fourth modification are 2'-F and the second and third modification are 2'-OMe. The nucleotides on the first strand are numbered consecutively starting with nucleotide number 1 at the 5' end of the first strand.

In one aspect of the nucleic acid, each of the nucleotides of the first strand and of the second strand is a modified nucleotide.

One aspect is a double-stranded nucleic acid for inhibiting expression of *LPA*, preferably in a cell, wherein the nucleic acid comprises a first strand and a second strand, wherein the first strand sequence comprises a sequence of at least 15 nucleotides differing by no more than 3 nucleotides from any one of the sequences SEQ ID NO: 9, 5, 1, 3, 7, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43, preferably SEQ ID NO: 9, wherein all the even-numbered nucleotides of the first strand are modified by a first modification, all the odd-numbered nucleotides of the first strand are modified by a second modification, all the nucleotides of the second strand in positions corresponding to nucleotides 11-13 of the first strand are modified by a fourth modification, all the nucleotides of the second strand other than the nucleotides corresponding to nucleotides 11-13 of the first strand modified by a third modification, wherein the first and fourth modification are 2'-F and the second and third modification are 2'-OMe.

One aspect are nucleic acids which are siRNA molecules wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleic acid comprises one or more or all of:

(i) an inverted nucleotide, preferably a 3'-3' linkage at the 3' end of the second strand;
(ii) one or more phosphorodithioate linkages;
(iii) the second strand nucleotide corresponding to position 11 or 13 of the first strand is not modified with a 2' O-methyl modification, preferably wherein one or both of these positions comprise a 2' fluoro modification;
(iv) the nucleic acid comprises at least 80% of all nucleotides having a 2'-O-methly modification;
(v) the nucleic acid comprises no more than 20% of nucleotides which have 2' fluoro modifications.

Also provided by the present invention is a nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand and the nucleotides at positions 7 and/or 9, or 7 - 9 from the 5' end of the second strand are modified with a 2' fluoro modification, and at least 90% of the remaining nucleotides are 2'-O methyl modified or comprise another naturally occurring 2' modification.

Specific preferred examples, for a blunt double stranded 19 base nucleic acid, with no overhang, are:

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotide

at position 7 from the 5' end of the second strand is not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotide at position 9 from the 5' end of the second strand is not modified with a 2' O-methyl modification

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotides at position 7 and 9 from the 5' end of the second strand are not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotides at positions 7 - 9 from the 5' end of the second strand are not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are not modified with a 2' O-methyl modification, and the nucleotides at positions 7 and/or 9, or 7-9 from the 5' end of the second strand are modified with a 2' fluoro modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides at positions 7 and/or 9, or 7 - 9 from the 5' end of the second strand are not modified with a 2' O-methyl modification.

A nucleic acid as disclosed herein, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides at positions 7 and/or 9, or 7 - 9 from the 5' end of the second strand are modified with a 2' fluoro modification.

A nucleic acid as disclosed herein wherein greater than 50% of the nucleotides of the first and/or second strand comprise a 2' O-methyl modification, such as greater than 55%, 60%, 65%, 70%, 75%, 80%, or 85%, or more, of the first and/or second strand comprise a 2' O-

methyl modification, preferably measured as a percentage of the total nucleotides of both the first and second strands.

A nucleic acid as disclosed herein wherein greater than 50% of the nucleotides of the first and/or second strand comprise a naturally occurring RNA modification, such as wherein greater than 55%, 60%, 65%, 70%, 75%, 80%, or 85% or more of the first and/or second strands comprise such a modification, preferably measured as a percentage of the total nucleotides of both the first and second strands. Suitable naturally occurring modifications include, as well as 2 O' methyl, other 2' sugar modifications, in particular a 2' H modification resulting in a DNA nucleotide.

A nucleic acid as disclosed herein comprising no more than 20%, such as no more than 15% such as more than 10%, of nucleotides which have 2' modifications that are not 2' O methyl modifications on the first and/or second strand, preferably as a percentage of the total nucleotides of both the first and second strands.

A nucleic acid as disclosed herein comprising no more than 20%, (such as no more than 15% or no more than 10%) of 2' fluoro modifications on the first and/or second strand, preferably as a percentage of the total nucleotides of both strands.

A nucleic acid as disclosed herein, wherein all nucleotides are modified with a 2' O-methyl modification except positions 2 and 14 from the 5' end of the first strand and the nucleotides at positions 7 and/or 9 from the 5' end of the second strand. Preferably the nucleotides that are not modified with 2' O-methyl are modified with fluoro at the 2' position.

A nucleic acid as disclosed herein, wherein all nucleotides are modified with a 2' O-methyl modification except positions 2 and 14 from the 5' end of the first strand and the nucleotides at positions 7 - 9 from the 5' end of the second strand. Preferably the nucleotides that are not modified with 2' O-methyl are modified with fluoro at the 2' position.

For a nucleic acid comprising a 20 base pair duplex region, the second strand preferably does not have a 2' O-methyl group at nucleotides 8 or 9 or 10 counting from the 5' end of the duplex corresponding to positions 13, 12, and 11 of the first strand respectively.

For a nucleic acid comprising a 21 base pair duplex region, the second strand preferably does not have a 2' O-methyl group at nucleotides 9 or 10 or 11 counting from the 5' end of the duplex corresponding to positions 13, 12, and 11 of the first strand respectively.

The nucleic acid of the present invention may include one or more phosphorothioate modifications on one or more of the ends of the first and/or the second strand. Optionally, each or either end of the first strand may comprise one or two or three phosphorothioate modified nucleotides. Optionally, each or either end of the second strand may comprise one or two or three phosphorothioate modified nucleotides.

In one embodiment, the first strand may include at least one phosphorothioate (ps) linkage.

In one embodiment, the first strand may further comprise a phosphorothioate linkage between the terminal two 3' nucleotides or phosphorothioate linkages between the terminal three 3' nucleotides.

In one embodiment, the linkages between the other nucleotides in the first strand are phosphodiester linkages.

In one embodiment, the first strand may include more than 1 phosphorothioate linkage.

In a further embodiment, the second strand may comprise a phosphorothioate linkage between the terminal two 3' nucleotides or phosphorothioate linkages between the terminal three 3' nucleotides.

In another further embodiment, the second strand may comprise a phosphorothioate linkage between the terminal two 5' nucleotides or phosphorothioate linkages between the terminal three 5' nucleotides.

In one aspect the nucleic acid comprises one or more phosphorodithioate linkages, such as 1, 2, 3 or 4 phosphorodithioate linkages. Preferably there are up to 4 phosphorodithioate linkages, one each at the 5' and 3' ends of the first and second strands.

The use of a phosphorodithioate linkage in the nucleic acid of the invention reduces the variation in the stereochemistry of a population of nucleic acid molecules compared to molecules comprising a phosphorothioate in that same position. Phosphorothioate linkage indeed introduce a chiral centre and it is difficult to control which non-linking oxygen is substituted for sulphur. The use of a phosphorodithioate ensures that no chiral centre exists in that linkage and thus reduces or eliminates any variation in the population of nucleic acid

molecules, depending on the number of phosphorodithioate and phosphorothioate linkages used in the nucleic acid molecule.

In one aspect, the nucleic acid comprises a phosphorothioate linkage between each of the three terminal 3' nucleotides and/or between each of the three terminal 5' nucleotides on the first strand, and/or between each of the three terminal 3' nucleotides and/or between each of the three terminal 5' nucleotides of the second strand when there is no phosphorodithioate linkage present at that end. No phosphorodithioate linkage being present at an end means that the linkage between the two terminal nucleotides, or preferably between the three terminal nucleotides of the nucleic acid end in question are linkages other than phosphorodithioate linkages.

The invention also provides a nucleic acid according to any aspect of the invention described herein, wherein the first RNA strand has a terminal 5' (E)-vinylphosphonate nucleotide, and the terminal 5' (E)-vinylphosphonate nucleotide is linked to the second nucleotide in the first strand by a phosphodiester linkage. The first strand may include more than one phosphodiester linkage. In one embodiment, the first strand may comprise phosphodiester linkages between at least the terminal three 5' nucleotides. In one embodiment, the first strand may comprise phosphodiester linkages between at least the terminal four 5' nucleotides.

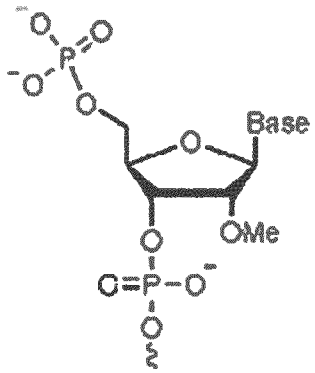
In one embodiment, the first strand may comprise formula (IV):

$$(vp)\text{-}N(po)[N(po)]_n\text{-} \qquad (IV)$$

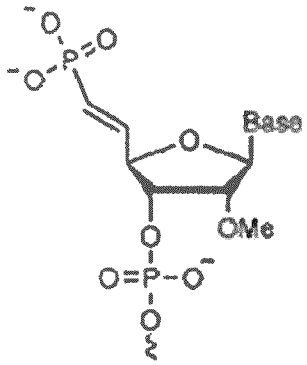
where '(vp)-' is the 5' (E)-vinylphosphonate, 'N' is a nucleotide, 'po' is a phosphodiester linkage, and n is from 1 to (the total number of nucleotides in the first strand – 2), preferably wherein n is from 1 to (the total number of nucleotides in the first strand -3), more preferably wherein n is from 1 to (the total number of nucleotides in the first strand -4).

In one aspect, if the 5'-most nucleotide of the first strand is a nucleotide other than A or U, this nucleotide is replaced by A or U in the sequence. Preferably, if the 5'-most nucleotide of the first strand is a nucleotide other than U, this nucleotide is replaced by U, and more preferably by U with a 5' vinylphosphonate, in the sequence.

A terminal 5' (E)-vinylphosphonate nucleotide is a nucleotide wherein the natural phosphate group at the 5'-end has been replaced with a E-vinylphosphonate, in which the bridging 5'-oxygen atom of the terminal nucleotide of the 5' phosphorylated strand is replaced with a methynyl (-CH=) group:



Nucleotides with a natural phosphate at the 5'-end



Nucleotide with a E-vinylphosphonate at the 5'-end

5' (E) vinylphosphonate is a 5' phosphate mimic. A biological mimic is a molecule that is capable of carrying out the same function as and is structurally very similar to the original molecule that is being mimicked. In the context of the present invention, 5' (E) vinylphosphonate mimics the function of a normal 5' phosphate, e.g. enabling efficient RISC loading. In addition, because of its slightly altered structure, 5' (E) vinylphosphonate is capable of stabilizing the 5'-end nucleotide by protecting it from dephosphorylation by enzymes such as phosphatases.

In an embodiment, the terminal 5' (E)-vinylphosphonate nucleotide is an RNA nucleotide.

In one aspect, the nucleic acid:

(i) has a phosphorothioate linkage between the terminal three 3' nucleotides and the terminal three 5' nucleotides of the first strand;
(ii) is conjugated to a triantennary ligand either on the 3' end nucleotide or on the 5' end nucleotide of the second strand;
(iii) has a phosphorothioate linkage between the terminal three nucleotides of the second strand at the end opposite to the one conjugated to the triantennary ligand; and
(iv) all remaining linkages between nucleotides of the first and/or of the second strand are phosphodiester linkages.

In one aspect, the nucleic acid:

(i) has a terminal 5' (E)-vinylphosphonate nucleotide at the 5' end of the first strand;
(ii) has a phosphorothioate linkage between the terminal three 3' nucleotides on the first and second strand and between the terminal three 5' nucleotides on the second strand; and

(iii) all remaining linkages between nucleotides of the first and/or of the second strand are phosphodiester linkages.

In one aspect, the nucleic acid, which is preferably an siRNA that inhibits expression of *LPA*, preferably via RNAi, comprises one or more or all of:

(i) a modified nucleotide;

(ii) a modified nucleotide other than a 2'-OMe modified nucleotide at positions 2 and 14 from the 5' end of the first strand, preferably a 2'-F modified nucleotide;

(iii) each of the odd-numbered nucleotides of the first strand as numbered starting from one at the 5' end of the first strand are 2'-OMe modified nucleotides;

(iv) each of the even-numbered nucleotides of the first strand as numbered starting from one at the 5' end of the first strand are 2'-F modified nucleotides;

(v) the second strand nucleotide corresponding to position 11 or 13 of the first strand is modified by a modification other than a 2'-OMe modification, preferably wherein one or both of these positions comprise a 2'-F modification;

(vi) an inverted nucleotide, preferably a 3'-3' linkage at the 3' end of the second strand;

(vii) one or more phosphorothioate linkages;

(viii) one or more phosphorodithioate linkages; and/or

(ix) the first strand has a terminal 5' (E)-vinylphosphonate nucleotide at its 5' end, in which case the terminal 5' (E)-vinylphosphonate nucleotide is preferably a uridine and is preferably linked to the second nucleotide in the first strand by a phosphodiester linkage.

The nucleic acids of the invention may include one or more inverted nucleotides, for example inverted thymidine or inverted adenine (for example see Takei, et al., 2002. JBC 277 (26):23800-06).

In one aspect the nucleic acid of the invention comprises one or more inverted ribonucleotides, preferably an inverted adenine, using a 5'-5' linkage or a 3'-3' linkage, preferably a 3'-3' linkage at the 3' end of the second strand.

The nucleic acid of the invention may comprise an inverted RNA nucleotide at one or several of the strand ends. Such inverted nucleotides provide stability to the nucleic acid. Preferably, the nucleic acid comprises at least an inverted nucleotide at one or several of the 3' end of at least one of the strands and/or at the 5' end of the of the second strand. More preferably, the nucleic acid comprises an inverted nucleotide at the 3' end of the second strand. Most preferably, the nucleic acid comprises an inverted RNA nucleotide at the 3' end of the second strand and this nucleotide is preferably an inverted A. The inverted

nucleotide is preferably present at an end of a strand not as an overhang but opposite a corresponding nucleotide in the other strand. A nucleic acid with such a modification is stable and easy to synthesise.

Ligands

The nucleic acid of the invention may be conjugated to a ligand. Efficient delivery of oligonucleotides, in particular double stranded nucleic acids of the invention, to cells *in vivo* is important and requires specific targeting and substantial protection from the extracellular environment, particularly serum proteins. One method of achieving specific targeting is to conjugate a ligand to the nucleic acid. The ligand helps in targeting the nucleic acid to the required target site. There is a need to conjugate appropriate ligands for the desired receptor molecules in order for the conjugated molecules to be taken up by the target cells by mechanisms such as different receptor-mediated endocytosis pathways or functionally analogous processes.

One example is the asialoglycoprotein receptor complex (ASGP-R) composed by varying ratios of multimers of membrane ASGR1 and ASGR2 receptors, which is highly abundant on hepatocytes and has high affinity to the here described GalNAc moiety. One of the first disclosures of the use of triantennary cluster glycosides as conjugated ligands was in US patent number US 5,885,968. Conjugates having three GalNAc ligands and comprising phosphate groups are known and are described in Dubber et al. (Bioconjug. Chem. 2003 Jan-Feb;14(1):239-46.). The ASGP-R complex shows a 50-fold higher affinity for N-Acetyl-D-Galactosylamine (GalNAc) than D-Gal.

The asialoglycoprotein receptor complex (ASGP-R), which recognizes specifically terminal β-galactosyl subunits of glycosylated proteins or other oligosaccharides (Weigel, P.H. et. al., Biochim. Biophys. Acta. 2002 Sep 19;1572(2-3):341-63) can be used for delivering a drug to the liver's hepatocytes expressing the receptor complex by covalent coupling of galactose or galactosamine to the drug substance (Ishibashi,S.; et. al., J Biol. Chem. 1994 Nov 11;269(45):27803-6). Furthermore the binding affinity can be significantly increased by the multi-valency effect, which is achieved by the repetition of the targeting moiety (Biessen EA, et al., J Med Chem. 1995 Apr 28;38(9):1538-46.).

The ASGP-R complex is a mediator for an active uptake of terminal β-galactosyl containing glycoproteins to the cell's endosomes. Thus, the ASGPR is highly suitable for targeted delivery of drug candidates conjugated to such ligands like, e.g., nucleic acids into receptor-expressing cells (Akinc et al., Mol Ther. 2010 Jul;18(7):1357-64).

More generally the ligand can comprise a saccharide that is selected to have an affinity for at least one type of receptor on a target cell. In particular, the receptor is on the surface of a mammalian liver cell, for example, the hepatic asialoglycoprotein receptor complex described before (ASGP-R).

The saccharide may be selected from N-acetyl galactosamine, mannose, galactose, glucose, glucosamine and fucose. The saccharide may be N-acetyl galactosamine (GalNAc).

A ligand for use in the present invention may therefore comprise (i) one or more N-acetyl galactosamine (GalNAc) moieties and derivatives thereof, and (ii) a linker, wherein the linker conjugates the GalNAc moieties to a sequence as defined in any preceding aspects. The linker may be a bivalent or trivalent or tetravalent branched structure. The nucleotides may be modified as defined herein.

"GalNAc" refers to 2-(Acetylamino)-2-deoxy-D- galactopyranose, commonly referred to in the literature as N-acetyl galactosamine. Reference to "GalNAc" or "N-acetyl galactosamine" includes both the β- form: 2-(Acetylamino)-2-deoxy-β -D-galactopyranose and the α-form: 2-(Acetylamino)-2-deoxy-α-D- galactopyranose. Both the β-form: 2-(Acetylarnino)-2-deoxy-β-D-galactopyranose and α-form: 2-(Acetylamino)-2-deoxy-α-D-galactopyranose may be used interchangeably. Preferably, the compounds of the invention comprise the β-form, 2-(Acetylarnino)-2-deoxy-β-D-galactopyranose.

The ligand may therefore comprise GalNAc.

The ligand may comprise a compound of formula (I):

$$[S\text{-}X^1\text{-}P\text{-}X^2]_3\text{-}A\text{-}X^3\text{-} \quad (I)$$

wherein:

S represents a saccharide, wherein the saccharide is N-acetyl galactosamine;

X^1 represents C_3-C_6 alkylene or $(\text{-}CH_2\text{-}CH_2\text{-}O)_m(\text{-}CH_2)_2\text{-}$ wherein m is 1, 2, or 3;

P is a phosphate or modified phosphate (preferably a thiophosphate);

X^2 is alkylene or an alkylene ether of the formula $(\text{-}CH_2)_n\text{-}O\text{-}CH_2\text{-}$ where n = 1- 6;

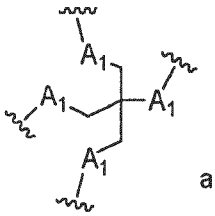
A is a branching unit;

X^3 represents a bridging unit;

wherein a nucleic acid according to the present invention is conjugated to X^3 via a phosphate or modified phosphate (preferably a thiophosphate).

In formula (I), branching unit "A" branches into three in order to accommodate the three saccharide ligands. The branching unit is covalently attached to the remaining tethered portions of the ligand and the nucleic acid. The branching unit may comprise a branched aliphatic group comprising groups selected from alkyl, amide, disulphide, polyethylene glycol, ether, thioether and hydroxyamino groups. The branching unit may comprise groups selected from alkyl and ether groups.

The branching unit A may have a structure selected from:



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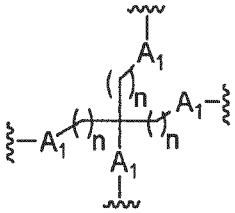
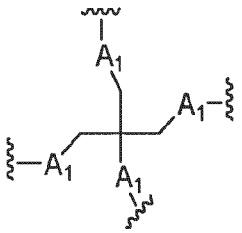


wherein each A_1 independently represents O, S, C=O or NH; and
each n independently represents an integer from 1 to 20.

The branching unit may have a structure selected from:



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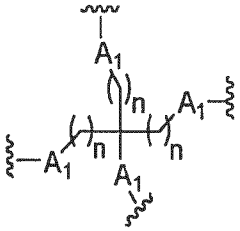

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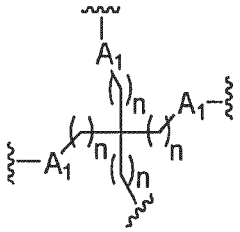
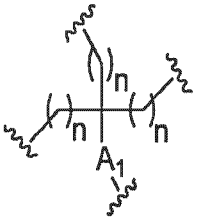
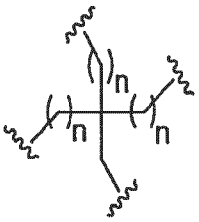


wherein each A_1 independently represents O, S, C=O or NH; and
each n independently represents an integer from 1 to 20.

The branching unit may have a structure selected from:

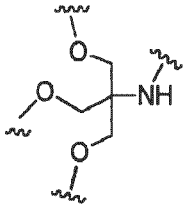


and

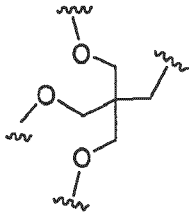


wherein A_1 is O, S, C=O or NH; and
each n independently represents an integer from 1 to 20.

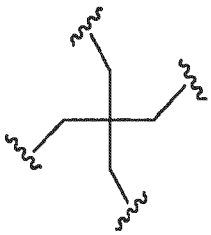
The branching unit may have the structure:



The branching unit may have the structure:



The branching unit may have the structure:



Optionally, the branching unit consists of only a carbon atom.

The "X^3" portion is a bridging unit. The bridging unit is linear and is covalently bound to the branching unit and the nucleic acid.

X^3 may be selected from -C_1-C_{20} alkylene-, -C_2-C_{20} alkenylene-, an alkylene ether of formula -(C_1-C_{20} alkylene)–O–(C_1-C_{20} alkylene)-, -C(O)-C_1-C_{20} alkylene-, -C_0-C_4 alkylene(Cy)C_0-C_4 alkylene- wherein Cy represents a substituted or unsubstituted 5 or 6 membered cycloalkylene, arylene, heterocyclylene or heteroarylene ring, -C_1-C_4 alkylene-NHC(O)-C_1-C_4 alkylene-, -C_1-C_4 alkylene-C(O)NH-C_1-C_4 alkylene-, -C_1-C_4 alkylene-SC(O)-C_1-C_4 alkylene-, -C_1-C_4 alkylene-C(O)S-C_1-C_4 alkylene-, -C_1-C_4 alkylene-OC(O)-C_1-C_4 alkylene-, -C_1-C_4 alkylene-C(O)O-C_1-C_4 alkylene-, and -C_1-C_6 alkylene-S-S-C_1-C_6 alkylene-.

X^3 may be an alkylene ether of formula -(C_1-C_{20} alkylene)–O–(C_1-C_{20} alkylene)-. X^3 may be an alkylene ether of formula -(C_1-C_{20} alkylene)–O–(C_4-C_{20} alkylene)-, wherein said (C_4-C_{20} alkylene) is linked to Z. X^3 may be selected from the group consisting of -CH_2-O-C_3H_6-, -CH_2-O-C_4H_8-, -CH_2-O-C_6H_{12}- and -CH_2-O-C_8H_{16}-, especially -CH_2-O-C_4H_8-, -CH_2-O-C_6H_{12}- and -CH_2-O-C_8H_{16}-, wherein in each case the -CH_2- group is linked to A.

The ligand may comprise a compound of formula (II):

$$[S\text{-}X^1\text{-}P\text{-}X^2]_3\text{-}A\text{-}X^3\text{-} \quad (II)$$

wherein:

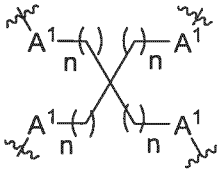
S represents a saccharide;

X^1 represents C_3-C_6 alkylene or $(\text{-}CH_2\text{-}CH_2\text{-}O)_m(\text{-}CH_2)_2\text{-}$ wherein m is 1, 2, or 3;

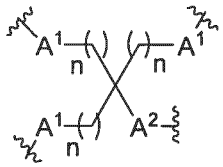
P is a phosphate or modified phosphate (preferably a thiophosphate);

X^2 is C_1-C_8 alkylene;

A is a branching unit selected from:



A^1 = O, NH
n = 1 to 4

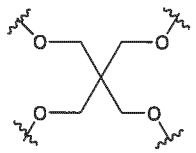


A^1 = O, NH A^2 = NH, CH_2, O
n = 1 to 4

X^3 is a bridging unit;.

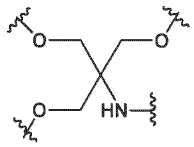
wherein a nucleic acid according to the present invention is conjugated to X^3 via a phosphate or modified phosphate (preferably a thiophosphate)

Branching unit A may have the structure:



.

Branching unit A may have the structure:



, wherein X^3 is attached to the nitrogen atom.

X^3 may be C_1-C_{20} alkylene. Preferably, X^3 is selected from the group consisting of $\text{-}C_3H_6\text{-}$, $\text{-}C_4H_8\text{-}$, $\text{-}C_6H_{12}\text{-}$ and $\text{-}C_8H_{16}\text{-}$, especially $\text{-}C_4H_8\text{-}$, $\text{-}C_6H_{12}\text{-}$ and $\text{-}C_8H_{16}\text{-}$.

The ligand may comprise a compound of formula (III):

$$[S\text{-}X^1\text{-}P\text{-}X^2]_3\text{-}A\text{-}X^3\text{-} \quad (III)$$

wherein:

S represents a saccharide;

X^1 represents C_3-C_6 alkylene or $(\text{-}CH_2\text{-}CH_2\text{-}O)_m(\text{-}CH_2)_2\text{-}$ wherein m is 1, 2, or 3;

P is a phosphate or modified phosphate (preferably a thiophosphate);

X^2 is an alkylene ether of formula $-C_3H_6-O-CH_2-$;

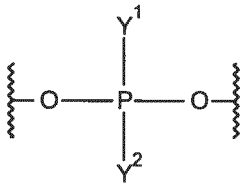
A is a branching unit;

X^3 is an alkylene ether of formula selected from the group consisting of $-CH_2-O-CH_2-$, $-CH_2-O-C_2H_4-$, $-CH_2-O-C_3H_6-$, $-CH_2-O-C_4H_8-$, $-CH_2-O-C_5H_{10}-$, $-CH_2-O-C_6H_{12}-$, $-CH_2-O-C_7H_{14}-$, and $-CH_2-O-C_8H_{16}-$, wherein in each case the $-CH_2-$ group is linked to A, and wherein X^3 is conjugated to a nucleic acid according to the present invention by a phosphate or modified phosphate (preferably a thiophosphate).

The branching unit may comprise carbon. Preferably, the branching unit is carbon.

X^3 may be selected from the group consisting of $-CH_2-O-C_4H_8-$, $-CH_2-O-C_5H_{10}-$, $-CH_2-O-C_6H_{12}-$, $-CH_2-O-C_7H_{14}-$, and $-CH_2-O-C_8H_{16}-$. Preferably, X^3 is selected from the group consisting of $-CH_2-O-C_4H_8-$, $-CH_2-O-C_6H_{12}-$ and $-CH_2-O-C_8H_{16}$.

For any of the above aspects, when P represents a modified phosphate group, P can be represented by:



wherein Y^1 and Y^2 each independently represent =O, =S, $-O^-$, -OH, -SH, $-BH_3$, $-OCH_2CO_2$, $-OCH_2CO_2R^x$, $-OCH_2C(S)OR^x$, and $-OR^x$, wherein R^x represents C_1-C_6 alkyl and wherein ⫞ indicates attachment to the remainder of the compound.

By modified phosphate it is meant a phosphate group wherein one or more of the non-linking oxygens is replaced. Examples of modified phosphate groups include phosphorothioate, phosphoroselenates, borano phosphates, borano phosphate esters, hydrogen phosphonates, phosphoroamidates, alkyl or aryl phosphonates and phosphotriesters. Phosphorodithioates have both non-linking oxygens replaced by sulphur. One, each or both non-linking oxygens in the phosphate group can be independently any one of S, Se, B, C, H, N, or OR (R is alkyl or aryl).

The phosphate can also be modified by replacement of a linking oxygen with nitrogen (bridged phosphoroamidates), sulfur (bridged phosphorothioates) and carbon (bridged methylenephosphonates). The replacement can occur at a terminal oxygen. Replacement of the non-linking oxygens with nitrogen is possible.

For example, Y^1 may represent -OH and Y^2 may represent =O or =S; or
Y^1 may represent $-O^-$ and Y^2 may represent =O or =S;
Y^1 may represent =O and Y^2 may represent $-CH_3$, -SH, $-OR^x$, or $-BH_3$
Y^1 may represent =S and Y^2 may represent $-CH_3$, OR^x or –SH.

It will be understood by the skilled person that in certain instances there will be delocalisation between Y^1 and Y^2.

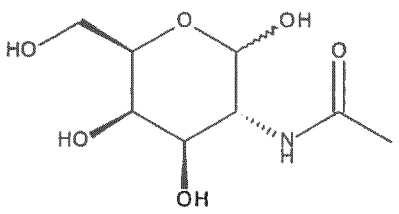
Preferably, the modified phosphate group is a thiophosphate group. Thiophosphate groups include bithiophosphate (i.e. where Y^1 represents =S and Y^2 represents $-S^-$) and monothiophosphate (i.e. where Y^1 represents $-O^-$ and Y^2 represents =S, or where Y^1 represents =O and Y^2 represents $-S^-$). Preferably, P is a monothiophosphate. The inventors have found that conjugates having thiophosphate groups in replacement of phosphate groups have improved potency and duration of action *in vivo*.

P may also be an ethylphosphate (i.e. where Y^1 represents =O and Y^2 represents OCH_2CH_3).

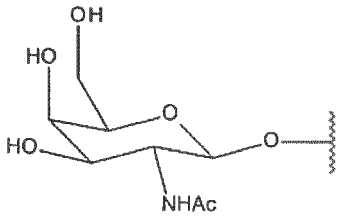
The saccharide may be selected to have an affinity for at least one type of receptor on a target cell. In particular, the receptor is on the surface of a mammalian liver cell, for example, the hepatic asialoglycoprotein receptor complex (ASGP-R).

For any of the above aspects, the saccharide may be selected from N-acetyl with one or more of galactosamine, mannose, galactose, glucose, glucosamine and fructose. Typically a ligand to be used in the present invention may include N-acetyl galactosamine (GalNAc). Preferably the compounds of the invention may have 3 ligands, which will each preferably include N-acetyl galactosamine.

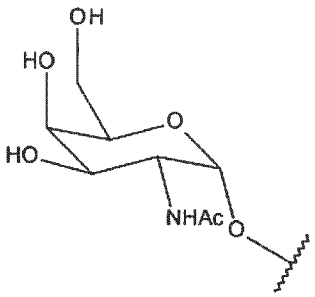
"GalNAc" refers to 2-(Acetylamino)-2-deoxy-D- galactopyranose, commonly referred to in the literature as N-acetyl galactosamine. Reference to “GalNAc” or “N-acetyl galactosamine” includes both the β- form: 2-(Acetylamino)-2-deoxy-β -D-galactopyranose and the α-form: 2-(Acetylamino)-2-deoxy-α-D- galactopyranose. In certain embodiments, both the β-form: 2-(Acetylarnino)-2-deoxy-β-D-galactopyranose and α-form: 2-(Acetylamino)-2-deoxy-α-D-galactopyranose may be used interchangeably. Preferably, the compounds of the invention comprise the β-form, 2-(Acetylarnino)-2-deoxy-β-D-galactopyranose.



2-(Acetylamino)-2-deoxy-D-galactopyranose



2-(Acetylamino)-2-deoxy-β-D-galactopyranose

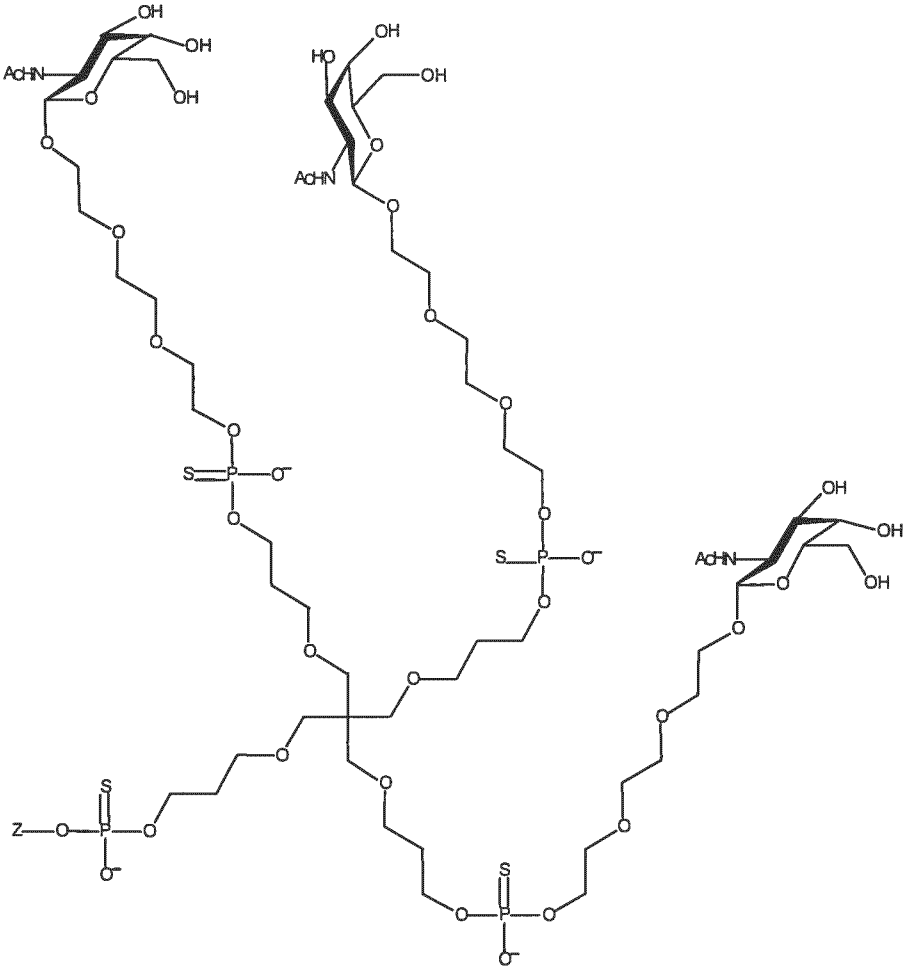


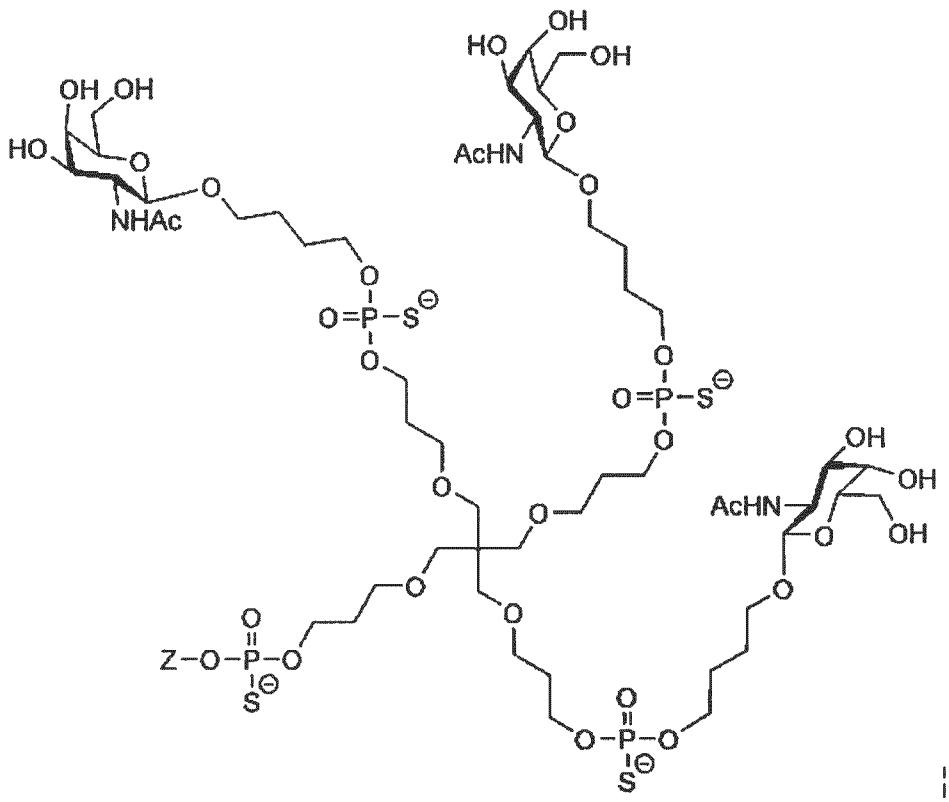
2-(Acetylamino)-2-deoxy-α-D-galactopyranose

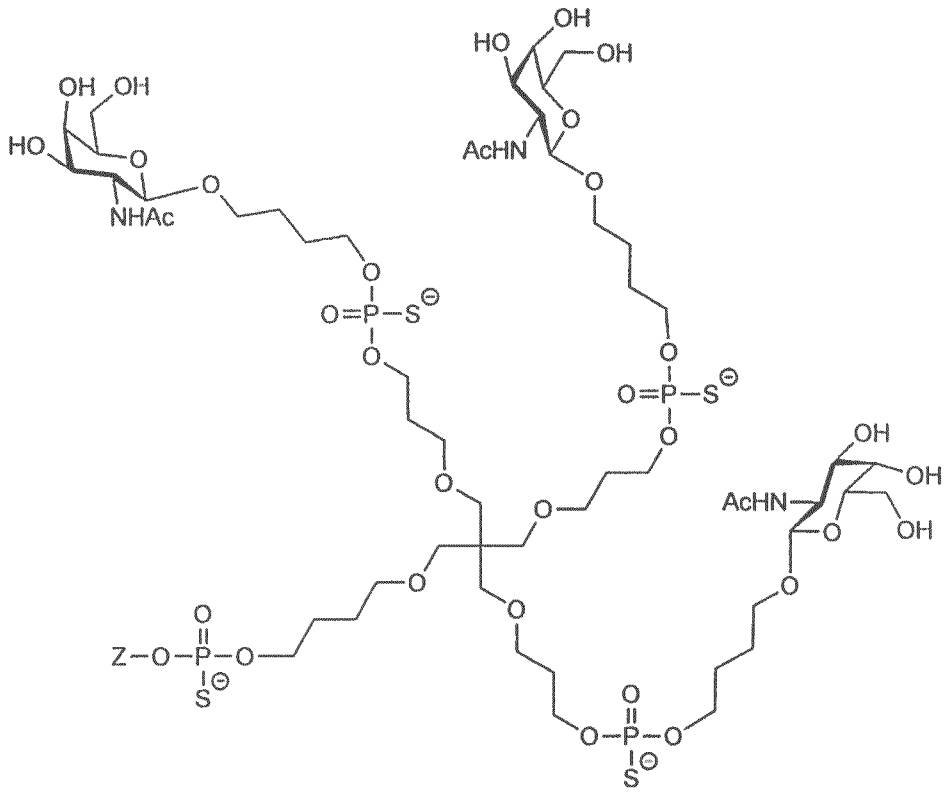
For any of the above compounds of formula (III), X^1 may be $(-CH_2-CH_2-O)(-CH_2)_2-$. X^1 may be $(-CH_2-CH_2-O)_2(-CH_2)_2-$. X^1 may be $(-CH_2-CH_2-O)_3(-CH_2)_2-$. Preferably, X^1 is $(-CH_2-CH_2-O)_2(-CH_2)_2-$. Alternatively, X^1 represents C_3-C_6 alkylene. X^1 may be propylene. X^1 may be butylene. X^1 may be pentylene. X^1 may be hexylene. Preferably the alkyl is a linear alkylene. In particular, X^1 may be butylene.

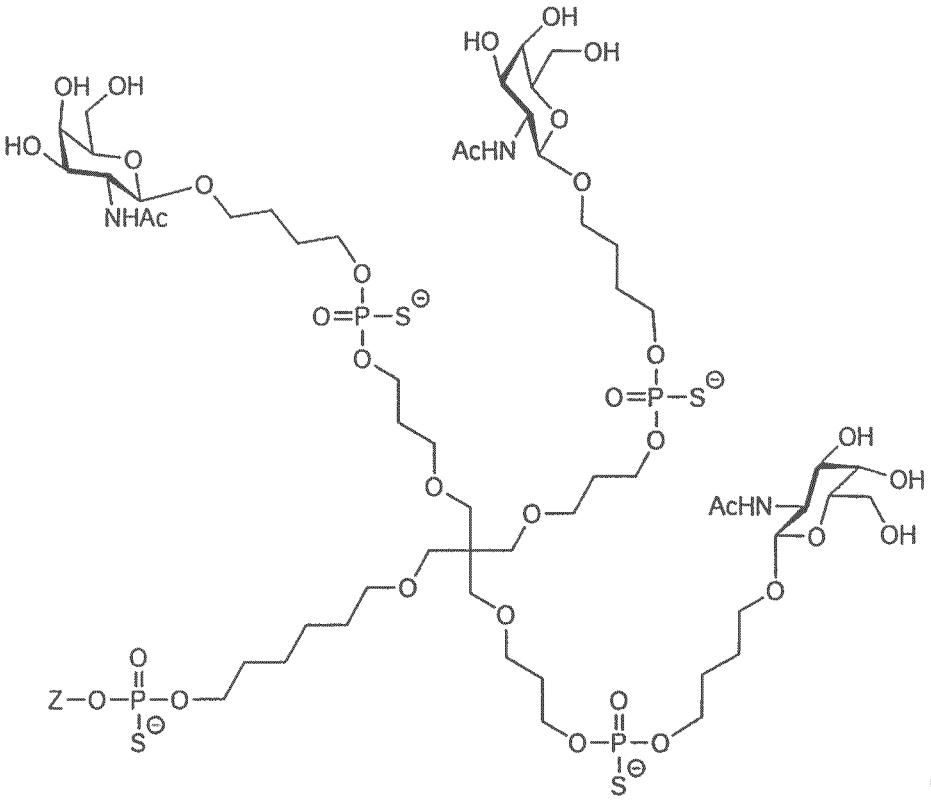
For compounds of formula (III), X^2 represents an alkylene ether of formula $-C_3H_6-O-CH_2-$ i.e. C_3 alkoxy methylene, or $–CH_2CH_2CH_2OCH_2-$.

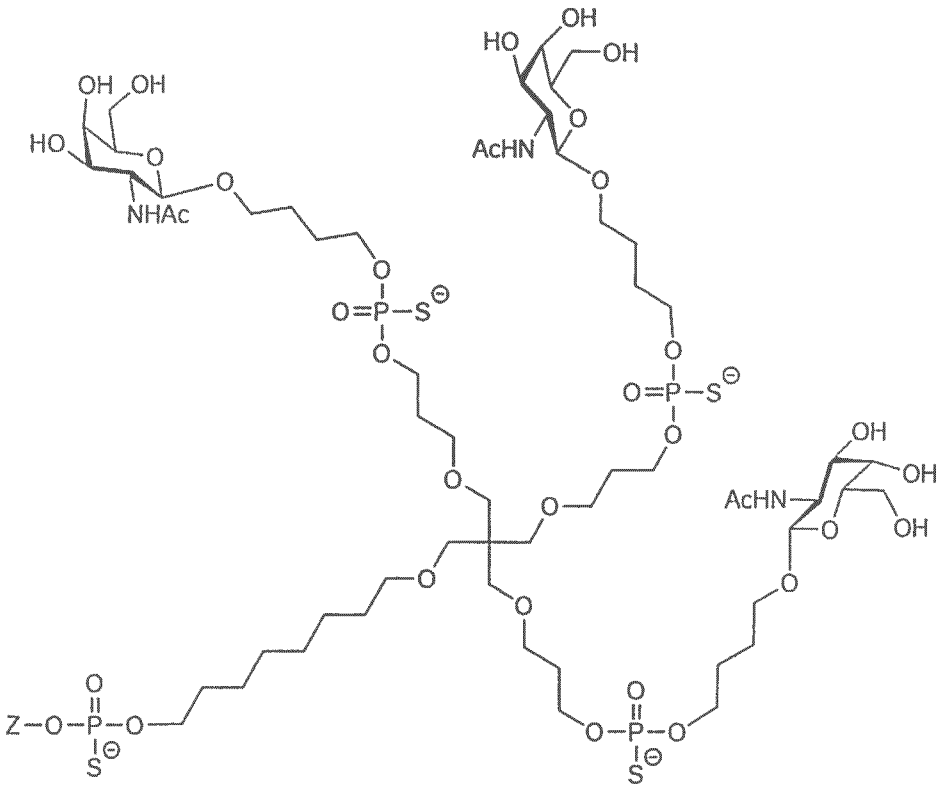
The invention provides a conjugated nucleic acid having one of the following structures:

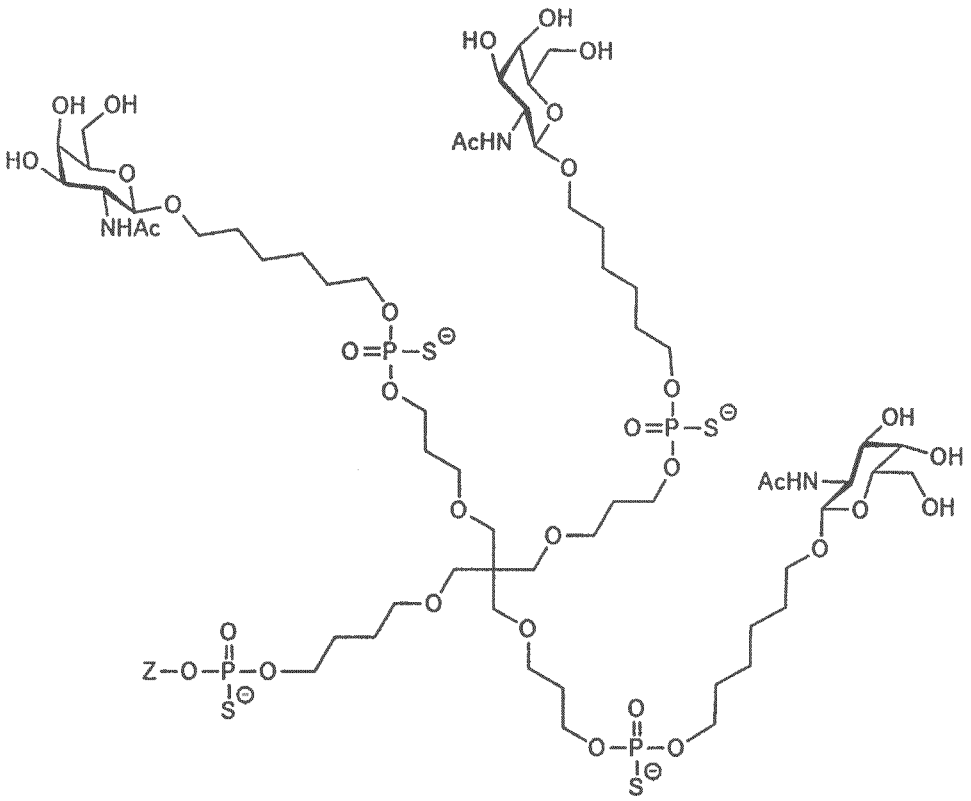


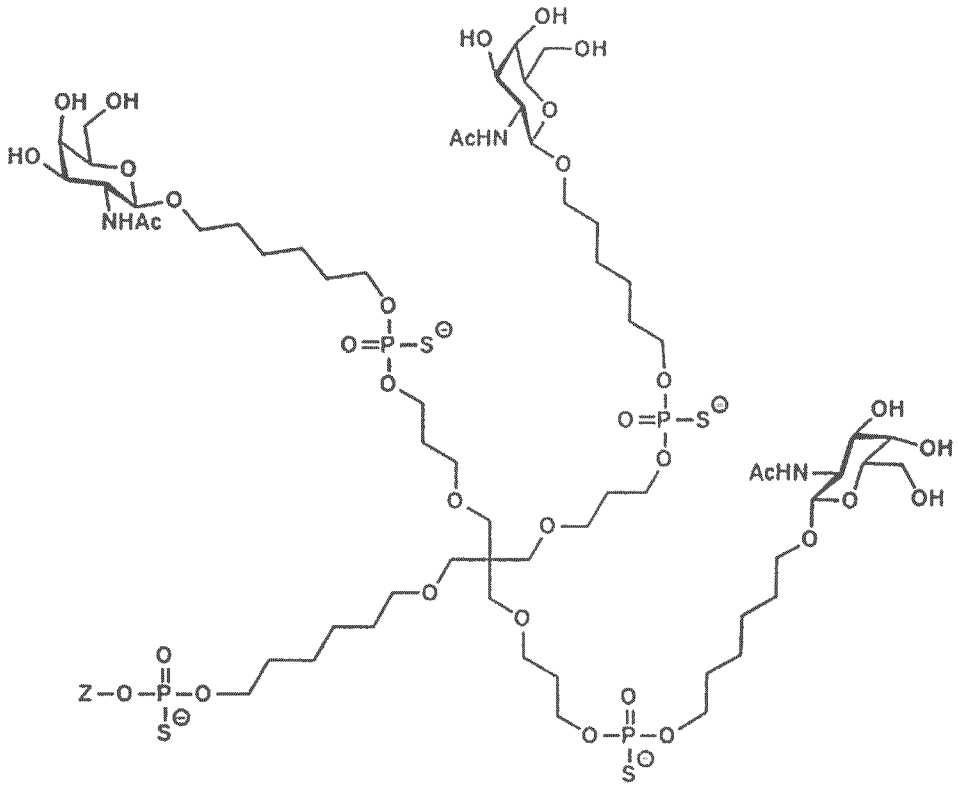


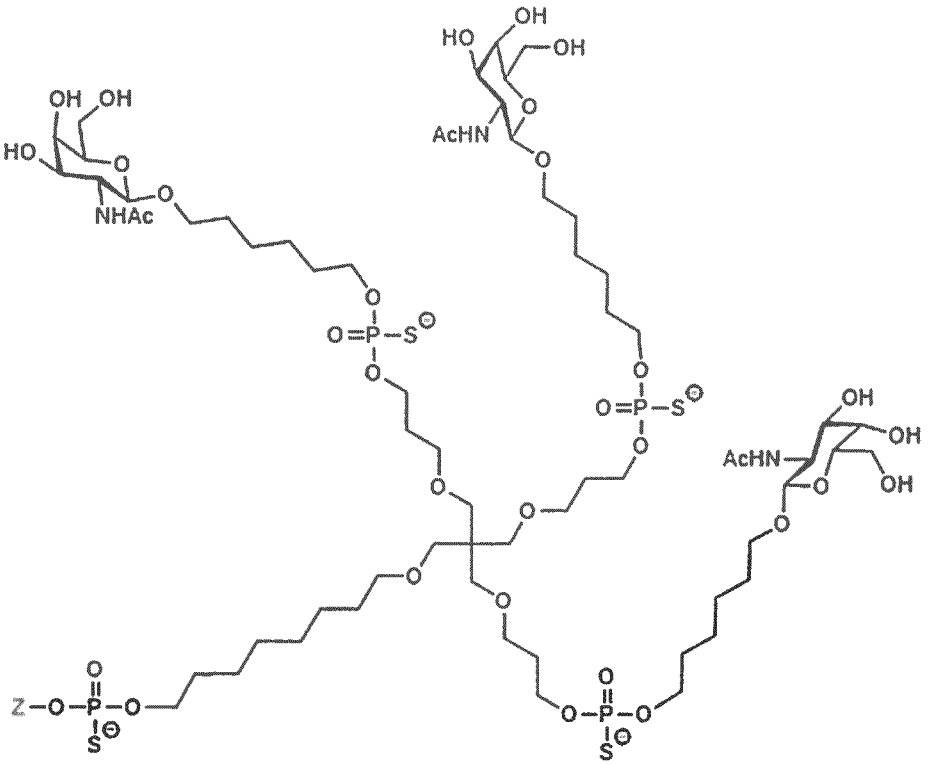






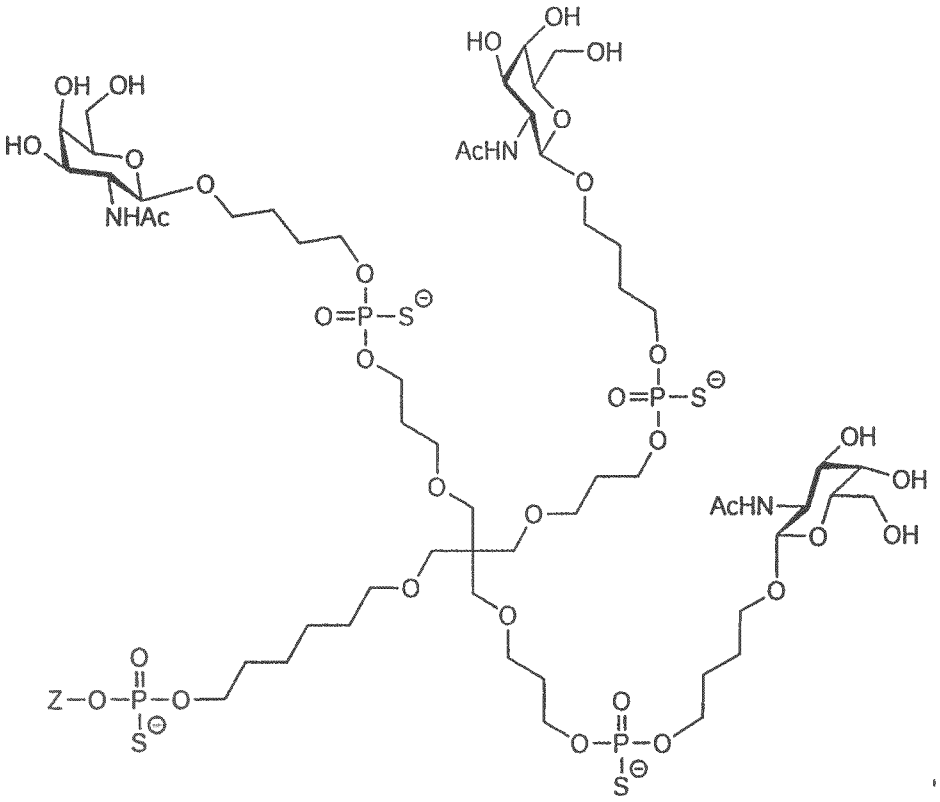






wherein Z is a nucleic acid as defined herein before and is preferably conjugated to the 5' end of the second strand of the nucleic acid.

Preferably, the conjugated nucleic acid has the following structure:



wherein Z is a nucleic acid as defined herein before and is preferably conjugated to the 5' end of the second strand.

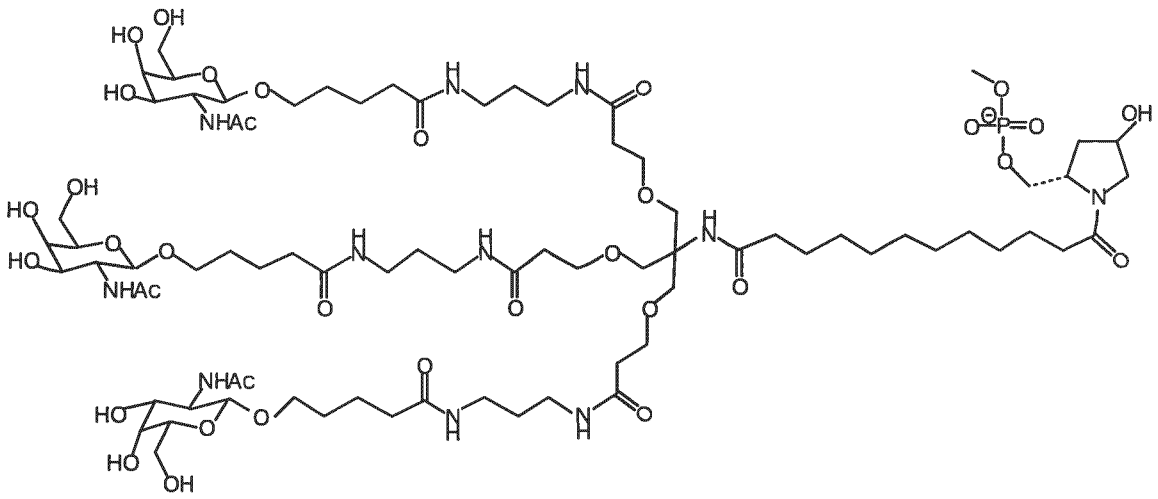
A ligand of formula (I), (II) or (III) can be attached at the 3'-end of the first (antisense) strand and/or at any of the 3'- and/or 5'-end of the second (sense) strand. The nucleic acid can comprise more than one ligand of formula (I), (II), or (III). However, a single ligand of formula (I), (II) or (III) is preferred because a single such ligand is sufficient for efficient targeting of the nucleic acid to the target cells. Preferably in that case, at least the last two, preferably at least the last three and more preferably at least the last four nucleotides at the end of the nucleic acid to which the ligand is attached are linked by a phosphodiester linkage.

Preferably, the 5'-end of the first (antisense) strand is not attached to a ligand of formula (I), (II) or (III), since a ligand in this position can potentially interfere with the biological activity of the nucleic acid.

A nucleic acid with a single ligand of formula (I), (II) or (III) at the 5'-end of a strand is easier and therefore cheaper to synthesis than the same nucleic acid with the same ligand at the 3'-end. Preferably therefore, a single ligand of any of formulae (I), (II) or (III) is covalently attached to (conjugated with) the 5'-end of the second strand of the nucleic acid.

In one embodiment, the nucleic acid is conjugated to a ligand that comprises a lipid, and more preferably a ligand that comprises a cholesterol.

Alternatively, a nucleic acid according to the present invention may be conjugated to a ligand of the following structure



A conjugate of the invention can comprise any nucleic acid as disclosed herein conjugated to any ligand or ligands as disclosed herein.

The present invention also relates to a conjugate for inhibiting expression of a *LPA* gene in a cell, said conjugate comprising a nucleic acid portion, comprising the nucleic acid of any aspect of the invention, and at least one ligand portion, said nucleic acid portion comprising at least one duplex region that comprises at least a portion of a first RNA strand and at least a portion of a second RNA strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from said *LPA* gene, said at least one ligand portion comprising a linker moiety, preferably a serinol-derived linker moiety, and a targeting ligand for *in vivo* targeting of cells and being conjugated exclusively to the 3' and/or 5' ends of one or both RNA strands, wherein the 5' end of the first RNA strand is not conjugated, wherein:

(i) the second RNA strand is conjugated at the 5' end to the targeting ligand, and wherein (a) the second RNA strand is also conjugated at the 3' end to the targeting ligand and the 3' end of the first RNA strand is not conjugated; or (b) the first RNA strand is conjugated at the 3' end to the targeting ligand and the 3' end of the second RNA strand is not conjugated; or (c) both the second RNA strand and the first RNA strand are also conjugated at the 3' ends to the targeting ligand; or

(ii) both the second RNA strand and the first RNA strand are conjugated at the 3' ends to the targeting ligand and the 5' end of the second RNA strand is not conjugated.

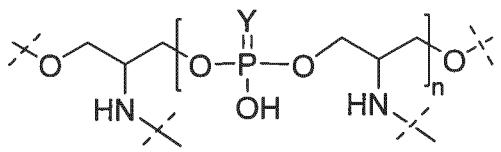
The ligands may be monomeric or multimeric (e.g. dimeric, trimeric, etc.).

Suitably, the ligands are monomeric, thus containing a single targeting ligand moiety, e.g. a single GalNAc moiety.

Alternatively, the ligands may be dimeric ligands wherein the ligand portions comprise two linker moieties, such as serinol-derived linker moieties or non-serinol linker moieties, each linked to a single targeting ligand moiety.

The ligands may be trimeric ligands wherein the ligand portions comprise three linker moieties, such as serinol-derived linker moieties or non-serinol linker moieties, each linked to a single targeting ligand moiety.

The two or three serinol-derived linker moieties may be linked in series e.g. as shown below:



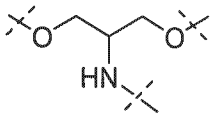
wherein n is 1 or 2 and Y is S or O.

Preferably, the ligands are monomeric.

Suitably, the conjugated RNA strands are conjugated to a targeting ligand via a linker moiety including a further linker wherein the further linker is or comprises a saturated, unbranched or branched C_{1-15} alkyl chain, wherein optionally one or more carbons (for example 1, 2 or 3 carbons, suitably 1 or 2, in particular 1) is/are replaced by a heteroatom selected from O, N, $S(O)_p$, wherein p is 0, 1 or 2 (for example a CH_2 group is replaced with O, or with NH, or with S, or with SO_2 or a $-CH_3$ group at the terminus of the chain or on a branch is replaced with OH or with NH_2) wherein said chain is optionally substituted by one or more oxo groups (for example 1 to 3, such as 1 group).

Suitably, the linker moiety is a serinol-derived linker moiety.

The term "serinol-derived linker moiety" means the linker moiety comprises the following structure:



An O atom of said structure typically links to an RNA strand and the N atom typically links to the targeting ligand.

More suitably, the further linker comprises a saturated, unbranched C_{1-15} alkyl chain wherein one or more carbons (for example 1, 2 or 3 carbons, suitably 1 or 2, in particular 1) is/are replaced by an oxygen atom.

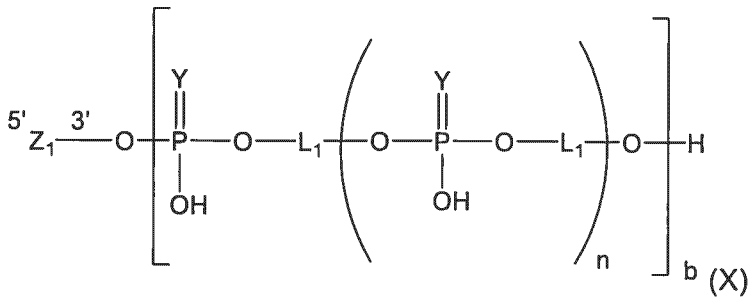
More suitably, the further linker comprises a PEG-chain.

More suitably, the further linker comprises a saturated, unbranched C_{1-15} alkyl chain.

More suitably, the further linker comprises a saturated, unbranched C_{1-6} alkyl chain.

More suitably, the further linker comprises a saturated, unbranched C_4 or C_6 alkyl chain, e.g. a C_4 alkyl chain.

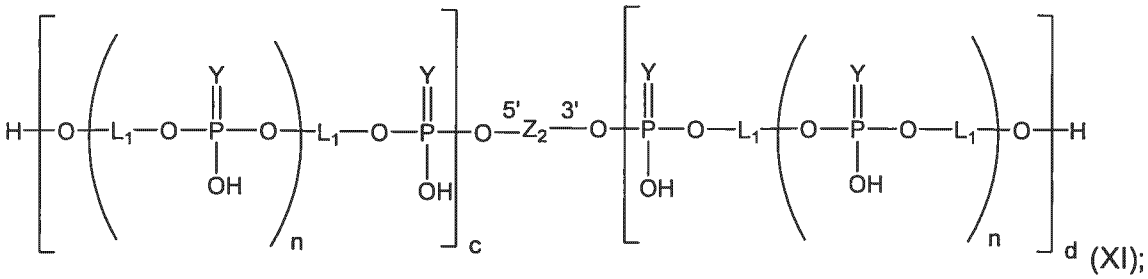
In an embodiment of the invention, the first RNA strand is a compound of formula (X):



(X)

wherein b is 0 or 1; and

the second RNA strand is a compound of formula (XI):



(XI);

wherein:

c and d are independently 0 or 1;

Z_1 and Z_2 are the RNA portions of the first and second RNA strands respectively;

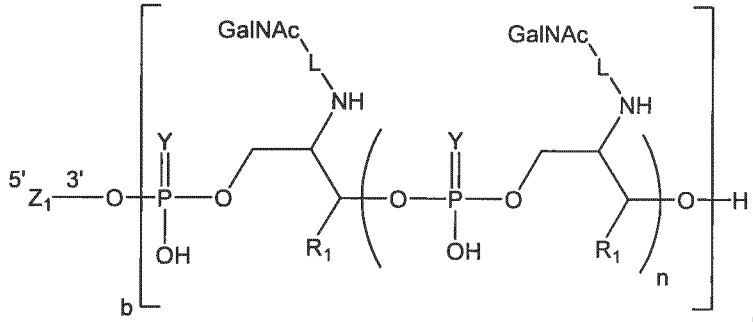
Y is O or S;

n is 0, 1, 2 or 3; and

L_1 is a linker to which a ligand is attached;

and wherein b + c + d is 2 or 3.

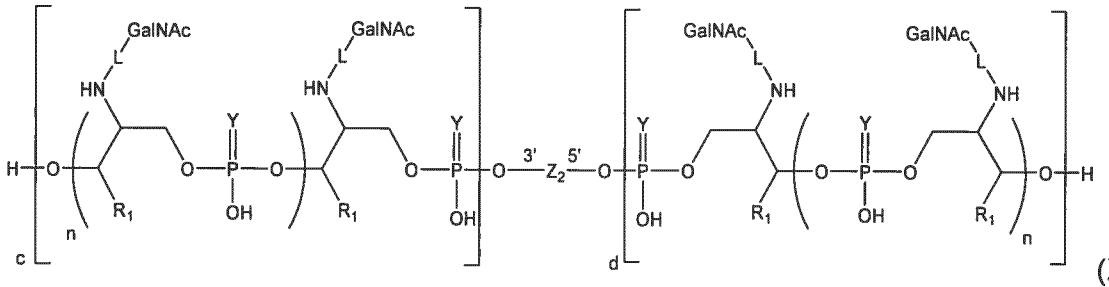
Suitably, the first RNA strand is a compound of formula (XV)



(XV)

wherein b is 0 or 1; and

the second RNA strand is a compound of formula (XVI):



(XVI);

wherein c and d are independently 0 or 1;

wherein:

Z_1 and Z_2 are the RNA portions of the first and second RNA strands respectively;

Y is O or S;

R_1 is H or methyl;

n is 0, 1, 2 or 3; and

L is the same or different in formulae (XV) and (XVI) and is selected from the group consisting of:

$-(CH_2)_r-C(O)-$, wherein r = 2-12;

$-(CH_2-CH_2-O)_s-CH_2-C(O)-$, wherein s = 1-5;

$-(CH_2)_t-CO-NH-(CH_2)_t-NH-C(O)-$, wherein t is independently 1-5;

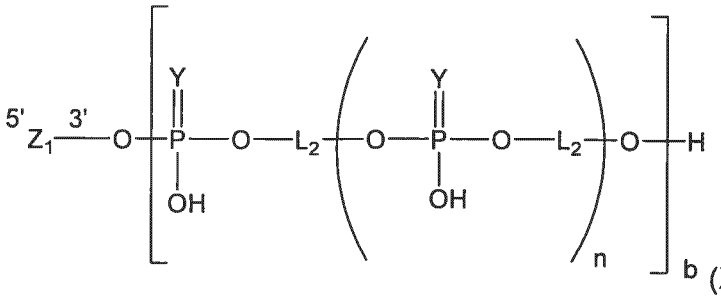
$-(CH_2)_u-CO-NH-(CH_2)_u-C(O)-$, wherein u is independently 1-5; and

$-(CH_2)_v-NH-C(O)-$, wherein v is 2-12; and

wherein the terminal C(O) (if present) is attached to the NH group;

and wherein b + c + d is 2 or 3.

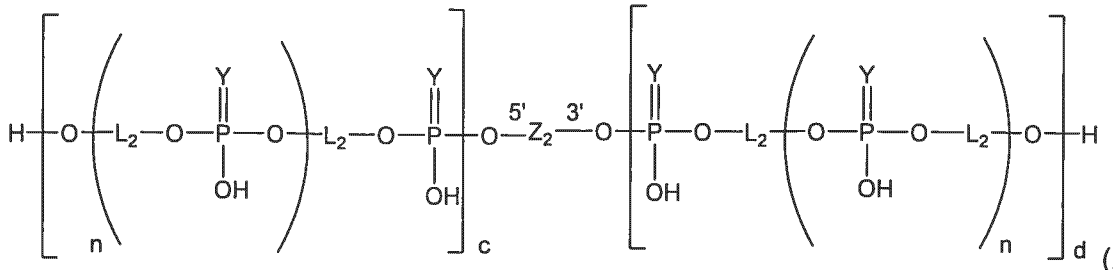
Suitably, the first RNA strand is a compound of formula (XII):



(XII)

wherein b is 0 or 1; and

the second RNA strand is a compound of formula (XIII):



(XIII);

wherein:

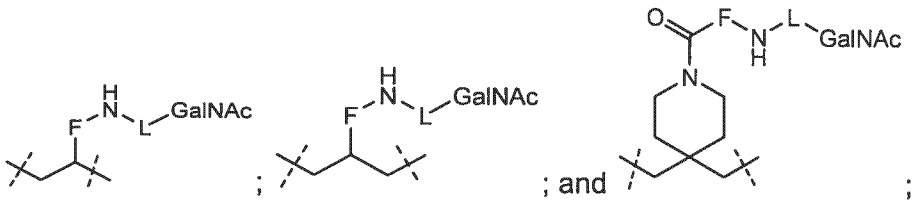
c and d are independently 0 or 1;

Z_1 and Z_2 are the RNA portions of the first and second RNA strands respectively;

Y is O or S;

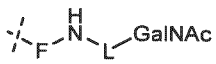
n is 0, 1, 2 or 3; and

L_2 is the same or different in formulae (XII) and (XIII) and is the same or different in moieties bracketed by b, c and d, and is selected from the group consisting of:

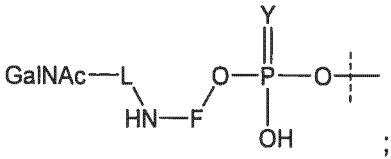


; and ; or

n is 0 and L_2 is:



and the terminal OH group is absent such that the following moiety is formed:



;

wherein

F is a saturated branched or unbranched (such as unbranched) C_{1-8}alkyl (e.g. C_{1-6}alkyl) chain wherein one of the carbon atoms is optionally replaced with an oxygen atom provided that said oxygen atom is separated from another heteroatom (e.g. an O or N atom) by at least 2 carbon atoms;

L is the same or different in formulae (XII) and (XIII) and is selected from the group consisting of:

$-(CH_2)_r-C(O)-$, wherein r = 2-12;

$-(CH_2-CH_2-O)_s-CH_2-C(O)-$, wherein s = 1-5;

$-(CH_2)_t-CO-NH-(CH_2)_t-NH-C(O)-$, wherein t is independently 1-5;

$-(CH_2)_u-CO-NH-(CH_2)_u-C(O)-$, wherein u is independently 1-5; and

$-(CH_2)_v-NH-C(O)-$, wherein v is 2-12; and

wherein the terminal C(O) (if present) is attached to the NH group;

and wherein b + c + d is 2 or 3.

In any one of the above formulae where GalNAc is present, the GalNAc may be substituted for any other targeting ligand, such as those mentioned herein.

Suitably, b is 0, c is 1 and d is 1; b is 1, c is 0 and d is 1; b is 1, c is 1 and d is 0; or b is 1, c is 1 and d is 1.

More suitably, b is 0, c is 1 and d is 1; b is 1, c is 0 and d is 1; or b is 1, c is 1 and d is 1.

Most suitably, b is 0, c is 1 and d is 1.

In one embodiment, Y is O. In another embodiment, Y is S.

In one embodiment, R_1 is H or methyl. In one embodiment, R_1 is H. In another embodiment, R_1 is methyl.

In one embodiment, n is 0, 1, 2 or 3. Suitably, n is 0.

In one embodiment, L is selected from the group consisting of:

$-(CH_2)_r-C(O)-$, wherein r = 2-12;

$-(CH_2-CH_2-O)_s-CH_2-C(O)-$, wherein s = 1-5;

$-(CH_2)_t-CO-NH-(CH_2)_t-NH-C(O)-$, wherein t is independently 1-5;

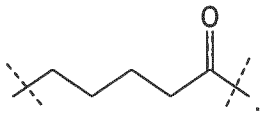
$-(CH_2)_u-CO-NH-(CH_2)_u-C(O)-$, wherein u is independently 1-5; and

$-(CH_2)_v-NH-C(O)-$, wherein v is 2-12;

wherein the terminal C(O) is attached to the NH group.

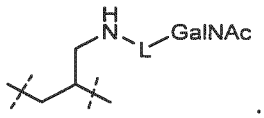
Suitably, L is $-(CH_2)_r-C(O)-$, wherein r = 2-12. Suitably, r = 2-6. More suitably, r = 4 or 6 e.g. 4.

Suitably, L is:

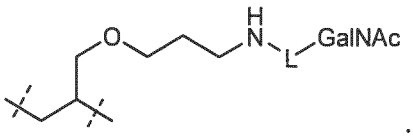


Example F moieties include $(CH_2)_{1-6}$ e.g. $(CH_2)_{1-4}$ e.g. CH_2, $(CH_2)_4$, $(CH_2)_5$ or $(CH_2)_6$, or $CH_2O(CH_2)_{2-3}$, e.g. $CH_2O(CH_2)CH_3$.

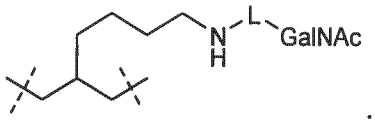
Suitably, L_2 is:



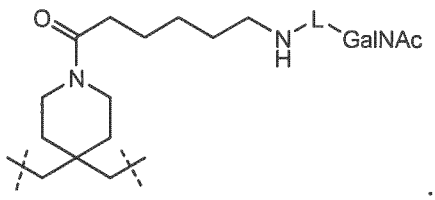
Suitably, L_2 is:



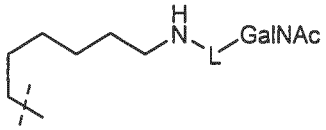
Suitably, L_2 is:



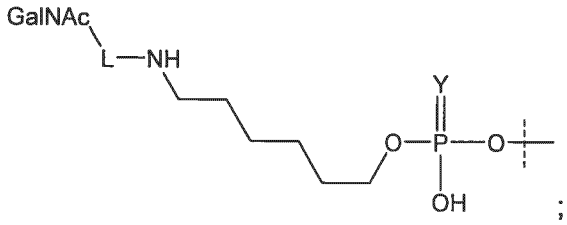
Suitably, L_2 is:



Suitably, n is 0 and L_2 is:



and the terminal OH group is absent such that the following moiety is formed:

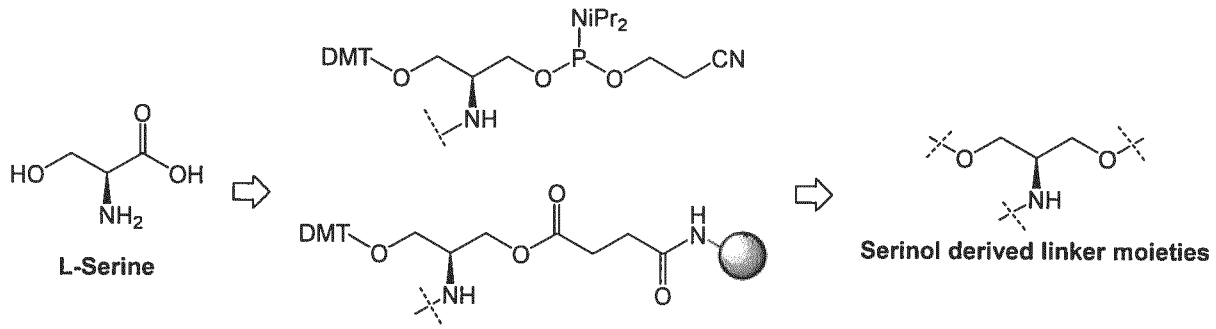


;

wherein Y is as defined elsewhere herein.

Within the moiety bracketed by b, c and d, L_2 is typically the same. Between moieties bracketed by b, c and d, L_2 may be the same or different. In an embodiment, L_2 in the moiety bracketed by c is the same as the L_2 in the moiety bracketed by d. In an embodiment, L_2 in the moiety bracketed by c is not the same as L_2 in the moiety bracketed by d. In an embodiment, the L_2 in the moieties bracketed by b, c and d is the same, for example when the linker moiety is a serinol-derived linker moiety.

Serinol derived linker moieties may be based on serinol in any stereochemistry i.e. derived from L-serine isomer, D-serine isomer, a racemic serine or other combination of isomers. In a preferred aspect of the invention, the serinol-GalNAc moiety (SerGN) has the following stereochemistry:



(S)-Serinol building blocks

i.e. is based on an (S)-serinol-amidite or (S)-serinol succinate solid supported building block derived from L-serine isomer.

In one embodiment, the targeted cells are hepatocytes.

One aspect is a nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of a RNA transcribed from the *LPA* gene, wherein said first strand comprises a nucleotide sequence selected from the following sequences: SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31,

33, 35, 37, 39, 41, or 43, wherein the nucleic acid is conjugated to a ligand. The second strand may comprise a nucleotide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, or 44. The nucleotides of the first and/or second strand may be modified, as herein described.

Preferably, the nucleic acid comprises SEQ ID NO:5 or SEQ ID NO:9 and SEQ ID NO:6 or SEQ ID NO:10 conjugated to a ligand of formula (I) (as set out above), wherein the ligand is conjugated to the nucleic acid as described and wherein the first strand is modified with a 2'OMe modification on the odd numbered nucleotides, and modified with a 2'F on the even numbered nucleotides, and the second strand is modified with a 2'OMe on the even numbered nucleotides and modified with a 2'F on the odd numbered nucleotides.

Particularly preferred is a nucleic acid wherein the first strand comprises, or preferably consists of SEQ ID NO: 165 and the second strand optionally comprises, or preferably consists of SEQ ID NO: 163. This nucleic acid can be further conjugated to a ligand. Even more preferred is a nucleic acid wherein the first strand comprises, or preferably consists of SEQ ID NO: 165 and the second strand optionally comprises, or preferably consists of SEQ ID NO: 164. Most preferred is an siRNA that consists of SEQ ID NO: 165 and SEQ ID NO: 164. One aspect of the invention is conjugate 21.

Compositions, uses and methods

The present invention also provides pharmaceutical compositions comprising the nucleic acid or conjugated nucleic acid of the invention. The pharmaceutical compositions may be used as medicaments or as diagnostic agents, alone or in combination with other agents. For example, one or more nucleic acid conjugates of the invention can be combined with a delivery vehicle (e.g., liposomes) and/or excipients, such as carriers, diluents. Other agents such as preservatives and stabilizers can also be added. Methods for the delivery of nucleic acids are known in the art and within the knowledge of the person skilled in the art.

The invention also includes a pharmaceutical composition comprising one or more nucleic acids or conjugated nucleic acids according to the present invention in a physiologically/pharmaceutically acceptable excipient, such as a stabilizer, preservative, diluent, buffer, and the like.

The pharmaceutical composition may be a sterile injectable aqueous suspension or solution, or in a lyophilised form or adhered, absorbed or included to or into any other

suitable galenic carrier substance such as pellets, tablets, capsules, nanoparticles, gels, tablets, beads or similar structures.

One aspect relates to a double-stranded nucleic acid that is capable of inhibiting expression *LPA*, preferably in a cell, for use as a medicament.

A further aspect of the invention relates to a nucleic acid or conjugated nucleic acid of the invention or the pharmaceutical composition comprising the nucleic acid or conjugated nucleic acid of the invention for use in the treatment of a disease, disorder or syndrome, preferably a disease, disorder or syndrome associated with elevated levels of Lp(a)-containing particles. The treatment may be to prevent and/or reduce the risk to suffer from and/or treat stroke, atherosclerosis, thrombosis or cardiovascular diseases such as coronary heart disease or aortic stenosis and any other disease or pathology associated to elevated levels of Lp(a)-containing particles. The treatment may be to prevent and/or reduce the risk of suffering from and/or treat an atherosclerotic cardiovascular disease, an atherosclerotic cerebrovascular disease, hyperlipidaemia, and dyslipidaemia, preferably wherein the disease is associated with elevated levels of Lp(a)-containing particles. The treatment may be to prevent and/or reduce the risk of suffering from and/or treat calcific aortic stenosis, ischaemic stroke, coronary artery disease, peripheral arterial disease, abdominal aortic aneurysm, heart failure secondary to ischaemic cardiomyopathy, or familial hypercholesterolaemia, preferably wherein the disease is associated with elevated levels of Lp(a)-containing particles. Preferable, the treatment is to prevent and/or reduce the risk of suffering from and/or treat aortic stenosis, such as calcific aortic stenosis, or familial hypercholesterolaemia, preferably in each case when the disease or disorder is associated with elevated levels of Lp(a)-containing particles. A desirable level of Lp(a)-containing particles in serum is generally described as a level of under 14 mg/dL. An elevated level of Lp(a)-containing particles is a level of at least 14, preferably at least 20, more preferably at least 30, more preferably at least 40 and most preferably at least 50 mg/dL of Lp(a)-containing particles in the serum of a subject.

The invention includes a pharmaceutical composition comprising one or more nucleic acids or conjugated nucleic acids according to the present invention in a physiologically/ pharmaceutically acceptable excipient, such as a stabiliser, preservative, diluent, buffer and the like.

The terms “Lp(a)-containing particles” and “Lp(a) particles” are used interchangeably throughout this disclosure.

The pharmaceutical compositions and medicaments of the present invention may be administered to a mammalian subject in a pharmaceutically effective dose. The mammal may be selected from a human, a non-human primate, a simian or prosimian, a dog, a cat, a horse, cattle, a pig, a goat, a sheep, a mouse, a rat, a hamster, a hedgehog and a guinea pig, or other species of relevance. On this basis, the wording "LPA" or "*LPA*" as used herein denotes nucleic acid or protein in any of the above-mentioned species, if expressed therein naturally or artificially, but preferably this wording denotes human nucleic acids or proteins.

The nucleic acid or conjugated nucleic acid of the present invention can also be administered in combination with other therapeutic compounds, either administrated separately or simultaneously, e.g., as a combined unit dose. The further therapeutic agent can be selected from the group comprising an oligonucleotide, a small molecule, a monoclonal antibody, a polyclonal antibody and a peptide. A molecular conjugation to other biologically active molecular entities such as peptides, cellular or artificial ligands or small and large molecules is also possible.

Dosage levels for the medicament and pharmaceutical compositions of the invention can be determined by those skilled in the art by routine experimentation. In one embodiment, a unit dose may contain between about 0.01 mg/kg and about 100 mg/kg body weight of nucleic acid or conjugated nucleic acid. Alternatively, the dose can be from 10 mg/kg to 25 mg/kg body weight, or 1 mg/kg to 10 mg/kg body weight, or 0.05 mg/kg to 5 mg/kg body weight, or 0.1 mg/kg to 5 mg/kg body weight, or 0.1 mg/kg to1 mg/kg body weight, or 0.1 mg/kg to 0.5 mg/kg body weight, or 0.5 mg/kg to 1 mg/kg body weight. Alternatively, the dose can be from about 0.5 mg/kg to about 10 mg/kg body weight, or about 0,6 mg/kg to about 8 mg/kg body weight, or about 0,7 mg/kg to about 5 mg/kg body weight, or about 0,8 mg/kg to about 4 mg/kg body weight, or about 0,9 mg/kg to about 3,5 mg/kg body weight, or about 1 mg/kg to about 3 mg/kg body weight, or about 1 mg/kg body weight, or about 3 mg/kg body weight, wherein "about" is a deviation of up to 30%, preferably up to 20%, more preferably up to 10%, yet more preferably up to 5% and most preferably 0% of the indicated value. Dosage levels may also be calculated via other parameters such as, e.g., body surface area.

The nucleic acid described herein may be capable of inhibiting the expression of *LPA*. The nucleic acid described herein may be capable of partially inhibiting the expression of *LPA*. Inhibition may be complete, i.e. 0% compared of the expression level of *LPA* in the absence of the nucleic acid of the invention. Inhibition of *LPA* expression may be partial, i.e. it may

be 15%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95% or intermediate values of *LPA* expression in the absence of a nucleic acid of the invention. Inhibition may last 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 10 weeks, 11 weeks, 12 weeks, 13 weeks, 14 weeks or up to 3 months, when used in a subject, such as a human patient. A nucleic acid or conjugated nucleic acid of the invention, or compositions including the same, may be for use in a regimen comprising treatments once or twice weekly, every week, every two weeks, every three weeks, every four weeks, every five weeks, every six weeks, every seven weeks, or every eight weeks, or in regimens with varying dosing frequency such as combinations of the before-mentioned intervals. The nucleic acid may be for use subcutaneously, intravenously or using any other application routes such as oral, rectal or intraperitoneal, preferably for use subcutaneously.

In cells and/or subjects treated with or receiving the nucleic acid or conjugated nucleic acid of the present invention, the *LPA* expression may be inhibited compared to untreated cells and/or subjects by a range from 15% up to 100% but at least about 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 100% or intermediate values. The level of inhibition may allow treatment of a disease associated with *LPA* expression or overexpression, or may serve to further investigate the functions and physiological roles of the *LPA* gene product.

A further aspect of the invention relates to a nucleic acid or conjugated nucleic acid of the invention in the manufacture of a medicament for treating a disease, disorder or syndromes, such as those as listed above or additional pathologies associated with elevated levels of Lp(a), or additional therapeutic approaches where inhibition of *LPA* expression is desired.

Also included in the invention is a method of treating or preventing a disease, disorder or syndrome, such as those listed above, comprising administration of a pharmaceutical composition comprising a nucleic acid or conjugated nucleic acid as described herein, to an individual in need of treatment (to improve such pathologies). The nucleic acid composition may be administered in a regimen comprising treatments twice every week, once every week, every two weeks, every three weeks, every four weeks, every five weeks, every six weeks, every seven weeks, or every eight weeks or at administration intervals of more than once every eight weeks or in regimens with varying dosing frequency such as combinations of the before-mentioned intervals. The nucleic acid or conjugated nucleic acid may be for use subcutaneously or intravenously or other application routes such as oral, rectal or intraperitoneal. Preferably the nucleic acid or conjugated nucleic acid is injected subcutaneously.

The nucleic acid or conjugated nucleic acid of the present invention can be produced using routine methods in the art including chemical synthesis or expressing the nucleic acid either *in vitro* (e.g., run off transcription) or *in vivo*. For example, using solid phase chemical synthesis or using a nucleic acid-based expression vector including viral derivates or partially or completely synthetic expression systems. In one embodiment, the expression vector can be used to produce the nucleic acid of the invention *in vitro*, within an intermediate host organism or cell type, within an intermediate or the final organism or within the desired target cell. Methods for the production (synthesis or enzymatic transcription) of the nucleic acid described herein are known to persons skilled in the art

All the features of the nucleic acids can be combined with all other aspects of the invention disclosed herein.

The present invention also relates to the unmodified sequences of all modified sequences disclosed herein.

The invention will now be described with reference to the following non-limiting Figures and Examples.

Figures

Figure 1 shows the results of a non-conjugated siRNA molecule screen for inhibition of *LPA* mRNA expression in human RT-4 cells.
Figures 2A and 2B show the dose response of non-conjugated *LPA*-targeting siRNA molecules on *LPA* mRNA expression in human RT-4 cells.
Figure 3 shows the inhibition of *LPA* mRNA expression in human and cynomolgus primary hepatocytes by different doses of GalNAc-L1 *LPA*-1038 conjugated siRNA molecules delivered by receptor-mediated uptake.
Figure 4 shows representative examples of the knockdown of *LPA*-mRNA by L6-conjugated GalNAc siRNAs indicated in primary human hepatocytes delivered by receptor-mediated uptake.
Figure 5 shows the synthesis of A0268, which is a 3' mono-GalNAc conjugated single stranded oligonucleotide and is the starting material in the synthesis of Conjugate 1 and Conjugate 3. (ps) denotes phosphorothioate linkage.

Figure 6 shows the synthesis of A0006 which is a 5' tri-antennary GalNAc conjugated single stranded oligonucleotide used for the synthesis of Reference Conjugate 4. (ps) denotes phosphorothioate linkage.

Figure 7 illustrates the *in vitro* determination of TTR knockdown. In particular, Figure 7A shows the *in vitro* determination of TTR knockdown by Reference Conjugates (RC) 1 and 3 as well as the untreated control "UT"; Figure 7B shows the *in vitro* determination of TTR knockdown by Reference Conjugates (RC) 2 and 3, as well as the untreated control "UT"; and Figure 7C shows the *in vitro* determination of TTR knockdown by Conjugates 1, 2 and 3, as well as by RC3 and untreated control "UT". Reference Conjugates 1 and 2 represent comparator conjugates. Reference Conjugate 3 represents a non-targeting GalNAc siRNA and "untreated" ("UT") represents untreated cells. Both RC3 and UT are negative controls. mRNA levels were normalised against PtenII.

Figure 8 shows a time course of serum TTR in c57BL/6 mice cohorts of n=4 at 7, 14, and 27 days post s.c. treatment with 1mg/kg - Conjugates 1-3, Reference Conjugates (RC) 1, 2 and 4 and mock treated (PBS) individuals.

Figure 9 shows oligonucleotide synthesis of 3' and 5' GalNAc conjugated oligonucleotides precursors (such as compound X0385B-prec).

Figure 10 shows equal dose response of knock down for *LPA* targeting siRNA with two single GalNAc units conjugated to the second strand as compared to a triantennary GalNAc unit at the 5' second strand in primary cynomolgus hepatocytes.

Figure 11 illustrates the *in vitro* determination of TTR knockdown. In particular, Figure 11A shows the *in vitro* determination of TTR knockdown by Conjugates 4, 5, 6 and 2 compared to "Luc" (Reference Conjugate 3) as well as the untreated control "UT"; Figure 11B shows the *in vitro* determination of TTR knockdown by Conjugates 7 and 2, compared to "Luc" (Reference Conjugate 3) as well as the untreated control "UT". Luc or Reference Conjugate 3 (RC3) represents a non-targeting GalNAc siRNA and "untreated" ("UT") represents untreated cells. Both RC3 and UT are negative controls. mRNA level were normalised against PtenII.

Figure 12 illustrates the *in vitro* determination of TTR knockdown. In particular, Figure 12A shows the *in vitro* determination of TTR knockdown by Conjugates 8, 9, 10, 11 and 2 compared to "Luc" (Reference Conjugate 3) as well as the untreated control "UT"; Figure 12B shows the *in vitro* determination of TTR knockdown by Conjugates 12 and 2, compared to "Luc" (Reference Conjugate 3) as well as the untreated control "UT". Luc or Reference Conjugate 3 represents a non-targeting GalNAc siRNA and "untreated" ("UT") represents untreated cells. Both RC3 and UT are negative controls. mRNA level were normalised against PtenII.

Figure 13 illustrates the *in vitro* determination of *LPA* mRNA knockdown by Conjugate 19 compared to controls. Ctr represents a non-targeting GalNAc siRNA and "untreated" ("UT") represents untreated cells. Both Ctr and UT are negative controls. mRNA level were normalised against *ACTB*.

Figure 14 shows a time course of *Aldh2* liver mRNA levels in c57BL/6 mice cohorts of n=6 at 14, 28 and 42 days post s.c. treatment with 1mg/kg - Conjugate 15, Reference Conjugate (RC) 6 and mock treated (PBS) individuals. mRNA level were normalised against *Pten*.

Figure 15 shows a time course of *Aldh2* liver mRNA levels in c57BL/6 mice cohorts of n=6 at 14, 28 and 42 days post s.c. treatment with 1mg/kg - Conjugate 16, Reference Conjugate (RC) 7 and mock treated (PBS) individuals. mRNA level were normalised against *Pten*.

Figure 16 shows a time course of *Tmprss6* liver mRNA levels in c57BL/6 mice cohorts of n=6 at 14, 28 and 42 days post s.c. treatment with 1mg/kg - Conjugate 18, Reference Conjugate (RC) 8 and mock treated (PBS) individuals. mRNA level were normalised against *Pten*.

Figure 17 shows serum stability of Conjugates 4, 5, 6, 7 and 2, and untreated control (UT) at 37 °C over 3 days.

Figure 18 shows serum stability of Conjugates 8, 9, 10, 11, 12 and 2, and untreated control (UT) at 37 °C over 3 days.

Figure 19 shows the reduction in *LPA* mRNA in primary human hepatocytes by Conjugate 21.

Figure 20 shows the reduction in *LPA* mRNA in primary cynomolgus hepatocytes by Conjugate 21.

Figure 21 shows that Conjugate 21 does not affect the level of *APOB* gene expression.

Figure 22 shows that Conjugate 21 does not affect the level of *PLG* gene expression.

Figure 23 shows a time course of serum Lp(a) inhibition over 29 days in cynomolgus with different dosages of conjugate 21.

Figure 24 shows a dose response curve of conjugate 21 showing reduction of serum Lp(a) at day 29 in cynomolgus.

Examples

The numbering referred to in each example is specific for said example.

Example 1

A number of modified and conjugated siRNA molecules used for functional examples are shown here.

LPA -1038 derivatives:

GalNAc-LPA-1038-L1

First strand (SEQ ID NO: 119, based on SEQ ID NO 5)
OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeA 3'

Second strand (SEQ ID NO: 120, based on SEQ ID NO SEQ ID NO 6)
5´[ST23 (ps)]3 long trebler (ps)FU-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU 3'

GalNAc-LPA-1038-L6

First strand (SEQ ID NO: 121, based on SEQ ID NO 5)
OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeA 3'

Second strand (SEQ ID NO: 122, based on SEQ ID NO 6)
5´[ST23 (ps)]3 ST43 (ps)FU-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU 3'

FN (N=A, C, G, U) denotes 2´Fluoro, 2´ DeoxyNucleosides
OMeN (N=A, C, G, U) denotes 2´O Methyl Nucleosides
(ps) indicates a phosphorothioate linkage

ST23 and ST43 are as below.

A further example are LPA 1041 derivatives:

GalNAc-LPA-1041-L1

First strand (SEQ ID NO: 123, based on SEQ ID NO 9)
5' OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeG 3'

Second strand (SEQ ID NO: 124, based on SEQ ID NO 10)
5´[ST23 (ps)]3 long trebler (ps) FC-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU 3'

GalNAc-LPA-1041-L6

First strand (SEQ ID NO: 125, based on SEQ ID NO 9)
5' OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeG 3'

Second strand (SEQ ID NO: 126, based on SEQ ID NO 10)
5´[ST23 (ps)]3 ST43 (ps) FC-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU 3'

FN (N=A, C, G, U) denotes 2´Fluoro, 2´ DeoxyNucleosides
OMeN (N=A, C, G, U) denotes 2´O Methyl Nucleosides
(ps) indicates a phosphorothioate linkage

All oligonucleotides were either obtained from commercial oligonucleotide manufacturers (Biospring, Frankfurt, Germany, or RiboBio, Guangzhou, Guangdong, PRC) or synthesized on an AKTA oligopilot synthesizer (in house) using standard phosphoramidite chemistry. Commercially available solid support and 2´O-Methyl RNA phosphoramidites, 2´Fluoro DNA phosphoramidites (all standard protection) and commercially available long trebler phosphoramidite (Glen research) were used. Synthesis was performed using 0.1 M solutions of the phosphoramidite in dry acetonitrile and benzylthiotetrazole (BTT) was used as activator (0.3M in acetonitrile). All other reagents were commercially available standard reagents.

Conjugation of the respective GalNac synthon (e.g., ST23, ST41 or ST43) was achieved by coupling of the respective phosphoramidite to the 5´end of the oligochain under standard phosphoramidite coupling conditions. Phosphorothioates were introduced using standard commercially available thiolation reagents (EDITH, Link technologies).

The single strands were cleaved off the CPG by using methylamine (40% aqueous) and the resulting crude oligonucleotide was purified by Ion exchange chromatography (Resource Q, 6mL, GE Healthcare) on a AKTA Pure HPLC System using a Sodium chloride gradient.

Product containing fractions were pooled, desalted on a size exclusion column (Zetadex, EMP Biotech) and lyophilised.

For annealing, equimolar amounts of the respective single strands were dissolved in water and heated to 80°C for 5min. After gradual cooling to RT the resulting duplex was lyophilised.

The sequences of the resulting nucleic acids (siRNAs) are set out in Table 1 below.

Table 1: Non-conjugated nucleic acid sequences tested for inhibition of *LPA* mRNA expression. Sequences and applied modification pattern are indicated

SEQ ID NO:	siRNA ID	strand	Sequence	Modifications
1	LPA-1014	first strand	5'ucguauaacaauaaggggc 3'	5381616272616284847
2		second strand	5'gccccuuauuguuauacga 3'	4737351615451616382
3	LPA-1024	first strand	5'gauaacucuguccauuacc 3'	8252635354537251637
4		second strand	5'gguaauggacagaguuauc 3'	4816254827282815253
5	LPA-1038	first strand	5'auaacucuguccauuacca 3'	6162717181736152736
6		second strand	5'ugguaauggacagaguuau 3'	1845261846364645161
7	LPA-1040	first strand	5'uaacucuguccauuaccgu 3'	5263535453725163745
8		second strand	5'acgguaauggacagaguua 3'	2748162548272828152
9	LPA-1041	first strand	5'auaacucuguccauuaccg 3'	6162717181736152738
10		second strand	5'cgguaauggacagaguuau 3'	3845261846364645161
11	LPA-1055	first strand	5'agaaugugccucgauaacu 3'	6462545473538252635
12		second strand	5'aguuaucgaggcacauucu 3'	2815253828472725171
13	LPA-1057	first strand	5'auaacucuguccaucacca 3'	6162717181736172736
14		second strand	5'uggugauggacagaguuau 3'	1845461846364645161
15	LPA-1058	first strand	5'auaacucuguccaucaccu 3'	6162717181736172735
16		second strand	5'aggugauggacagaguuau 3'	2845461846364645161
17	LPA-1061	first strand	5'uaacucuguccauuaccau 3'	5263535453725163725
18		second strand	5'augguaauggacagaguua 3'	2548162548272828152

19	LPA-1086	first strand	5'augugccuugauaacucug 3'	6181837154616271718
20		second strand	5'cagaguuaucaaggcacau 3'	3646451617264836361
21	LPA-1099	first strand	5'aguuggugcugcuucagaa 3'	6451845471835172826
22		second strand	5'uucugaagcagcaccaacu 3'	1535462836472736271
23	LPA-1102	first strand	5'aauaaggggcugccacagg 3'	6252648483547363648
24		second strand	5'ccuguggcagccccuuauu 3'	3718184728373715251
25	LPA-1116	first strand	5'uaacucuguccaucaccau 3'	5263535453725363725
26		second strand	5'auggugauggacagaguua 3'	2548182548272828152
27	LPA-1127	first strand	5'augagccucgauaacucug 3'	6182837174616271718
28		second strand	5'cagaguuaucgaggcucau 3'	3646451617464835361
29	LPA-1128	first strand	5'aaugagccucgauaacucu 3'	6254647353825263535
30		second strand	5'agaguuaucgaggcucauu 3'	2828152538284717251
31	LPA-1141	first strand	5'aaugcuuccaggacauuuc 3'	6254715372846361517
32		second strand	5'gaaauguccuggaagcauu 3'	4626181735482647251
33	LPA-1151	first strand	5'acagugguggagaaugugc 3'	6364548184646254547
34		second strand	5'gcacauucuccaccacugu 3'	4727251717363727181
35	LPA-1171	first strand	5'guaugugccucgauaacuc 3'	8161818371746162717
36		second strand	5'gaguuaucgaggcacauac 3'	4645161746483636163
37	LPA-1177	first strand	5'ucgauaacucuguccauca 3'	5382526353545372536
38		second strand	5'ugauggacagaguuaucga 3'	1825482728281525382
39	LPA-1189	first strand	5'ugucacuggacauuguguc 3'	5453635482725181817
40		second strand	5'gacacaauguccagugaca 3'	4636362545372818272
41	LPA-1244	first strand	5'cugggauccaugguguaac 3'	7184825372548181627
42		second strand	5'guuacaccauggaucccag 3'	4516363725482537364
43	LPA-1248	first strand	5'agaugaccaagcuuggcag 3'	6461827362835184728
44		second strand	5'cugccaagcuuggucaucu 3'	3547362835184536171

Table 1

Table 1: Nucleotides modifications are depicted by the following numbers (column 4), 1=2´F-dU, 2=2'F-dA, 3=2´F-dC, 4=2´F-dG, 5=2'-OMe-rU; 6=2'-OMe-rA; 7=2'-OMe-rC; 8=2'-OMe-rG.

Table 2: Sequences of *LPA, APOB, beta-Actin* and *PTEN* qPCR amplicon sets that were used to measure mRNA levels are shown below.

Gene	Species	Sequences	SEQ ID NO:
LPA: (upper)	human	5' AAGTGTCCTTGCGACGTCC 3'	45
LPA: (lower)		5' CCTGGACTGTGGGGCTTT 3'	46
LPA: (probe)		5' CTGTTTCTGAACAAGCACCAACGGAGC 3'	47
LPA (upper)	cynomolgus	5' GTGTCCTCGCAACGTCCA 3'	48
LPA (lower)		5' GACCCCGGGGCTTTG 3'	49
LPA (probe)		5'TGGCTGTTTCTGAACAAGCACCAATGG 3'	50
APOB (upper)	human	5' TCATTCCTTCCCCAAAGAGACC 3'	51
APOB (lower)		5' CACCTCCGTTTTGGTGGTAGAG 3'	52
APOB (probe)		5' CAAGCTGCTCAGTGGAGGCAACACATTA 3'	53
beta-Actin (upper)	human	5' GCATGGGTCAGAAGGATTCCTAT 3'	54
beta-Actin (lower)		5' TGTAGAAGGTGTGGTGCCAGATT 3'	55
beta-Actin (probe)		5' TCGAGCACGGCATCGTCACCAA 3'	56
beta-Actin (upper)	cynomolgus	5' AAGGCCAACCGCGAGAAG 3'	57
beta-Actin (lower)		5' AGAGGCGTACAGGGACAGCA 3'	58
beta-Actin (probe)		5' TGAGACCTTCAACACCCCAGCCATGTAC 3'	59
PPIB (upper)	human	5' AGATGTAGGCCGGGTGATCTTT 3'	60
PPIB (lower)		5' GTAGCCAAATCCTTTCTCTCCTGT 3'	61
PPIB (probe)		5' TGTTCCAAAAACAGTGGATAATTTTGTGGCC 3'	62

Table 2

Example 2

Screening of non-conjugated siRNA molecules (Table 1) for inhibition of *LPA* mRNA expression in human RT-4 cells.

Liposomal transfection complexes were prepared in triplicate at a ratio of 1.5 µl RNAiMax (ThermoFisher) / 80 pmol of the indicated siRNA molecules. The complex was diluted to the indicated concentrations of 2,5nM and 25 nM, respectively (values represented pairwise as light and darker grey bars). RT4 human urinary bladder transitional cell papilloma cells expressing endogenously *LPA* were seeded at a density of 125.000 cells per well in 24-well format on top of previously plated transfection complexes (reverse transfection) at the

indicated concentration. 24 hours after transfection total RNA was isolated using the Spin Cell Mini Kit 250 (Stratec). *LPA* mRNA levels were determined by qRT-PCR relative to *PPIB* mRNA expression in the respective samples as housekeeping transcript. Values were normalized to the amount of *LPA* mRNA detected in untreated cells (intraplate). A non-silencing siRNA compound was transfected as an additional control. Means and SD of normalized triplicate values are shown. Results are shown in Figure 1.

Example 3

Dose response of non-conjugated *LPA*-targeting siRNA compounds on *LPA* mRNA expression in human RT-4 cells.

RT4 human urinary bladder transitional cell papilloma cells were reversely transfected as described above (Example 2) and treated at the indicated concentration (range 100 nM to 0.2 nM) with the different non-conjugated siRNA compounds (Table 1) as labeled. 24 h post transfection, total RNA was isolated using the Spin Cell Mini Kit 250 (Stratec). *LPA* mRNA levels were determined by qRT-PCR relative to *PPIB* mRNA expression in the respective samples as housekeeping transcript. Values were normalized to the amount of *LPA* mRNA detected in untreated cells. The bars represent the remaining *LPA* mRNA expression for each data point. Results are shown in Figure 2.

Example 4

Inhibition of *LPA* mRNA expression in human and cynomolgus primary hepatocytes by different doses of GalNAc-L1 LPA-1038 conjugated siRNA molecule delivered by receptor-mediated uptake.

Primary hepatocytes (ThermoFisher) were plated on collagen-coated 96-well plates at densities of 45,000 cells per well (cynomolgus) and 30,000 cells per well (human). GalNAc-L1-conjugated LPA-1038 was added immediately after plating at the indicated concentrations (nM). 24 hours after siRNA treatment total RNA was isolated using the InviTrap RNA cell HTS 96 well kit (Stratec). *LPA* mRNA levels were determined by qRT-PCR relative to *Actin* (cynomolgus) or *APOB* (human) mRNA levels in the respective samples as housekeeping transcript. Values were normalized to *LPA* expression in untreated cells. Means and SD of normalized triplicate values of remaining *LPA* mRNA levels are shown as black bars. Results shown in Figure 3.

Example 5

Knockdown of *LPA*-mRNA in human primary hepatocytes by the different indicated L6-GalNAc conjugated siRNAs in primary human hepatocytes upon receptor-mediated delivery.

Primary human hepatocytes (ThermoFisher) were plated on collagen-coated 96-well plates at 30,000 cells per well (96 well format). GalNAc-L6-conjugated siRNAs including a non-silencing control were added immediately after cell plating at the two indicated concentrations. 24 hours after siRNA treatment total RNA was isolated using the InviTrap RNA cell HTS 96 well kit (Stratec). *LPA* mRNA expression levels were determined by qRT-PCR relative to *APOB* mRNA as housekeeping transcript. Values were normalized to *LPA* mRNA expression in untreated cells and remaining *LPA* mRNA levels represented pairwise as bars (100 nM black bars, 20 nM grey bars). Means and SD of normalized triplicate values are shown in Figure 4.

Example 6 – *In vitro* determination of TTR knockdown of various TTR siRNA GalNAc conjugates

Murine primary hepatocytes were seeded into collagen pre-coated 96 well plates (Thermo Fisher Scientific, #A1142803) at a cell density of 30,000 cells per well and treated with siRNA-conjugates at concentrations ranging from 10nM to 0.0001nM. 24h post treatment cells were lysed and RNA extracted with InviTrap® RNA Cell HTS 96 Kit / C24 x 96 preps (Stratec #7061300400) according to the manufactures protocol. Transcripts levels of TTR and housekeeping mRNA (PtenII) were quantified by TaqMan analysis.

Target gene expression in primary murine hepatocytes 24h following treatment with the conjugates of the invention, Conjugates 1-3, showed that target gene expression decreases as the dose of the conjugate increased compared to the negative controls (see "UT" column and Reference Conjugate 3), as shown in Figure 7. This indicates that the first strand is binding to the target gene, thus lowering gene expression. Figure 7 also shows the target gene expression levels of Reference Conjugates 1 and 2 which act as comparator conjugates. As can be seen from a comparison between the data presented in Figures 7A and 7C, and 7B and 7C, the conjugates of the invention (Conjugates 1-3) decrease the target gene expression compared to Reference Conjugates 1 and 2. The most effective conjugate at 0.01 nM appears to be Conjugate 2. The most effective conjugate at 0.1 nM, 0.5 nM, 1 nM and 10 nM appears to be Conjugate 3.

Example 7 – *In vivo* time course of serum TTR in mice

C57BL/6 mice were treated s.c. with 1mg/kg siRNA-conjugates at day 0. Serum samples were taken at day 7, 14, and 27 by orbital sinus bleeding and stored at -20°C until analysis. Serum TTR quantification was performed with a Mouse Prealbumin ELISA (ALPCO, 41-PALMS/lot 22, 2008003B) according to the manufacturers protocol (sample dilution 1:8000 or 1:800).

The results of the time course of serum TTR in c57BL/6 mice cohorts of n=4 at 7, 14, and 27 days post s.c. treatment with 1 mg/kg Conjugates 1-3, Reference Conjugates 1, 2 and 4, and mock treated (PBS) individuals is shown in Figure 8. As indicated by the data in Figure 8, the conjugates of the invention are particularly effective at reducing target gene expression compared to the negative control (PBS) and Reference Conjugates 1, 2, and in particular to Reference Conjugate 4. Conjugates 2 and 3 are also more effective than Reference Conjugates 1, 2 and 4. The most effective conjugate is Conjugate 2. Thus, it may be expected that the dosing level of Conjugate 3 would be about three times lower to achieve the same initial knock down and would also result in longer duration of knock down as compared to Reference Conjugate 4.

More specifically, Conjugate 2 resulted in 3-fold lower target protein level in serum at day seven and 4-fold lower target protein level in serum at day 27 compared to Reference Conjugate 4 at equimolar dose in wild type mice. Furthermore, Conjugate 2 resulted in 85% reduction of target serum protein level at day 27 after single injection, compared to 36% reduction by equimolar amount of Reference Conjugate 4.

Example 8

Equal dose response of knock down for *LPA* targeting siRNA with two single GalNAc units conjugated to the second strand as compared to a triantennary GalNAc unit at the 5' second strand in primary cynomolgus hepatocytes.

The siRNAs are modified with alternating 2'-OMe/2'-F and contain each two phosphorothioate (PS) internucleotide linkages at their 5' and 3' terminal two internucleotide linkages. In conjugate 19 one serinol-GalNAc unit each is attached via a PS-bond to the 5' and 3' of the second strand. In conjugate 20 the two terminal 5' internucleotides of the second strand are phosphodiesters and a triantennary GalNAc linker is attached via a PS bond to this end.

Dose response of *LPA* knockdown in primary cynomolgus hepatocytes was assessed 24h post treatment with 100, 20, 4, 0.8, 0.16, 0.032, and 0.006 nM siRNA. The reference control is construct 2, the non-targeting control is named Cte. The transcript ct-value for each

treatment group was normalized to the transcript ct value for the house keeping gen ACTB (Δct) and to untreated hepatocytes, named ut (ΔΔct).

Data are shown in Figure 10

Material & Methods:

siRNAs

SEQ ID NO:	name	batch	strand	sequence
135	Conjugate 19	X0373	X0373A	mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG
136			X0373B	Ser(GN) (ps) fC (ps) mG (ps) fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU (ps) Ser(GN)
135	Ref. Conjugate 9	STS20041L6	STS2041A	mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG
137			STS2041B	ST23 (ps) ST23 (ps) ST23 (ps) C6XLT (ps) fC mG fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU
138	Reference Conjugate 5 (CTR)	X0125	X0125A	mC (ps) fU (ps) mU fA mC fU mC fU mC fG mC fC mC fA mA fG mC (ps) fG (ps) mA
139			X0125B	[(ST23) (ps)]$_3$ (C6XLT) (ps) fU mC fG mC fU mU fG mG fG mC fG mA fG mA fG mU fA (ps) mA (ps) fG

Legend

mA, mU, mC, mG	2'-O-Methyl RNA
fA, fU, fC, fG	2'-deoxy-2'-fluoro RNA
(ps)	phosphorothioate
(po)	phosphodiester

Primer:

			SEQ ID NO:
LPA	fw	GTGTCCTCGCAACGTCCA	48
	rev	GACCCCGGGGCTTTG	49
	probe	BHQ1-TGGCTGTTTCTGAACAAGCACCAATGG-FAM	140
ACTB	fw	GCATGGGTCAGAAGGATTCCTAT	54
	rev	TGTAGAAGGTGTGGTGCCAGATT	55
	probe	BHQ1-TCGAGCACGGCATCGTCACCAA-VIC	141

General Methods

In vitro experiments

Primary murine hepatocytes (Thermo Scientific: GIBCO Lot: #MC798) were thawed and cryo-preservation medium exchanged for Williams E medium supplemented with 5% FBS, 1 µM dexamethasone, 2 mM GlutaMax, 1% PenStrep, 4mg/ml human recombinant insulin,

15mM Hepes. Cell density was adjusted to 250000 cells per 1ml. 100µl per well of this cell suspension were seeded into collagen pre-coated 96 well plates. The test article was prediluted in the same medium (5 times concentrated) for each concentration and 25µl of this prediluted siRNA or medium only were added to the cells. Cells were cultured in at 37°C and 5% CO_2. 24 h post treatment the supernatant was discarded, and cells were washed in cold PBS and 250 µl RNA- Lysis Buffer S (Stratec) was added. Following 15 min incubation at room temperature plates were storage at -80°C until RNA isolation according to the manufacturers protocol.

TaqMan analysis

For mTTR & PTEN MultiPlex TaqMan analysis 10µl isolated RNA for each treatment group were mixed with 10 µl PCR mastermix (TAKYON low Rox) containing 600 nM mTTR-primer, 400 nM ApoB-primer and 200nM of each probe as well as 0.5 units Euroscript II RT polymerase with 0.2 units RNAse inhibitor. TaqMan analysis was performed in 384-well plate with a 10 min RT step at 48°C, 3 min initial denaturation at 95°C and 40 cycles of 95°C for 10 sec and 60°C for 1 min. The primers contain two of BHQ1, FAM and YY, one at each end of the sequence.

For TMPRSS6 & ApoB MultiPlex TaqMan analysis 10 µl isolated RNA for each treatment group were mixed with 10 µl PCR mastermix (TAKYON low Rox) containing 800 nM TMPRSS6 primer, 100 nM ApoB primer and 200 nM of either probe as well as 0.5 units Euroscript II RT polymerase with 0.2 units RNAse inhibitor. TaqMan analysis was performed in 384-well plate with a 10min RT step at 48°C, 3min initial denaturation at 95°C and 40 cycles of 95°C for 10 sec and 60°C for 1 min.

In vivo experiments

To compare *in vivo* potency of different siRNA conjugates 1mg/kg siRNA dissolved in PBS was administered sub cutaneous in the scapular region of c57BL/6 mice. Cohorts of of n=6 for were treated with siRNA targeting *Aldh2* or *Tmprss6* at day 1 and sacrificed at selected times points post treatment. Liver samples were snap frozen in liquid nitrogen and stored at -80°C until extraction RNA with InviTrap Spin Tissue RNA Mini Kit (stratec) according to the manufacturers manual. Following, transcript level of *Aldh2*, *Tmprss6* and *Pten* were quantified as described above.

Tritosome stability assay

To probe for RNAase stability in the endosomal / lysosomal compartment of hepatic cells *in vitro* siRNA was incubated for 0 h, 4 h, 24 h or 72 h in Sprague Dawley Rat Liver Tritosomes

(Tebu- Bio, CatN.: R0610.LT, lot: 1610405, pH: 7.4, 2.827 Units/ml). To mimic the acidified environment the Tritosomes were mixed 1:10 with low pH buffer (1.5M acetic acid, 1.5M sodium acetate pH 4.75). 30 µl of this acidified Tritosomes. Following 10µl siRNA (20µM) were mixed with and incubated for the indicated times at 37°C. Following incubation RNA was isolated with the Clarity OTX Starter Kit-Cartriges (Phenomenex CatNo: KSO-8494) according to the manufactures protocol for biological fluids. Lyophilized RNA was reconstituted in 30 µl H_2O, mixed with 4xloading buffer and 5 µl were loaded to a 20% TBE-polyacrylamide gel electrophoresis (PAGE) for separation qualitative semi-quantitative analysis. PAGE was run at 120 V for 2 h and RNA visualized by Ethidum-bromide staining with subsequent digital imaging with a Biorad Imaging system.

Example 9 - Synthesis of conjugates

Example compounds were synthesised according to methods described below and methods known to the person skilled in the art. Assembly of the oligonucleotide chain and linker building blocks was performed by solid phase synthesis applying phosphoramidite methodology. GalNAc conjugation was achieved by peptide bond formation of a GalNAc-carboxylic acid building block to the prior assembled and purified oligonucleotide having the necessary number of amino modified linker building blocks attached.

Oligonucleotide synthesis, deprotection and purification followed standard procedures that are known in the art.

All Oligonucleotides were synthesized on an AKTA oligopilot synthesizer using standard phosphoramidite chemistry. Commercially available solid support and 2´O-Methyl RNA phosphoramidites, 2´Fluoro, 2´Deoxy RNA phosphoramidites (all standard protection, ChemGenes, LinkTech) and commercially available 3'-Amino Modifier TFA Amino C-6 lcaa CPG 500Å (Chemgenes), Fmoc-Amino-DMT C-7 CE phosphoramidite (GlyC3Am), 3'-Amino Modifier C-3 lcaa CPG 500Å (C3Am), Fmoc-Amino-DMT C-3 CED phosphoramidite (C3Am) and TFA-Amino C-6 CED phosphoramidite (C6Am) (Chemgenes), 3'-Amino-Modifier C7 CPG (C7Am) (Glen Research), Non-nucleosidic TFA amino Phosphoramidite (Pip), Non-nucleosidic TFA amino Solid Support (PipAm) (AM Chemicals) were used. Per-acetylated galactose amine **8** is commercially available.

Ancillary reagents were purchased from EMP Biotech. Synthesis was performed using a 0.1 M solution of the phosphoramidite in dry acetonitrile and benzylthiotetrazole (BTT) was used as activator (0.3M in acetonitrile). Coupling time was 15 min. A Cap/OX/Cap or

Cap/Thio/Cap cycle was applied (Cap: Ac_2O/NMI/Lutidine/Acetonitrile, Oxidizer: 0.1M I_2 in pyridine/H_2O). Phosphorothioates were introduced using standard commercially available thiolation reagent (EDITH, Link technologies). DMT cleavage was achieved by treatment with 3% dichloroacetic acid in toluene. Upon completion of the programmed synthesis cycles a diethylamine (DEA) wash was performed. All oligonucleotides were synthesized in DMT-off mode.

Attachment of the serinol-derived linker moiety was achieved by use of either base-loaded (S)-DMT-Serinol(TFA)-succinate-lcaa-CPG **10** or a (S)-DMT-Serinol(TFA) phosphoramidite **7** (synthesis was performed as described in literature Hoevelmann *et al.* Chem. Sci., 2016,7, 128-135). Tri-antennary GalNAc clusters (ST23/C4XLT or ST23/C6XLT) were introduced by successive coupling of the respective trebler amidite derivatives (C4XLT-phos or C6XLT-phos) followed by the GalNAc amidite (ST23-phos).

Attachment of amino modified moieties (non-serinol-derived linkers) was achieved by use of either the respective commercially available amino modified building block CPG or amidite.

The single strands were cleaved off the CPG by 40% aq. methylamine treatment. The resulting crude oligonucleotide was purified by ion exchange chromatography (Resource Q, 6mL, GE Healthcare) on a AKTA Pure HPLC System using a sodium chloride gradient. Product containing fractions were pooled, desalted on a size exclusion column (Zetadex, EMP Biotech) and lyophilised.

Individual single strands were dissolved in a concentration of 60 OD/mL in H_2O. Both individual oligonucleotide solutions were added together in a reaction vessel. For easier reaction monitoring a titration was performed. The first strand was added in 25% excess over the second strand as determined by UV-absorption at 260nm. The reaction mixture was heated to 80°C for 5min and then slowly cooled to RT. Double strand formation was monitored by ion pairing reverse phase HPLC. From the UV-area of the residual single strand the needed amount of the second strand was calculated and added to the reaction mixture. The reaction was heated to 80°C again and slowly cooled to RT. This procedure was repeated until less than 10% of residual single strand was detected.

*Synthesis of compounds **2-10***

Compounds **2** to **5** and (S)-DMT-Serinol(TFA)-phosphoramidite **7** were synthesised according to literature published methods (Hoevelmann et al. Chem. Sci., 2016,7, 128-135).

(S)-4-(3-(bis(4-methoxyphenyl)(phenyl)methoxy)-2-(2,2,2-trifluoroacetamido)propoxy)-4-oxobutanoic acid (6).

To a solution of **5** in pyridine was added succinic anhydride, followed by DMAP. The resulting mixture was stirred at room temperature overnight. All starting material was consumed, as judged by TLC. The reaction was concentrated. The crude material was chromatographed in silica gel using a gradient 0% to 5% methanol in DCM (+ 1% triethylamine) to afford 1.33 g of **6** (yield = 38%). m/z (ESI-): 588.2 (100%), (calcd. for $C30H29F3NO8^-$ $[M-H]^-$ 588.6). 1 H-NMR: (400 MHz, CDCl3) δ [ppm] = 7.94 (d, 1H, NH), 7.39 - 7.36 (m, 2H, CHaryl), 7.29 - 7.25 (m, 7H, CHaryl), 6.82-6.79 (m, 4H, CHaryl), 4.51 – 4.47 (m, 1H), 4.31 – 4.24 (m, 2H), 3.77 (s, 6H, 2xDMTr-OMe), 3.66 - 3.60 (m, 16H, $HNEt_3^+$), 3.26 - 3.25 (m, 2H), 2.97 – 2.81 (m, 20H, NEt_3), 2.50-2.41 (4H, m), 1.48 – 1.45 (m, 26H, $HNEt_3^+$), 1.24 - 1.18 (m, 29H, NEt_3).

(S)-DMT-Serinol(TFA)-succinate-lcaa-CPG (10)

The (S)-DMT-Serinol(TFA)-succinate (159 mg, 270 umol) and HBTU (113 mg, 299 umol) were dissolved in CH_3CN (10 mL). Diisopropylethylamine (DIPEA, 94 µL, 540 umol) was added to the solution, and the mixture was swirled for 2 min followed by addition native amino-lcaa-CPG (500 A, 3 g, amine content: 136 umol/g). The suspension was gently shaken at room temperature on a wrist-action shaker for 16h then filtered, and washed with DCM and EtOH. The solid support was dried under vacuum for 2 h. The unreacted amines on the support were capped by stirring with acetic anhydride/lutidine/N-methylimidazole at room temperature. The washing of the support was repeated as above. The solid was dried under vacuum to yield solid support **10** (3 g, 26 umol/g loading).

GalNAc Synthon (9)

Synthesis of the GalNAc synthon **9** was performed as described in Nair et al. J. Am. Chem. Soc., 2014, 136 (49), pp 16958–16961, in 46% yield over two steps.

The characterising data matched the published data.

Synthesis of Oligonucleotides

All single stranded oligonucleotides were synthesised according to the reaction conditions described above and in Figure 5 and 6, and are outlined in Tables 3 and 4.

All final single stranded products were analysed by AEX-HPLC to prove their purity. Purity is given in %FLP (% full length product) which is the percentage of the UV-area under the assigned product signal in the UV-trace of the AEX-HPLC analysis of the final product.

Identity of the respective single stranded products (non-modified, amino-modified precursors or GalNAc conjugated oligonucleotides) was proved by LC-MS analysis.

Table 3: Single stranded un-conjugated oligonucleotides

Product (11)	Name	MW calc.	MW (ESI-) found	%FLP (AEX-HPLC)
A0002	STS16001A	6943.3 Da	6943.0 Da	86.6%
A0006	STS16001BL4	8387.5 Da	8387.5 Da	94.1%
A0114	STS22006A	6143.8 Da	6143.7 Da	94.3%
A0115	STS22006BL1	7855.1 Da	7855.1 Da	92.8%
A0122	STS22009A	6260.9 Da	6260.6 Da	92.8%
A0123	STS22009BL1	7783.0 Da	7782.9 Da	87.1%
A0130	STS18001A	6259.9 Da	6259.8 Da	76.5%
A0131	STS18001BL4	7813.2 Da	7813.1 Da	74.3%
A0220	STS16001B-5'1xNH2	6982.2 Da	6982.1 Da	95.7%
A0237	STS16001A	6943.3 Da	6943.3 Da	95.6%
A0244	STS16001BV1	6845.2 Da	6844.9 Da	98.2%
A0264	STS16001AV4-3'1xNH2	7112.4 Da	7112.2 Da	95.4%
A0329	STS16001BV6-3'5'1xNH2	7183.3 Da	7183.2 Da	88.8%
A0560	STS16001A	6943.3 Da	6943.3 Da	96.7%
A0541	STS16001BV1-3'5'NH2	7151,3 Da	7151,0 Da	85,6%
A0547	STS16001BV16-3'5'NH2	7119,3 Da	7119,1 Da	89,9%
A0617	STS16001BV20-3'5'NH2	7087,3Da	7086,7 Da	90,1%
A0619	STS16001BV1-3'5'2xNH2	7521,3 Da	7521,3 Da	93.4%
A0680	STS16001A	6943.3 Da	6942.9 Da	91.2%
A0514	STS22006A	6143.8 Da	6143.7 Da	94.6%
A0516	STS22009BV11-3'5'NH2	6665.0 Da	6664.8 Da	87.0%
A0517	STS22009BV11-3'5'NH2	6593.0 Da	6593.0 Da	86.0%
A0521	STS12009BV1-3'5'NH2	6437,7 Da	6437.8 Da	91.1%
A0303	STS12209BL4	7665.0 Da	7664.9 Da	90.4%
A0304	STS12209A	6393.1 Da	6392.9 Da	77.6%
A0319	STS22009A	6260,9 Da	6260.5 Da	86.9%
A0353	STS12009A	6416.1 Da	6416.1 Da	94.1%
A0216	STS17001A	6178.8 Da	6178.7 Da	87.2%
A0217	STS17001BL6	7937.2 Da	7937.2 Da	78.3%

5'1 x NH2 means refers to the position (5' end) and number (1 x NH2) of free serinol derived amino groups which are available for conjugation. For example, 1x3'NH2 on **A0264** means there is free amino group which can be reacted with GalNAc synthon **9** at the 3' end of the strand **A0264**. 3'5'1xNH2 means there is one serinol-derived free amino group which can be reacted with GalNAc linker **9** at the 3' end and the 5' end of the strand.

Table 4: Single stranded oligonucleotides with 5' and 3' modifications

Product	Name	5'mod	3'mod	MW calc.	MW (ESI-) found	%FLP (AEX-HPLC)
A0561	STS16001BV1-3'5'1xNH2	C6Am	GlyC3Am	7267.5 Da	7267.5 Da	66.7%
A0563	STS16001BV1-3'5'1xNH2	C3Am	C3Am	7183.4 Da	7183.1 Da	75.1%
A0651	STS16001BV1-3'5'1xNH2	C6Am	C7Am	7265.6 Da	7265.2 Da	99.6%
A0653	STS16001BV1-3'5'1xNH2	GlyC3Am	GlyC3Am	7299.5 Da	7299.3 Da	88.1%
A0655	STS16001BV1-3'5'1xNH2	PipAm	PipAm	7517.7 Da	7517.5 Da	89.8%

Similarly, 3'5'1 x NH2 refers to the position (3' and 5' end) and number (1 x NH2 each) of free amino groups which are available for conjugation. For example, 3'5'1xNH2 on **A0561** means there are 2 free amino group (1 at the 3' AND 1 at the 5' end) which can be reacted with GalNAc synthon **9** at the 3' end of the strand **A0561**.

Synthesis of certain conjugates and reference conjugates 1-2

Conjugation of the GalNac synthon (**9**) was achieved by coupling to the serinol-amino function of the respective oligonucleotide strand **11** using a peptide coupling reagent. Therefore, the respective amino-modified precursor molecule **11** was dissolved in H_2O (500 OD/mL) and DMSO (DMSO/H_2O, 2/1, v/v) was added, followed by DIPEA (2.5% of total volume). In a separate reaction vessel pre-activation of the GalN(Ac4)-C4-acid (**9**) was performed by reacting 2 eq. (per amino function in the amino-modified precursor oligonucleotide **11**) of the carboxylic acid component with 2 eq. of HBTU in presence of 8 eq. DIPEA in DMSO. After 2 min the pre-activated compound **9** was added to the solution of the respective amino-modified precursor molecule. After 30 min the reaction progress was monitored by LCMS or AEX-HPLC. Upon completion of the conjugation reaction the crude product was precipitated by addition of 10x *i*PrOH and 0.1x 2M NaCl and harvested by centrifugation and decantation. To set free the acetylated hydroxyl groups in the GalNAc moieties the resulting pellet was dissolved in 40% MeNH2 (1mL per 500 OD) and after 15 min at RT diluted in H_2O (1:10) and finally purified again by anion exchange and size exclusion chromatography and lyophilised to yield the final product **12** (Table 5).

Table 5: Single stranded GalNAc-conjugated oligonucleotides

Product (12)	**Starting Material**	**Name**	**MW calc.**	**MW (ESI-) found**	**%FLP (AEX-HPLC)**
A0241	A0220	STS16001BL20	7285.5 Da	7285.3 Da	91.8%
A0268	A0264	STS16001AV4L33	7415.7 Da	7415.4 Da	96.9%
A0330	A0329	STS16001BV6L42	7789.8 Da	7789.8 Da	95.5%
A0544	A0541	STS16001BV1L75	7757,9 Da	7757,7 Da	93.3%
A0550	A0547	STS16001BV16L42	7725,9 Da	7725.7 Da	88.5%
A0620	A0617	STS16001BV20L75	7693,91 Da	7693,2 Da	90.9%
A0622	A0619	STS16001BV1L94	8734,3 Da	8734,6 Da	82.9%
A0519	A0516	STS22006BV11L42	7271.7 Da	7271.7 Da	90.0%
A0520	A0517	STS22009BV11L42	7199.6 Da	7199.7 Da	92.9%
A0522	A0521	STS12009BV1L42	7044.4 Da	7044.4 Da	96.0%
A0603	A0602	STS20041BV1L42	7280.7 Da	7280.4 Da	93.4%

Synthesis of certain conjugates of the invention

Conjugation of the GalNac synthon (**9**) was achieved by coupling to the amino function of the respective oligonucleotide strand **14** using a peptide coupling reagent. Therefore, the respective amino-modified precursor molecule **14** was dissolved in H_2O (500 OD/mL) and DMSO (DMSO/H_2O, 2/1, v/v) was added, followed by DIPEA (2.5% of total volume). In a separate reaction vessel pre-activation of the GalN(Ac4)-C4-acid (**9**) was performed by reacting 2 eq. (per amino function in the amino-modified precursor oligonucleotide **14**) of the carboxylic acid component with 2 eq. of HBTU in presence of 8 eq. DIPEA in DMSO. After 2 min the pre-activated compound **9** was added to the solution of the respective amino-modified precursor molecule. After 30 min the reaction progress was monitored by LCMS or AEX-HPLC. Upon completion of the conjugation reaction the crude product was precipitated by addition of 10x *i*PrOH and 0.1x 2M NaCl and harvested by centrifugation and decantation. To set free the acetylated hydroxyl groups in the GalNAc moieties the resulting pellet was dissolved in 40% MeNH2 (1mL per 500 OD) and after 15 min at RT diluted in H_2O (1:10) and finally purified again by anion exchange and size exclusion chromatography and lyophilised to yield the final product **15** (Table 6).

Table 6: Single stranded GalNAc-conjugated oligonucleotides

Product (15)	Starting Material	Name	MW calc.	MW (ESI-) found	%FLP (AEX-HPLC)
A0562	A0561	STS16001BV1L87	7874.2 Da	7874.0 Da	82.7%
A0564	A0563	STS16001BV1L88	7790.0 Da	7789.4 Da	90.4%
A0652	A0651	STS16001BV1L96	7872.2 Da	7871.8 Da	94.6%
A0654	A0653	STS16001BV1L97	7906.2 Da	7905.6 Da	89.9%
A0656	A0655	STS16001BV1L98	8124.3 Da	8124.0 Da	93.6%

Double strand formation

Double strand formation was performed according to the methods described above.

The double strand purity is given in % double strand which is the percentage of the UV-area under the assigned product signal in the UV-trace of the IP-RP-HPLC analysis (Table 7).

Table 7: Nucleic acid conjugates

Product	Starting Materials		Name	% double strand
	First Strand	Second Strand		
Ref. Conj. 1	A0237	A0241	STS16001L20	97.7%
Ref. Conj. 2	A0268	A0244	STS16001L33	97.8%
Ref. Conj. 3	A0130	A0131	STS18001L4	96.8%
Ref. Conj. 4	A0002	A0006	STS16001L4	90.1%
Ref. Conj. 5	A0216	A0217	STS17001L6	88.4%
Conjugate 1	A0268	A0241	STS16001L24	96.0%
Conjugate 2	A0237	A0330	STS16001V1L42	98.5%
Conjugate 3	A0268	A0330	STS16001V1L43	98.2%
Conjugate 4	A0560	A0544	STS16001V1L75	92.5%
Conjugate 5	A0560	A0550	STS16001V16L42	95.3%

Conjugate 6	A0237	A0620	STS16001V20L75	97.8%
Conjugate 7	A0237	A0622	STS16001V1L94	93.7%
Conjugate 8	A0680	A0652	STS16001V1L96	98.4%
Conjugate 9	A0680	A0654	STS16001V1L97	95.8%
Conjugate 10	A0680	A0656	STS16001V1L98	97.6%
Conjugate 11	A0560	A0564	STS16001V1L88	95.0%
Conjugate 12	A0237	A0562	STS16001V1L87	96.8%
Conjugate 13	A0114	A0115	STS22006L1	85.6%
Conjugate 14	A0122	A0123	STS22009L1	96.4%
Conjugate 15	A0514	A0519	STS22006V11L42	98.6%
Conjugate 16	A0319	A0520	STS22009V11L42	97.0%
Conjugate 17	A0304	A0303	STS12209L4	93.0%
Conjugate 18	A0353	A0522	STS12009V1L42	98.0%
Conjugate 19	A0601	A0603	STS20041BL42	97.6%

Sequences

Modifications key for the following sequences:

f denotes 2´Fluoro 2´deoxyribonucleotide or 2'-fluoro ribonucleotide (the terms are interchangeable)

m denotes 2´O Methyl ribonucleotide

(ps) denotes phosphorothioate linkage

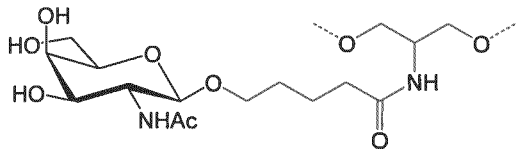
FAM = 6-Carboxyfluorescein

BHQ = Black Hole Quencher 1

YY = Yakima Yellow

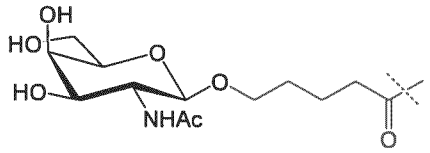
Definitions

Ser(GN) is a GalNAc-C4 building block attached to serinol derived linker moiety:

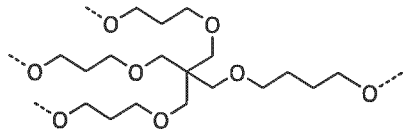


wherein the O--- is the linkage between the oxygen atom and e.g. H, phosphordiester linkage or phosphorothioate linkage.

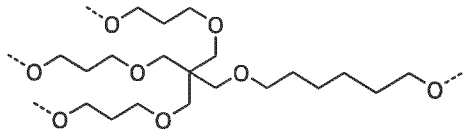
GN is:



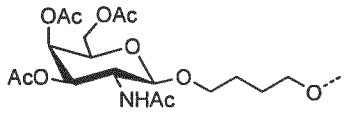
C4XLT is:



C6XLT is:

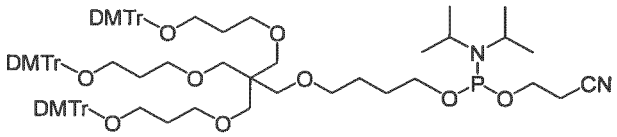


ST23 is:

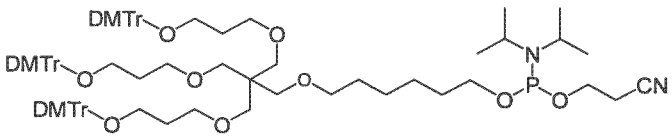


Synthesis of the phosphoramidite derivatives of C4XLT (C4XLT-phos), C6XLT (C6XLT-phos) as well as ST23 (ST23-phos) can be performed as described in WO2017/174657.

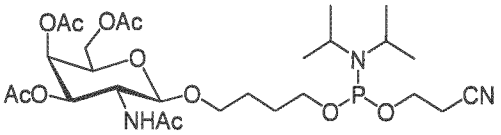
C4XLT-phos:

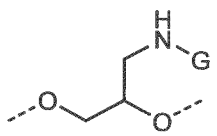
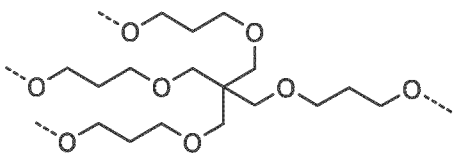
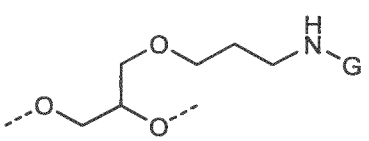


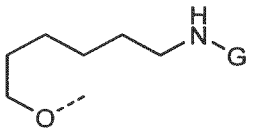
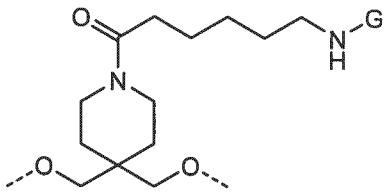
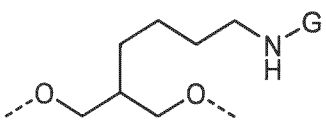
C6XLT-phos:



ST23-phos:



C3Am is:	Itrb is:	GlyC3Am is:
		

C6Am is:	Pip Am is:	C7Am is:
		

wherein G = H (pre conjugation) or G = GN (post conjugation).

Conjugate 1

Antisense strand - STS16001AL33 (SEQ ID NO: 127)

5′ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(GN) 3′

Sense strand - STS16001BL20 (SEQ ID NO: 128)

5′ Ser(GN) (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA 3′

Conjugate 2

Antisense strand - STS16001A (SEQ ID NO: 129)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand - STS16001BV1L42 (SEQ ID NO: 130)

Ser(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) Ser(GN)

Conjugate 3

Antisense strand - STS16001AL33 (SEQ ID NO: 127)

5′ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(GN) 3′

Sense strand - STS16001BV1L42 (SEQ ID NO: 130)

5′ Ser(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) Ser(GN) 3′

Conjugate 4

Antisense strand - STS16001A (SEQ ID NO: 129)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand - STS16001BV1L75 (SEQ ID NO: 142)

5´ Ser(GN) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA Ser(GN) 3´

Conjugate 5

Antisense strand - STS16001A (SEQ ID NO: 129)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand - STS16001BV16L42 (SEQ ID NO: 143)

5´ Ser(GN) (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU mA fA (ps) Ser(GN) 3´

Conjugate 6

Antisense strand - STS16001A (SEQ ID NO: 129)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand - STS16001BV20L75 (SEQ ID NO: 144)

5´ Ser(GN) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU mA fA Ser(GN) 3´

Conjugate 7

Antisense strand - (SEQ ID NO: 129)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand - STS16001BV1L94 (SEQ ID NO: 145)

5´ Ser(GN) (ps) Ser(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) Ser(GN) (ps) Ser(GN) 3´

Conjugate 8

Antisense strand - STS16001A (SEQ ID NO: 129)

5‘ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU 3‘

Sense strand - STS16001V1BL96 (SEQ ID NO: 146)

5‘ C6Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) C7Am(GN) 3´

Conjugate 9

Antisense strand - STS16001A (SEQ ID NO: 129)

5‘ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU 3‘

Sense strand - STS16001V1BL97 (SEQ ID NO: 147)

5´ GlyC3Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) GlyC3Am(GN) 3´

Conjugate 10

Antisense strand - STS16001A (SEQ ID NO: 129)

5´ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU 3‘

Sense strand (SEQ ID NO: 148)

5´ PipAm(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) PipAm(GN) 3´

Conjugate 11

Antisense strand - STS16001A (SEQ ID NO: 129)

5´ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU 3‘

Sense strand - STS16001V1BL88 (SEQ ID NO: 149)

5´ C3Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) C3Am(GN) 3´

Conjugate 12

Antisense strand - STS16001A (SEQ ID NO: 129)

5′ mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU 3‘

Sense strand - STS16001V1BL87 (SEQ ID NO: 150)

5′ C6Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) GlyC3Am(GN) 3′

Conjugate 15

Antisense strand (SEQ ID NO: 151)

mU (ps) fC (ps) mU fU mC fU mU fA mA fA mC fU mG fA mG fU mU (ps) fU (ps) mC

Sense strand (SEQ ID NO: 152)

Ser(GN) (ps) fG (ps) mA (ps) fA mA fC mU fC mA fG mU fU mU fA mA fG mA fA (ps) mG (ps) fA (ps) Ser(GN)

Conjugate 16

Antisense strand (SEQ ID NO: 153)

mA (ps) fU (ps) mG fU mA fG mC fC mG fA mG fG mA fU mC fU mU (ps) fC (ps) mU

Sense strand (SEQ ID NO: 154)

Ser(GN) (ps) fA (ps) mG (ps) fA mA fG mA fU mC fC mU fC mG fG mC fU mA fC (ps) mA (ps) fU (ps) Ser(GN)

Conjugate 18

Antisense strand (SEQ ID NO: 155)

mA (ps) fA (ps) mC fC mA fG mA fA mG fA mA fG mC fA mG fG mU (ps) fG (ps) mA

Sense strand (SEQ ID NO: 156)

Ser(GN) (ps) fU (ps) mC (ps) fA mC fC mU fG mC fU mU fC mU fU mC fU mG fG (ps) mU (ps) fU (ps) Ser(GN)

Conjugate 19

Antisense strand (SEQ ID NO: 135)

mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG

Sense strand (SEQ ID NO: 136)

Ser(GN) (ps) fC (ps) mG (ps) fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU (ps) Ser(GN)

Reference conjugate 1

Antisense strand - STS16001A (SEQ ID NO: 129)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand – STS16001BL20 (SEQ ID NO: 128)

Ser(GN) (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA

Reference conjugate 2

Antisense strand - STS16001AL33 (SEQ ID NO: 127)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(GN)

Sense strand - STS16001BV1 (SEQ ID NO: 157)

fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA

Reference Conjugate 3 – "Luc"

Antisense strand - STS18001A (A0130, SEQ ID NO: 132)

mU (ps) fC (ps) mG fA mA fG mU fA mU fU mC fC mG fC mG fU mA (ps) fC (ps) mG

Sense strand - STS18001BL4 (A0131, SEQ ID NO: 133)

$[(ST23)\ (ps)]_3$ C4XLT (ps) fC mG fU mA fC mG fC mG fG mA fA mU fA mC fU mU fC (ps) mG (ps) fA

Reference Conjugate 4

Antisense strand - STS16001AL33 (SEQ ID NO: 127)

mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU

Sense strand - STS16001BL4 (SEQ ID NO: 134)

5´[(ST23) (ps)]$_3$ C4XLT(ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA

Reference Conjugate 5 – "Ctr"

Antisense strand (SEQ ID NO: 138)

mC (ps) fU (ps) mU fA mC fU mC fU mC fG mC fC mC fA mA fG mC (ps) fG (ps) mA

Sense strand (SEQ ID NO: 139)

[(ST23) (ps)]3 (C6XLT) (ps) fU mC fG mC fU mU fG mG fG mC fG mA fG mA fG mU fA (ps) mA (ps) fG

Reference Conjugate 6

Antisense strand (SEQ ID NO: 151)

mU (ps) fC (ps) mU fU mC fU mU fA mA fA mC fU mG fA mG fU mU (ps) fU (ps) mC

Sense strand (SEQ ID NO: 158)

[ST23 (ps)]3 ltrb (ps) fG mA fA mA fC mU fC mA fG mU fU mU fA mA fG mA fA (ps) mG (ps) fA

Reference Conjugate 7

Antisense strand (SEQ ID NO: 153)

mA (ps) fU (ps) mG fU mA fG mC fC mG fA mG fG mA fU mC fU mU (ps) fC (ps) mU

Sense strand (SEQ ID NO: 159)

[ST23 (ps)]3 ltrb (ps) fA mG fA mA fG mA fU mC fC mU fC mG fG mC fU mA fC (ps) mA (ps) fU

Reference Conjugate 8

Antisense strand (SEQ ID NO: 160)

mU (ps) fA (ps) mC fC mA fG mA fA mG fA mA fG mC fA mG fG mU (ps) fG (ps) mA

Sense strand (SEQ ID NO: 161)

[ST23 (ps)]3 ST41 (ps)fU mC fA mC fC mU fG mC fU mU fC mU fU mC fU mG fG (ps) mU (ps) fA

Reference Conjugate 9

Antisense strand (SEQ ID NO: 135)

mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG

Sense strand (SEQ ID NO: 162)

[ST23 (ps)]3 C6XLT (ps) fC mG fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU

Example 10 – *In vitro* determination of TTR knockdown of various TTR siRNA GalNAc conjugates

Conjugates 4 to 7

The method described above under "In vitro experiments" in the General Method section was followed.

Target gene expression in primary murine hepatocytes 24h following treatment at 0.01 nM, 0.1 nM, 0.5 nM, 1nM and 10nM with the conjugates of the invention, Conjugates 4-7, showed that target gene expression decreases as the dose of the conjugate increased compared to the negative controls (see "UT" column and Luc [Reference Conjugate 3]), as shown in Figure 11. This indicates that the first strand is binding to the target gene, thus lowering gene expression.

The *in vitro* data show that in the context of one or two serinol-derived linker moieties being provided at 5' and 3' ends of the sense strand in Conjugates 4-7, the number of phosphorothioate (PS) bonds between the terminal nucleotide and the linker, and/or between the terminal three nucleotides in the sense strand, can be varied whilst maintaining efficacy for decreasing target gene expression.

Conjugates 8 to 12 and 19

The method described above under "In vitro experiments" in the General Method section was followed.

Target gene expression in primary murine hepatocytes 24h following treatment at 0.01 nM, 0.1 nM, 0.5 nM, 1nM and 10nM with the conjugates of the invention, Conjugates 8-12, showed that target gene expression decreases as the dose of the conjugate increased compared to the negative controls (see "UT" column and Luc [Reference Conjugate 3]), as shown in Figure 12. This indicates that the first strand is binding to the target gene, thus lowering gene expression. In particular, Conjugates 8, 9, 10 and 11 appear to be

comparable to or better than Conjugate 2 which was previously shown to be the most effective conjugate at 0.01 nM.

Conjugate 19 was also shown to decrease target gene expression compared to the negative controls (see "UT" column and Ctr which is a non-targeting siRNA and also referred to as Reference Conjugate 5), as shown in Figure 13. This indicates that the first strand is binding to the target gene, thus lowering gene expression.

The *in vitro* data for Conjugates 8-12 and 19 show that a number of linkers which are structurally diverse and which are conjugated at both termini of the sense strand are effective at decreasing target gene expression. Conjugates 8-12 and 19 decrease target gene expression more effectively than "Luc" which is Reference Conjugate 3 (for Conjugates 8-12), "Ctr" which is Reference Conjugate 5 (for Conjugate 19) and untreated control.

Example 11 – *In vivo* time course of serum *Ttr*, *Aldh2* and *Tmprss6* in mice

Conjugates 15 to 18

The method described above under "*In vivo* experiments" in the General Method section was followed.

The results of the time course of serum *Aldh2* in c57BL/6 mice cohorts of n=6 at 14, 28 and 42 days post s.c. treatment with 1mg/kg Conjugates 15 and 16, Reference Conjugates 6 and 7, and mock treated (PBS) individuals is shown in Figures 14 and 15. As indicated by the data in Figures 14 and 15, the conjugates of the invention are particularly effective at reducing target gene expression compared to the negative control (PBS) and Reference Conjugates 6 and 7 respectively.

The results of the time course of serum *Tmprss6* in c57BL/6 mice cohorts of n=6 at 14, 28 and 42 days post s.c. treatment with 1mg/kg Conjugate 18, Reference Conjugate 8, and mock treated (PBS) individuals is shown in Figure 16. As indicated by the data in Figure 16, the conjugates of the invention are particularly effective at reducing target gene expression compared to the negative control (PBS) and Reference Conjugate 8.

Overall, the *in vivo* data show that a variety of example linkers which are conjugated at both termini of the second strand are effective at decreasing target gene expression *in vivo*. The positioning of the linker improves *in vivo* potency conjugates, as compared to a triantennary GalNAc-linker control at the 5' terminus of the second strand (Reference Conjugates 6, 7 and 8).

Example 12 – Serum Stability Studies

The method described above under "Tritosome stability assay" in the General Method section was followed.

Figure 17 shows the results from the serum stability studies in respect of Conjugates 2, 4, 5, 6 and 7. Figure 18 shows the serum stability of Conjugates 2, 8, 9, 10, 11 and 12.

All conjugates of the invention that were tested are more stable in serum compared to control.

All tested conjugates contain each one GalNAc linker unit at the 5' end and another at the 3' end of the second strand. The siRNAs are modified with alternating 2'-OMe/2'-F and contain each two phosphorothioate (PS) internucleotide linkages at their 5' and 3' terminal two internucleotide linkages, unless stated differently.

In Conjugate 4 the serinol-GalNAc units are attached via a phosphodiester bond. In Conjugate 5 the serinol-GalNAc units are conjugated via PS, whereas all internucleotide linkage in the second strand are phosphodiesters. In Conjugate 6 the second strand contains no PS. In Conjugate 7 two serinol-GalNAc units are attached to each second strand terminus and to each other via a PS-bonds at the respective ends. In Conjugate 8 a C6-amino-modifier at 5' and a C7-amino-modifier at the 3' end of the second strand were applied for ligand attachment. In Conjugate 9 Gly-C3-amino-modifiers, in Conjugate 10 piperidyl-amino-modifiers, in Conjugate 11 C3-amino-modifiers and in Conjugate 2 serinol-GalNAc units were used as linkers for conjugation to both ends of the second strand. In Conjugate 2 both terminal internucleotides as well as the nucleotide-serinol bonds are PS. In Conjugate 12 a C6-amino-modifier at the 5' and a GlyC3-amino-modifier at the 3' end of second strand were applied for ligand attachment. "ut" indicates an untreated sample which the other samples were normalised to. "Luc" indicates an siRNA targeting Luciferase (Reference Conjugate 3), which was used as non-targeting control and does not reduce target mRNA levels.

The data show that in context of a serinol-derived linker moiety being provided at 5' and 3' ends of the sense strand, the number of phosphorothioate (PS) bonds between the terminal nucleotide and the linker, and/or between the terminal three nucleotides in the sense strand, can be varied whilst maintaining stability in serum.

Example 13

Primary human (Lot Hu1823) and cynomolgus (Lot CY367) hepatocytes and media were sourced from Life Technologies. As described by the manufacturer, primary hepatocytes were thawed and plated in plating media consisting of Williams' E medium (Life Technologies), supplemented with 5% fetal bovine serum, 1 µM Dexamethasone in DMSO (final concentration of DMSO = 0.01 %) and 3.6 % v/v of Thawing/Plating Cocktail-A (Thermo Fisher Scientific, CM3000).

Human primary hepatocytes were seeded into collagen I-coated 96-well plates (Life Technologies) at a density of 30,000 cells per well. Cynomolgus hepatocytes were seeded at a density of 45,000 cells per well. Conjugate 21 and a control GalNAc-conjugated siRNA were serially diluted 5-fold at a concentration range of 0.006 – 100 nM and added immediately after plating in plating media. Plates were then incubated at 37°C in a 5% CO_2 atmosphere for 24 hours. Subsequently, cells were lysed and RNA was isolated using the method described below.

Conjugate 21 sequences

Antisense strand – Conjugate 21 (SEQ ID NO: 165)

5´ mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG 3´

Sense strand - STS16001BL20 (SEQ ID NO: 164)

5´ [ST23 (ps)]3 C6XLT (ps) mC mG mG mU mA mA fU fG fG mA mC mA mG mA mG mU mU (ps) mA (ps) mU 3´

Total RNA was extracted using the InviTrap HTS 96-well kit (Stratec Molecular GmbH, Berlin, Germany) according to the manufacturer's instructions with the following changes to the protocol: After the last washing step, plates were centrifuged at 6,000 rpm for twenty minutes. Subsequently, the RNA binding plate was positioned on top of an elution plate, and RNA was eluted by two rounds of adding 30 µl of elution buffer and incubating for two minutes at room temperature, followed by one minute of centrifugation at 1,000 rpm. A final elution step was performed by centrifuging at 1700 g (4000 rpm) for 3 minutes RNA was stored at -80°C.

Ten µl of RNA-solution was used for gene expression analysis by reverse transcription quantitative polymerase chain reaction (RT-qPCR) performed with amplicon

sets/sequences for *LPA*, *ACTB* (Eurogentec Deutschland GmbH, Cologne, Germany), *APOB* and *PLG* (BioTez GmbH, Berlin, Germany).

The RT-qPCR reactions were carried out with an ABI StepOne Plus (Applied Biosystems, part of Thermo Fisher Scientific, Massachusetts, USA) using standard protocols for RT-PCR (48 °C 30 min, 95 °C 10 min, 40 cycles at 95 °C 15 s followed by 60 °C 1 min).

In primary hepatocytes, *LPA* and *PLG* analyses were performed in singleplex assays (primers: 300 nM, probe: 100 nM). *APOB* (200 nM) and *ACTB* (300 nM) were run in a multiplex assay adding 100 nM of each probe to the standard mixture.

The data were calculated by using the comparative CT method also known as the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001 and Schmittgen and Livak, 2008). Here the amount of *APOB*, *LPA* or *PLG* mRNA normalised to the endogenous reference *ACTB* relative to a calibrator (untreated control) is given by the formula

$$\text{Fold-change} = 2^{-\Delta\Delta Ct}.$$

Unless stated otherwise, all values presented in the example refer to mean ± SD. IC_{50} values were calculated using a sigmoidal 4 parameter dose response curve in GraphPad Prism 7.

Figure 19 shows the knockdown of *LPA* mRNA by Conjugate 21 through receptor-mediated uptake into primary human hepatocytes 24 hours post siRNA treatment (IC_{50} = 3.6nM). *LPA* mRNA expression levels were normalised to *ACTB* and relative to cells treated with a non-targeting siRNA control measured by RT-qPCR. Data is presented as the mean ± SD of a single experiment. Figure 20 shows the knockdown of *LPA* mRNA by Conjugate 21 through receptor-mediated uptake into primary cynomolgus hepatocytes 24 hours post siRNA treatment (IC_{50} = 0.7nM). *LPA* mRNA expression levels were normalised to *ACTB* and relative to cells treated with a non-targeting siRNA control measured by RT-qPCR. Data is presented as the mean ± SD of a single experiment.

Figure 21 shows Knockdown of *APOB* mRNA by Conjugate 21 through receptor-mediated uptake into primary human hepatocytes 24 hours post siRNA treatment. *APOB* mRNA expression levels were normalised to *ACTB* and relative to cells treated with a non-targeting siRNA control measured by RT-qPCR. Data is presented as the mean ± SD of a single experiment.

Figure 22 shows Knockdown of *PLG* mRNA by Conjugate 21 through receptor-mediated uptake into primary human hepatocytes 24 hours post siRNA treatment. *PLG* mRNA expression levels were normalised to *ACTB* and relative to cells treated with a non-targeting siRNA control measured by RT-qPCR. Data is presented as the mean ± SD of a single experiment.

Conjugate 21 achieves high levels of *LPA* mRNA inhibition without affecting the levels of *APOB* and *PLG* mRNAs.

Example 14

To test the efficacy of conjugate 21 *in vivo*, male cynomolgus monkeys were used to perform a pharmacodynamic study. Animals were grouped into 4 groups, 3 animals per group. Before dosing, serum was prepared to establish the baseline Lp(a) level for each animal. On day 1, conjugate 21 was formulated in 0.9% saline and each animal received a single dose of conjugate 21 at doses of 0.1, 0.3, 1.0 and 3.0 mg/kg.

Serial samples were taken over 29 days and Lp(a) levels were measured by ELISA (Mercodia, Catalogue No. 10-1106-01Lot: 27736; Uppsala, Sweden). All values were normalised to the baseline values for each individual animal taken before dosing and presented as a percentage of the starting level (Figure 23). Doses of 1.0 and 3.0 mg/kg showed marked reduction of the serum Lp(a) levels (69.4 and 77.3% after 29 days respectively). The dose dependent effect results in an ED_{50} dose of 0.56 mg/kg (Figure 24). These data indicate that a significant and sustained reduction in serum Lp(a) is achievable through a single dose of conjugate 21. Based on this data, dosing would be expected to be infrequent, not more often than once every two months.

Statements of Invention

The following are statements of the invention:

1. A nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from the *LPA* gene, wherein said first strand comprises a nucleotide sequence

selected from the following sequences: SEQ ID NO: 9, 5, 1, 3, 7, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43.

2. The nucleic acid of statement 1, wherein said first strand comprises a nucleotide sequence of SEQ ID NO: 9, and optionally wherein said second strand comprises a nucleotide sequence of SEQ ID NO: 10; or wherein said first strand comprises a nucleotide sequence of SEQ ID NO: 5, and optionally wherein said second strand comprises a nucleotide sequence of SEQ ID NO: 6.

3. A nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from the *LPA* gene, wherein said first strand comprises a nucleotide sequence selected from the following sequences: SEQ ID NO: 9 or 5.

4. The nucleic acid of any of the preceding statements, wherein said first strand and/or said second strand are each from 17-35 nucleotides in length.

5. The nucleic acid of any of the preceding statements, wherein the at least one duplex region consists of 17-25, preferably 19-25, consecutive nucleotide base pairs.

6. The nucleic acid of any of the preceding statements, wherein the nucleic acid:

   a) is blunt ended at both ends; or
   b) has an overhang at one end and a blunt end at the other; or
   c) has an overhang at both ends.

7. The nucleic acid of any of the preceding statements, wherein one or more nucleotides on the first and/or second strand are modified, to form modified nucleotides.

8. The nucleic acid of any of the preceding statements, wherein the nucleic acid comprises a phosphorothioate linkage between the terminal one, two or three 3' nucleotides and/or 5' nucleotides of one or both ends of the first and/or the second strand.

9. The nucleic acid of any of the preceding statements, wherein the nucleic acid is conjugated to a ligand.

10. The nucleic acid of statement 9, wherein the ligand comprises (i) one or more N-acetyl galactosamine (GalNAc) moieties or derivatives thereof, and (ii) a linker, wherein the linker conjugates the at least one GalNAc moiety or derivative thereof to the nucleic acid.

11. The nucleic acid of any of statements 9-10, wherein the nucleic acid is conjugated to a ligand comprising a compound of formula (I):

$$[S\text{-}X^1\text{-}P\text{-}X^2]_3\text{-}A\text{-}X^3\text{-} \qquad (I)$$

wherein:

S represents a saccharide, preferably wherein the saccharide is N-acetyl galactosamine;

X^1 represents C_3-C_6 alkylene or $(\text{-}CH_2\text{-}CH_2\text{-}O)_m(\text{-}CH_2)_2\text{-}$ wherein m is 1, 2, or 3;

P is a phosphate or modified phosphate, preferably a thiophosphate;

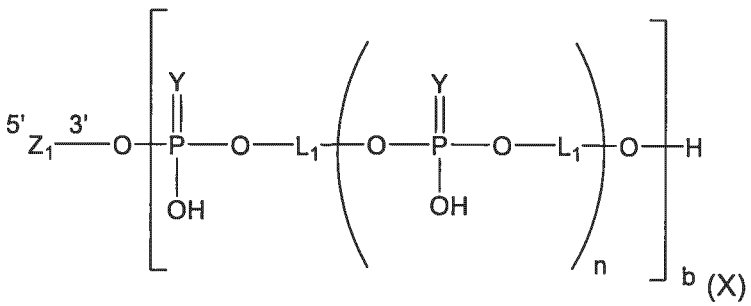
X^2 is alkylene or an alkylene ether of the formula $(\text{-}CH_2)_n\text{-}O\text{-}CH_2\text{-}$ where n = 1-6;

A is a branching unit;

X^3 represents a bridging unit;

wherein a nucleic acid as defined in any of statements 1 to 8 is conjugated to X^3 via a phosphate or modified phosphate, preferably a thiophosphate.

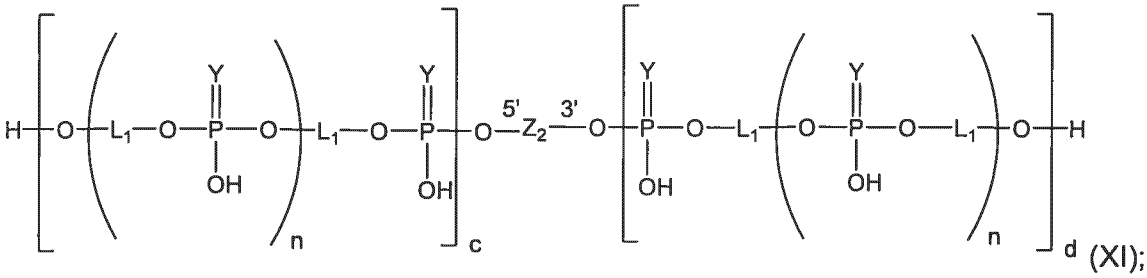
12. The nucleic acid of any of statements 9-10, wherein the first RNA strand is a compound of formula (X):



(X)

wherein b is 0 or 1; and

the second RNA strand is a compound of formula (XI):



(XI);

wherein:

c and d are independently 0 or 1;

Z_1 and Z_2 are the RNA portions of the first and second RNA strands respectively;

Y is O or S;

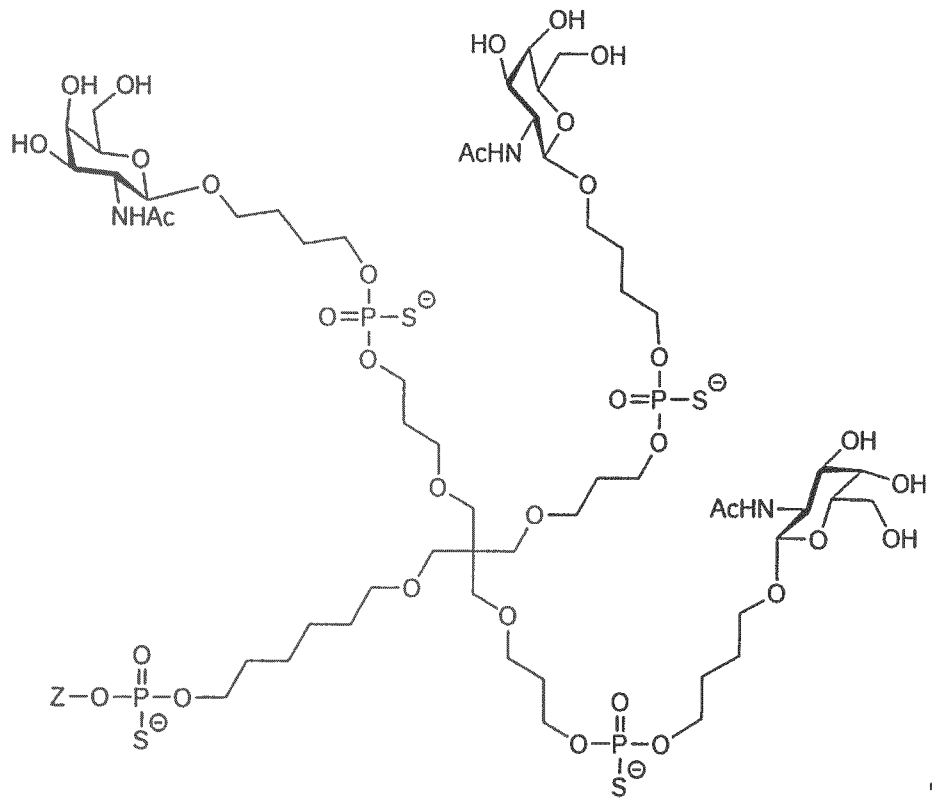
n is 0, 1, 2 or 3; and

L_1 is a linker to which a ligand is attached; and

wherein b + c + d is 2 or 3.

13. A nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from the *LPA* gene, wherein said first strand comprises, and preferably consists of, the nucleotide sequence of SEQ ID NO: 9 and optionally, wherein said second strand comprises, and preferably consists of, the nucleotide sequence of SEQ ID NO. 10.

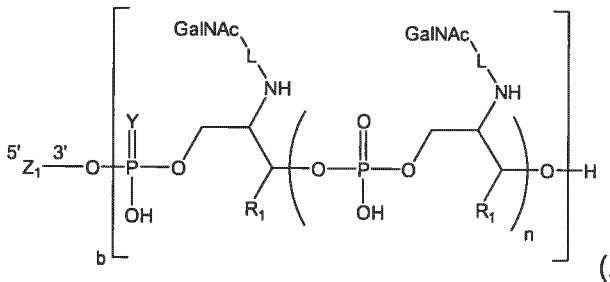
14. The nucleic acid of statement 13, wherein the nucleic acid is conjugated to a ligand and has the following structure



wherein Z is a nucleic acid according ot statement 13 and is preferably conjugated to the 5' end of the second strand.

15. The nucleic acid of statement 14, wherein the nucleic acid comprises two phosphorothioate linkages between each of the three terminal 3' and between each of the three terminal 5' nucleotides on the first strand, and two phosphorothioate linkages between the three terminal nucleotides of the 3' end of the second strand and wherein the ligand is conjugated to the 5' end of the second strand.

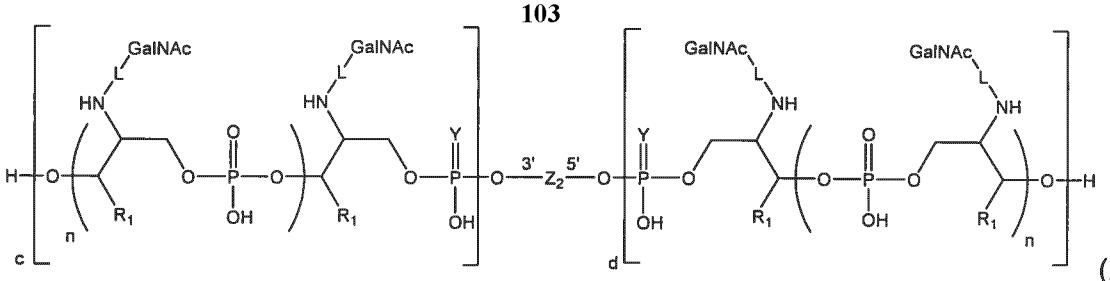
16. The nucleic acid of statement 13, wherein the nucleic acid is conjugated to a ligand, wherein the first RNA strand is a compound of formula (XV):



(XV)

wherein b is 0 or 1; and

the second RNA strand is a compound of formula (XVI):



(XVI);

wherein c and d are independently 0 or 1;

wherein:

Z_1 and Z_2 are the RNA portions of the first and second RNA strands respectively;

Y is O or S;

R_1 is H or methyl;

n is 0, 1, 2 or 3; and

L is the same or different in formulae (XV) and (XVI) and is selected from the group consisting of:

$-(CH_2)_q$, wherein q = 2-12;

$-(CH_2)_r-C(O)-$, wherein r = 2-12;

$-(CH_2-CH_2-O)_s-CH_2-C(O)-$, wherein s = 1-5;

$-(CH_2)_t-CO-NH-(CH_2)_t-NH-C(O)-$, wherein t is independently is 1-5;

$-(CH_2)_u-CO-NH-(CH_2)_u-C(O)-$, wherein u is independently is 1-5; and

$-(CH_2)_v-NH-C(O)-$, wherein v is 2-12; and

wherein the terminal C(O), if present, is attached to the NH group;

and wherein b + c + d is 2 or 3.

17. The nucleic acid of any of statements 13-16, comprising a sequence and modifications as shown below:

SEQ ID NO:	sequence	modifications
9	5' AUAACUCUGUCCAUUACCG 3	6162717181736152738
10	5' CGGUAAUGGACAGAGUUAU 3'	3845261846364645161

wherein, the specific modifications are depicted by numbers

1=2´F-dU,

2=2'F-dA,

3=2´F-dC,

4=2´F-dG,

5=2'-OMe-rU;

6=2'-OMe-rA;

7=2'-OMe-rC;

8=2'-OMe-rG.

18. The nucleic acid of any of statements 13-16, wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to position 11, or 13, or 11 and 13, or 11-13 of the first strand are modified with a 2' fluoro modification.

19. A composition comprising a nucleic acid of any of statements 1-18 and optionally a delivery vehicle and/or a physiologically acceptable excipient and/or a carrier and/or a diluent and/or a buffer and/or a preservative, for use as a medicament, preferably for the prevention or treatment or risk reduction of a disease or pathology, wherein the disease or pathology preferably is a cardiovascular disease, wherein the cardiovascular disease preferably is a stroke, atherosclerosis, thrombosis, a coronary heart disease or aortic stenosis and/or any other disease or pathology associated to elevated levels of Lp(a)-containing particles.

20. A pharmaceutical composition comprising a nucleic acid of any of statements 1-18 and further comprising a delivery vehicle, preferably liposomes and/or a physiologically acceptable excipient and/or a carrier and/or a diluent.

21. Use of a nucleic acid of any of statements 1-18 or a pharmaceutical composition of statement 20 for the prevention or treatment or risk reduction of a disease or pathology, wherein the disease or pathology preferably is a cardiovascular disease, wherein the cardiovascular disease preferably is a stroke, atherosclerosis, thrombosis, a coronary heart disease or aortic stenosis and any other disease or pathology associated to elevated levels of Lp(a)-containing particles.

22. A method of preventing or treating a disease, disorder or syndrome comprising administering a composition comprising a nucleic acid of any of statements 1-18 or a composition according to statements 19-20 to an individual in need of treatment, preferably wherein the nucleic acid or composition is administered to the subject subcutaneously, intravenously or using any other application routes such as oral, rectal or intraperitoneal.

Summary sequence table

SEQ ID NO	Name	Sequence (5'-3')	Unmodified Sequence counterpart (5'-3')
1	LPA-1014 first strand	UCGUAUAACAAUAAGGGGC	UCGUAUAACAAUAAGGGGC
2	LPA-1014 second strand	GCCCCUUAUUGUUAUACGA	GCCCCUUAUUGUUAUACGA
3	LPA-1024 first strand	GAUAACUCUGUCCAUUACC	GAUAACUCUGUCCAUUACC
4	LPA-1024 second strand	GGUAAUGGACAGAGUUAUC	GGUAAUGGACAGAGUUAUC
5	LPA-1038 first strand	AUAACUCUGUCCAUUACCA	AUAACUCUGUCCAUUACCA
6	LPA-1038 second strand	UGGUAAUGGACAGAGUUAU	UGGUAAUGGACAGAGUUAU
7	LPA-1040 first strand	UAACUCUGUCCAUUACCGU	UAACUCUGUCCAUUACCGU
8	LPA-1040 second strand	ACGGUAAUGGACAGAGUUA	ACGGUAAUGGACAGAGUUA
9	LPA-1041 first strand	AUAACUCUGUCCAUUACCG	AUAACUCUGUCCAUUACCG
10	LPA-1041 second strand	CGGUAAUGGACAGAGUUAU	CGGUAAUGGACAGAGUUAU
11	LPA-1055 first strand	AGAAUGUGCCUCGAUAACU	AGAAUGUGCCUCGAUAACU
12	LPA-1055 second strand	AGUUAUCGAGGCACAUUCU	AGUUAUCGAGGCACAUUCU
13	LPA-1057 first strand	AUAACUCUGUCCAUCACCA	AUAACUCUGUCCAUCACCA
14	LPA-1057 second strand	UGGUGAUGGACAGAGUUAU	UGGUGAUGGACAGAGUUAU
15	LPA-1058 first strand	AUAACUCUGUCCAUCACCU	AUAACUCUGUCCAUCACCU
16	LPA-1058 second strand	AGGUGAUGGACAGAGUUAU	AGGUGAUGGACAGAGUUAU
17	LPA-1061 first strand	UAACUCUGUCCAUUACCAU	UAACUCUGUCCAUUACCAU
18	LPA-1061 second strand	AUGGUAAUGGACAGAGUUA	AUGGUAAUGGACAGAGUUA
19	LPA-1086 first strand	AUGUGCCUUGAUAACUCUG	AUGUGCCUUGAUAACUCUG
20	LPA-1086 second strand	CAGAGUUAUCAAGGCACAU	CAGAGUUAUCAAGGCACAU
21	LPA-1099 first strand	AGUUGGUGCUGCUUCAGAA	AGUUGGUGCUGCUUCAGAA
22	LPA-1099 second strand	UUCUGAAGCAGCACCAACU	UUCUGAAGCAGCACCAACU
23	LPA-1102 first strand	AAUAAGGGGCUGCCACAGG	AAUAAGGGGCUGCCACAGG
24	LPA-1102 second strand	CCUGUGGCAGCCCCUUAUU	CCUGUGGCAGCCCCUUAUU
25	LPA-1116 first strand	UAACUCUGUCCAUCACCAU	UAACUCUGUCCAUCACCAU
26	LPA-1116 second strand	AUGGUGAUGGACAGAGUUA	AUGGUGAUGGACAGAGUUA
27	LPA-1127 first strand	AUGAGCCUCGAUAACUCUG	AUGAGCCUCGAUAACUCUG
28	LPA-1127 second strand	CAGAGUUAUCGAGGCUCAU	CAGAGUUAUCGAGGCUCAU
29	LPA-1128 first strand	AAUGAGCCUCGAUAACUCU	AAUGAGCCUCGAUAACUCU

30	LPA-1128 second strand	AGAGUUAUCGAGGCUCAUU	AGAGUUAUCGAGGCUCAUU
31	LPA-1141 first strand	AAUGCUUCCAGGACAUUUC	AAUGCUUCCAGGACAUUUC
32	LPA-1141 second strand	GAAAUGUCCUGGAAGCAUU	GAAAUGUCCUGGAAGCAUU
33	LPA-1151 first strand	ACAGUGGUGGAGAAUGUGC	ACAGUGGUGGAGAAUGUGC
34	LPA-1151 second strand	GCACAUUCUCCACCACUGU	GCACAUUCUCCACCACUGU
35	LPA-1171 first strand	GUAUGUGCCUCGAUAACUC	GUAUGUGCCUCGAUAACUC
36	LPA-1171 second strand	GAGUUAUCGAGGCACAUAC	GAGUUAUCGAGGCACAUAC
37	LPA-1177 first strand	UCGAUAACUCUGUCCAUCA	UCGAUAACUCUGUCCAUCA
38	LPA-1177 second strand	UGAUGGACAGAGUUAUCGA	UGAUGGACAGAGUUAUCGA
39	LPA-1189 first strand	UGUCACUGGACAUUGUGUC	UGUCACUGGACAUUGUGUC
40	LPA-1189 second strand	GACACAAUGUCCAGUGACA	GACACAAUGUCCAGUGACA
41	LPA-1244 first strand	CUGGGAUCCAUGGUGUAAC	CUGGGAUCCAUGGUGUAAC
42	LPA-1244 second strand	GUUACACCAUGGAUCCCAG	GUUACACCAUGGAUCCCAG
43	LPA-1248 first strand	AGAUGACCAAGCUUGGCAG	AGAUGACCAAGCUUGGCAG
44	LPA-1248 second strand	CUGCCAAGCUUGGUCAUCU	CUGCCAAGCUUGGUCAUCU
45	LPA: (upper) human	AAGTGTCCTTGCGACGTCC	AAGTGTCCTTGCGACGTCC
46	LPA: (lower) human	CCTGGACTGTGGGGCTTT	CCTGGACTGTGGGGCTTT
47	LPA: (probe) human	CTGTTTCTGAACAAGCACCAACGGAGC	CTGTTTCTGAACAAGCACCAACGGAGC
48	LPA (upper) cynomolgus	GTGTCCTCGCAACGTCCA	GTGTCCTCGCAACGTCCA
49	LPA (lower) cynomolgus	GACCCCGGGGCTTTG	GACCCCGGGGCTTTG
50	LPA (probe) cynomolgus	TGGCTGTTTCTGAACAAGCACCAATGG	TGGCTGTTTCTGAACAAGCACCAATGG
51	APOB (upper) human	TCATTCCTTCCCCAAAGAGACC	TCATTCCTTCCCCAAAGAGACC
52	APOB (lower) human	CACCTCCGTTTTGGTGGTAGAG	CACCTCCGTTTTGGTGGTAGAG
53	APOB (probe) human	CAAGCTGCTCAGTGGAGGCAACACATTA	CAAGCTGCTCAGTGGAGGCAACACATTA
54	beta-Actin (upper) human	GCATGGGTCAGAAGGATTCCTAT	GCATGGGTCAGAAGGATTCCTAT
55	beta-Actin (lower) human	TGTAGAAGGTGTGGTGCCAGATT	TGTAGAAGGTGTGGTGCCAGATT
56	beta-Actin (probe) human	TCGAGCACGGCATCGTCACCAA	TCGAGCACGGCATCGTCACCAA
57	beta-Actin (upper) cynomolgus	AAGGCCAACCGCGAGAAG	AAGGCCAACCGCGAGAAG
58	beta-Actin (lower)cynomolgus	AGAGGCGTACAGGGACAGCA	AGAGGCGTACAGGGACAGCA
59	beta-Actin (probe)cynomolgus	TGAGACCTTCAACACCCCAGCCATGTAC	TGAGACCTTCAACACCCCAGCCATGTAC

60	PPIB (upper) human	AGATGTAGGCCGGGTGATCTTT	AGATGTAGGCCGGGTGATCTTT
61	PPIB (lower) human	GTAGCCAAATCCTTTCTCTCCTGT	GTAGCCAAATCCTTTCTCTCCTGT
62	PPIB (probe) human	TGTTCCAAAAACAGTGGATAATTTTGTGGCC	TGTTCCAAAAACAGTGGATAATTTTGTGGCC
63	LPA: (upper) human	AAGTGTCCTTGCGACGTCC	AAGTGTCCTTGCGACGTCC
64	LPA: (lower) human	CCTGGACTGTGGGGCTTT	CCTGGACTGTGGGGCTTT
65	LPA: (probe) human	CTGTTTCTGAACAAGCACCAACGGAGC	CTGTTTCTGAACAAGCACCAACGGAGC
66	LPA (upper) cynomolgus	GTGTCCTCGCAACGTCCA	GTGTCCTCGCAACGTCCA
67	LPA (lower) cynomolgus	GACCCCGGGGCTTTG	GACCCCGGGGCTTTG
68	LPA (probe) cynomolgus	TGGCTGTTTCTGAACAAGCACCAATGG	TGGCTGTTTCTGAACAAGCACCAATGG
69	APOB (upper) human	TCATTCCTTCCCCAAAGAGACC	TCATTCCTTCCCCAAAGAGACC
70	APOB (lower) human	CACCTCCGTTTTGGTGGTAGAG	CACCTCCGTTTTGGTGGTAGAG
71	APOB (probe) human	CAAGCTGCTCAGTGGAGGCAACACATTA	CAAGCTGCTCAGTGGAGGCAACACATTA
72	beta-Actin (upper) human	GCATGGGTCAGAAGGATTCCTAT	GCATGGGTCAGAAGGATTCCTAT
73	beta-Actin (lower) human	TGTAGAAGGTGTGGTGCCAGATT	TGTAGAAGGTGTGGTGCCAGATT
74	beta-Actin (probe) human	TCGAGCACGGCATCGTCACCAA	TCGAGCACGGCATCGTCACCAA
75	Modified SEQ ID NO: 1	5381616272616284847	UCGUAUAACAAUAAGGGGC
76	Modified SEQ ID NO: 2	4737351615451616382	GCCCCUUAUUGUUAUACGA
77	Modified SEQ ID NO: 3	8252635354537251637	GAUAACUCUGUCCAUUACC
78	Modified SEQ ID NO: 4	4816254827282815253	GGUAAUGGACAGAGUUAUC
79	Modified SEQ ID NO: 5	6162717181736152736	AUAACUCUGUCCAUUACCA
80	Modified SEQ ID NO: 6	1845261846364645161	UGGUAAUGGACAGAGUUAU
81	Modified SEQ ID NO: 7	5263535453725163745	UAACUCUGUCCAUUACCGU
82	Modified SEQ ID NO: 8	2748162548272828152	ACGGUAAUGGACAGAGUUA
83	Modified SEQ ID NO: 9	6162717181736152738	AUAACUCUGUCCAUUACCG
84	Modified SEQ ID NO: 10	3845261846364645161	CGGUAAUGGACAGAGUUAU
85	Modified SEQ ID NO: 11	6462545473538252635	AGAAUGUGCCUCGAUAACU
86	Modified SEQ ID NO: 12	2815253828472725171	AGUUAUCGAGGCACAUUCU
87	Modified SEQ ID NO: 13	6162717181736172736	AUAACUCUGUCCAUCACCA
88	Modified SEQ ID NO: 14	1845461846364645161	UGGUGAUGGACAGAGUUAU
89	Modified SEQ ID NO: 15	6162717181736172735	AUAACUCUGUCCAUCACCU
90	Modified SEQ ID NO: 16	2845461846364645161	AGGUGAUGGACAGAGUUAU
91	Modified SEQ ID NO: 17	5263535453725163725	UAACUCUGUCCAUUACCAU
92	Modified SEQ ID NO: 18	2548162548272828152	AUGGUAAUGGACAGAGUUA

93	Modified SEQ ID NO: 19	6181837154616271718	AUGUGCCUUGAUAACUCUG
94	Modified SEQ ID NO: 20	3646451617264836361	CAGAGUUAUCAAGGCACAU
95	Modified SEQ ID NO: 21	6451845471835172826	AGUUGGUGCUGCUUCAGAA
96	Modified SEQ ID NO: 22	1535462836472736271	UUCUGAAGCAGCACCAACU
97	Modified SEQ ID NO: 23	6252648483547363648	AAUAAGGGGCUGCCACAGG
98	Modified SEQ ID NO: 24	3718184728373715251	CCUGUGGCAGCCCCUUAUU
99	Modified SEQ ID NO: 25	5263535453725363725	UAACUCUGUCCAUCACCAU
100	Modified SEQ ID NO: 26	2548182548272828152	AUGGUGAUGGACAGAGUUA
101	Modified SEQ ID NO: 27	6182837174616271718	AUGAGCCUCGAUAACUCUG
102	Modified SEQ ID NO: 28	3646451617464835361	CAGAGUUAUCGAGGCUCAU
103	Modified SEQ ID NO: 29	6254647353825263535	AAUGAGCCUCGAUAACUCU
104	Modified SEQ ID NO: 30	2828152538284717251	AGAGUUAUCGAGGCUCAUU
105	Modified SEQ ID NO: 31	6254715372846361517	AAUGCUUCCAGGACAUUUC
106	Modified SEQ ID NO: 32	4626181735482647251	GAAAUGUCCUGGAAGCAUU
107	Modified SEQ ID NO: 33	6364548184646254547	ACAGUGGUGGAGAAUGUGC
108	Modified SEQ ID NO: 34	4727251717363727181	GCACAUUCUCCACCACUGU
109	Modified SEQ ID NO: 35	8161818371746162717	GUAUGUGCCUCGAUAACUC
110	Modified SEQ ID NO: 36	4645161746483636163	GAGUUAUCGAGGCACAUAC
111	Modified SEQ ID NO: 37	5382526353545372536	UCGAUAACUCUGUCCAUCA
112	Modified SEQ ID NO: 38	1825482728281525382	UGAUGGACAGAGUUAUCGA
113	Modified SEQ ID NO: 39	5453635482725181817	UGUCACUGGACAUUGUGUC
114	Modified SEQ ID NO: 40	4636362545372818272	GACACAAUGUCCAGUGACA
115	Modified SEQ ID NO: 41	7184825372548181627	CUGGGAUCCAUGGUGUAAC
116	Modified SEQ ID NO: 42	4516363725482537364	GUUACACCAUGGAUCCCAG
117	Modified SEQ ID NO: 43	6461827362835184728	AGAUGACCAAGCUUGGCAG
118	Modified SEQ ID NO: 44	3547362835184536171	CUGCCAAGCUUGGUCAUCU
119	GalNAc-LPA-1038-L1 first strand	OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeA	AUAACUCUGUCCAUUACCA
120	GalNAc-LPA-1038-L1 second strand	[ST23 (ps)]3 long trebler (ps)FU-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU	UGGUAAUGGACAGAGUUAU

121	GalNAc-LPA-1038-L6 first strand	OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeA	AUAACUCUGUCCAUUACCA
122	GalNAc-LPA-1038-L6 second strand	[ST23 (ps)]3 ST43 (ps)FU-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU	UGGUAAUGGACAGAGUUAU
123	GalNAc-LPA-1041-L1 first strand	OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeG	AUAACUCUGUCCAUUACCG
124	GalNAc-LPA-1041-L1 second strand	[ST23 (ps)]3 long trebler (ps) FC-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU	CGGUAAUGGACAGAGUUAU
125	GalNAc-LPA-1041-L6 first strand	OMeA-(ps)-FU-(ps)-OMeA-FA-OMeC-FU-OMeC-FU-OMeG-FU-OMeC-FC-OMeA-FU-OMeU-FA-OMeC-(ps)-FC-(ps)-OMeG	AUAACUCUGUCCAUUACCG
126	GalNAc-LPA-1041-L6 second strand	[ST23 (ps)]3 ST43 (ps) FC-OMeG-FG-OMeU-FA-OMeA-FU-OMeG-FG-OMeA-FC-OMeA-FG-OMeA-FG-OMeU-FU-(ps)-OMeA-(ps)-FU	CGGUAAUGGACAGAGUUAU
127	STS16001AL33	mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(GN)	UUAUAGAGCAAGAACACUGUU
128	STS16001BL20	Ser(GN) (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA	AACAGUGUUCUUGCUCUAUAA
129	STS16001A	mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU	UUAUAGAGCAAGAACACUGUU
130	STS16001BV1L42	Ser(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) Ser(GN)	AACAGUGUUCUUGCUCUAUAA
131	STS16001V1B	fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA	AACAGUGUUCUUGCUCUAUAA
132	STS18001A	mU (ps) fC (ps) mG fA mA fG mU fA mU fU mC fC mG fC mG fU mA (ps) fC (ps) mG	UCGAAGUAUUCCGCGUACG
133	STS18001BL4	[(ST23) (ps)]$_3$ C4XLT (ps) fC mG fU mA fC mG fC mG fG mA fA mU fA mC fU mU fC (ps) mG (ps) fA	CGUACGCGGAAUACUUCGA

134	STS16001BL4	[(ST23) (ps)]3 C4XLT(ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA	AACAGUGUUCUUGCUCUAUAA
135	X0373A	mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG	AUAACUCUGUCCAUUACCG
136	X0373B	Ser(GN) (ps) fC (ps) mG (ps) fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU (ps) Ser(GN)	CGGUAAUGGACAGAGUUAU
137	STS2041B	ST23 (ps) ST23 (ps) ST23 (ps) C6XLT (ps) fC mG fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU	CGGUAAUGGACAGAGUUAU
138	X0125A	mC (ps) fU (ps) mU fA mC fU mC fU mC fG mC fC mC fA mA fG mC (ps) fG (ps) mA	CUUACUCUCGCCCAAGCGA
139	X0125B	[(ST23) (ps)]$_3$ (C6XLT) (ps) fU mC fG mC fU mU fG mG fG mC fG mA fG mA fG mU fA (ps) mA (ps) fG	UCGCUUGGGCGAGAGUAAG
140	Probe based on SEQ ID NO: 50	BHQ1-TGGCTGTTTCTGAACAAGCACCAATGG-FAM	TGGCTGTTTCTGAACAAGCACCAATGG
141	Probe based on SEQ ID NO: 56	BHQ1-TCGAGCACGGCATCGTCACCAA-VIC	TCGAGCACGGCATCGTCACCAA
142	STS16001BV1L75	Ser(GN) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA Ser(GN)	AACAGUGUUCUUGCUCUAUAA
143	STS16001BV16L42	Ser(GN) (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU mA fA (ps) Ser(GN)	AACAGUGUUCUUGCUCUAUAA
144	STS16001BV20L75	Ser(GN) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU mA fA Ser(GN)	AACAGUGUUCUUGCUCUAUAA
145	STS16001BV1L94	Ser(GN) (ps) Ser(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) Ser(GN) (ps) Ser(GN)	AACAGUGUUCUUGCUCUAUAA
146	STS16001V1BL96	C6Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) C7Am(GN)	AACAGUGUUCUUGCUCUAUAA

147	STS16001V1BL97	GlyC3Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) GlyC3Am(GN)	AACAGUGUUCUUGCUCUAUAA
148	Conjugate 10 second strand	PipAm(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) PipAm(GN)	AACAGUGUUCUUGCUCUAUAA
149	STS16001V1BL88	C3Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) C3Am(GN)	AACAGUGUUCUUGCUCUAUAA
150	STS16001V1BL87	C6Am(GN) (ps) fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA (ps) GlyC3Am(GN)	AACAGUGUUCUUGCUCUAUAA
151	Conjugate 15 antisense strand	mU (ps) fC (ps) mU fU mC fU mU fA mA fA mC fU mG fA mG fU mU (ps) fU (ps) mC	UCUUCUUAAACUGAGUUUC
152	Conjugate 15 sense strand	Ser(GN) (ps) fG (ps) mA (ps) fA mA fC mU fC mA fG mU fU mU fA mA fG mA fA (ps) mG (ps) fA (ps) Ser(GN)	GAAACUCAGUUUAAGAAGA
153	Conjugate 16 antisense strand	mA (ps) fU (ps) mG fU mA fG mC fC mG fA mG fG mA fU mC fU mU (ps) fC (ps) mU	AUGUAGCCGAGGAUCUUCU
154	Conjugate 16 antisense strand	Ser(GN) (ps) fA (ps) mG (ps) fA mA fG mA fU mC fC mU fC mG fG mC fU mA fC (ps) mA (ps) fU (ps) Ser(GN)	AGAAGAUCCUCGGCUACAU
155	Conjugate 18 antisense strand	mA (ps) fA (ps) mC fC mA fG mA fA mG fA mA fG mC fA mG fG mU (ps) fG (ps) mA	AACCAGAAGAAGCAGGUGA
156	Conjugate 18 sense strand	Ser(GN) (ps) fU (ps) mC (ps) fA mC fC mU fG mC fU mU fC mU fU mC fU mG fG (ps) mU (ps) fU (ps) Ser(GN)	UCACCUGCUUCUUCUGGUU
157	STS16001BV1	fA (ps) mA (ps) fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA	AACAGUGUUCUUGCUCUAUAA
158	Reference Conjugate 6 sense strand	[ST23 (ps)]3 ltrb (ps) fG mA fA mA fC mU fC mA fG mU fU mU fA mA fG mA fA (ps) mG (ps) fA	GAAACUCAGUUUAAGAAGA
159	Reference Conjugate 7 sense strand	[ST23 (ps)]3 ltrb (ps) fA mG fA mA fG mA fU mC fC mU fC mG fG mC fU mA fC (ps) mA (ps) fU	AGAAGAUCCUCGGCUACAU

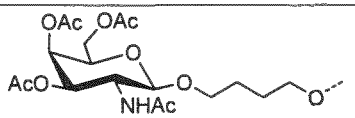
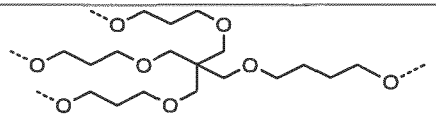
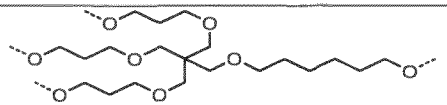
160	Reference Conjugate 8 antisense strand	mU (ps) fA (ps) mC fC mA fG mA fA mG fA mA fG mC fA mG fG mU (ps) fG (ps) mA	UACCAGAAGAAGCAGGUGA
161	Reference Conjugate 8 sense strand	[ST23 (ps)]3 ST41 (ps)fU mC fA mC fC mU fG mC fU mU fC mU fU mC fU mG fG (ps) mU (ps) fA	UCACCUGCUUCUUCUGGUA
162	Reference Conjugate 9 sense strand	[ST23 (ps)]3 C6XLT (ps) fC mG fG mU fA mA fU mG fG mA fC mA fG mA fG mU fU (ps) mA (ps) fU	CGGUAAUGGACAGAGUUAU
163	Conjugate 21 sense strand without ligand	mC mG mG mU mA mA fU fG fG mA mC mA mG mA mG mU mU (ps) mA (ps) mU	CGGUAAUGGACAGAGUUAU
164	Conjugate 21 sense strand	[ST23 (ps)]3 C6XLT (ps) mC mG mG mU mA mA fU fG fG mA mC mA mG mA mG mU mU (ps) mA (ps) mU	CGGUAAUGGACAGAGUUAU
165	Conjugate 21 antisense strand	mA (ps) fU (ps) mA fA mC fU mC fU mG fU mC fC mA fU mU fA mC (ps) fC (ps) mG	AUAACUCUGUCCAUUACCG

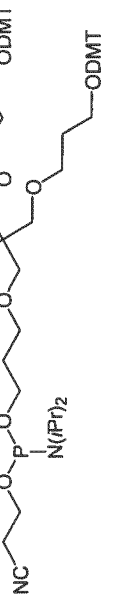
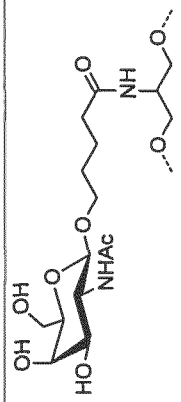
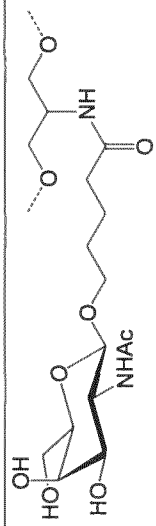
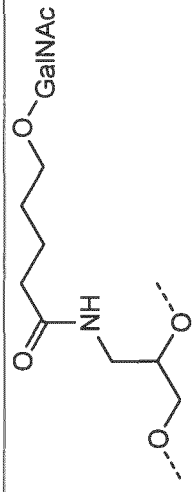
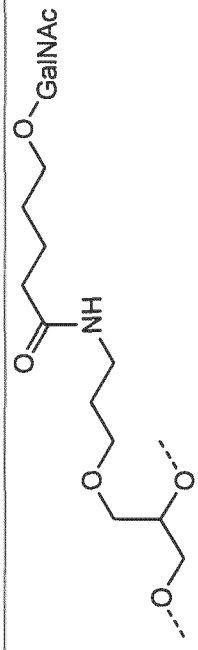
A single sequence may have more than one name. In those cases, one of those names is given in the summary sequence table.

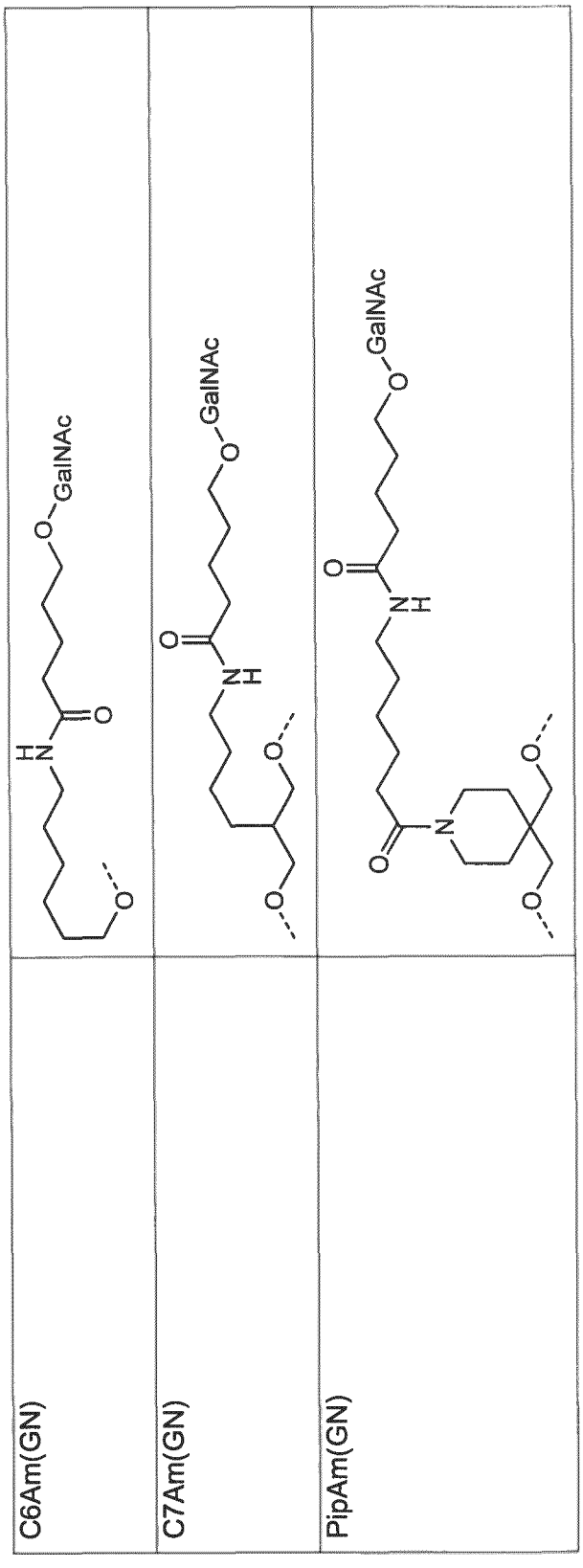
Where specific linkers and or modified linkages are taught within an RNA sequence, such as (ps) and [ST23 (ps)]3 ST41 (ps) etc, these are optional parts of the sequence, but are a preferred embodiment of that sequence.

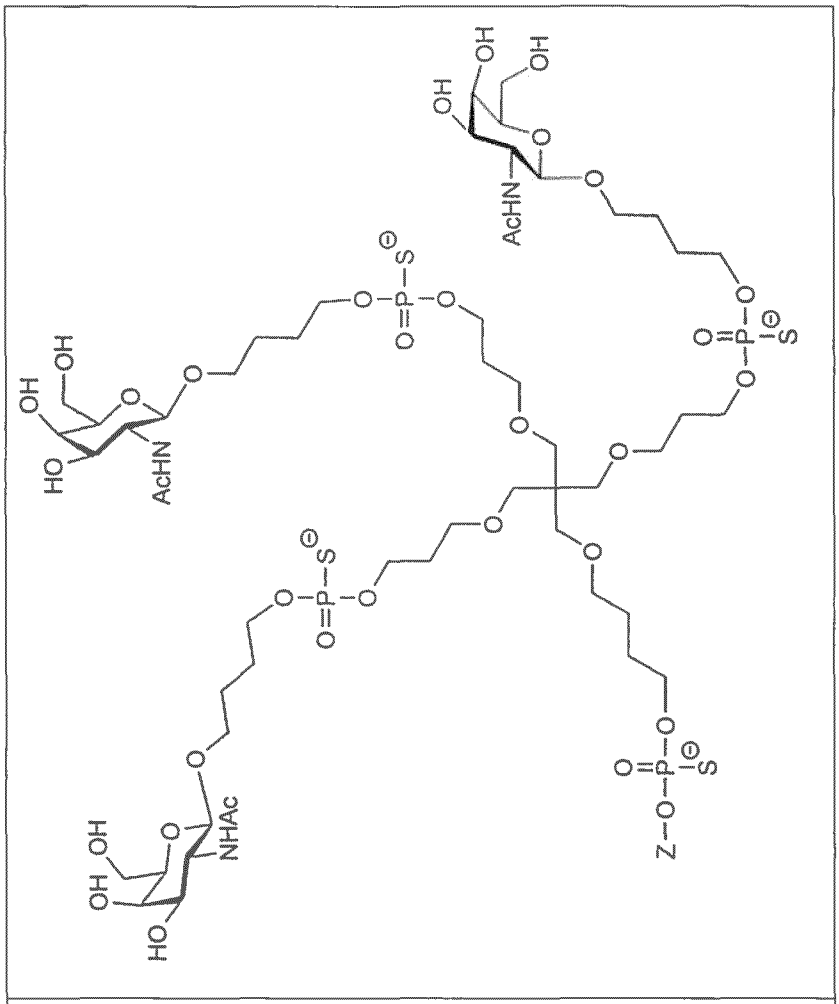
The following abbreviations may be used, particularly in listed sequences:

Abbreviation	**Meaning**
1	2'F-dU
2	2'F-dA
3	2'F-dC
4	2'F-dG
5	2'OMe-rU
6	2'OMe-rA

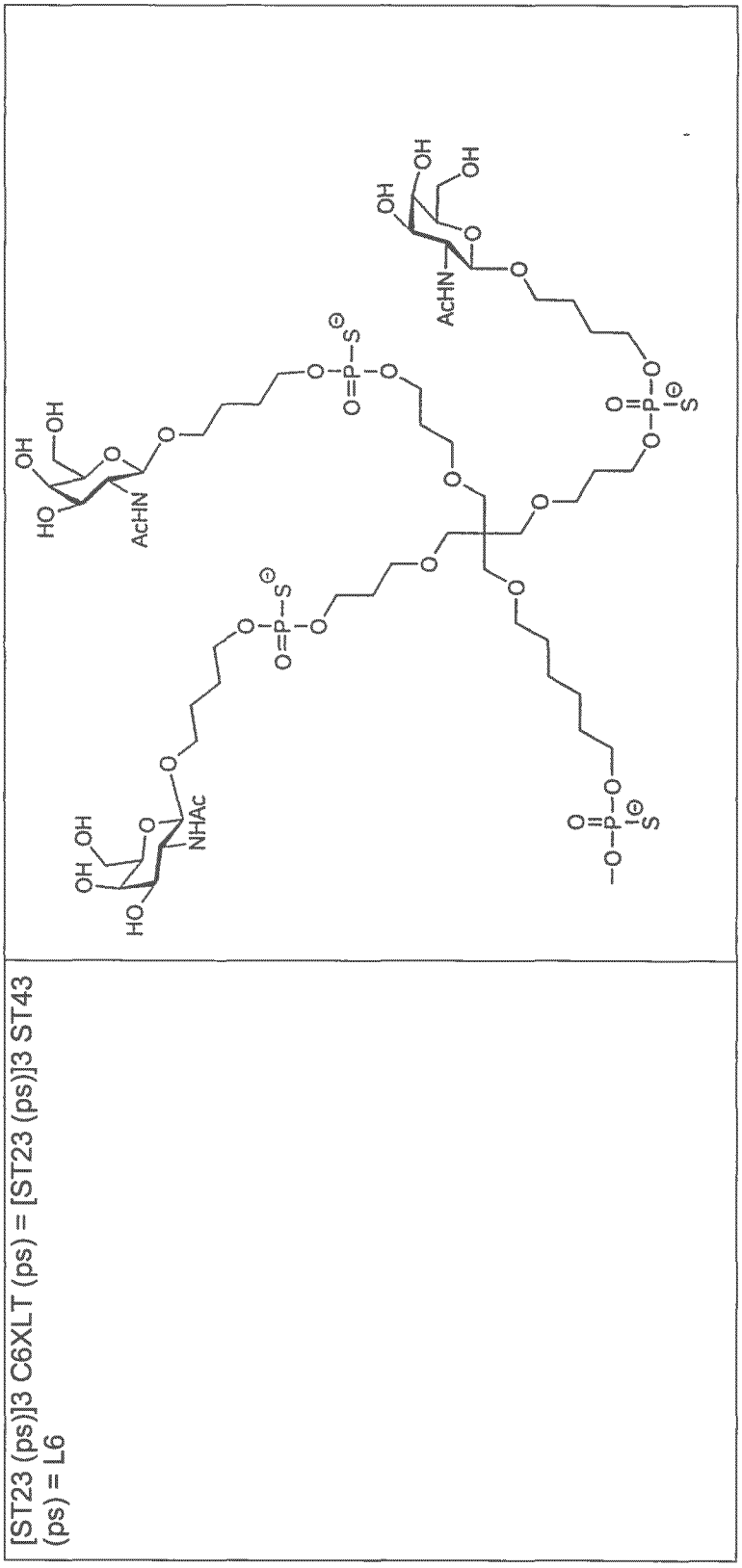
7	2'OMe-rC
8	2'OMe-rG
mA, mU, mC, mG, OMeA, OMeU, OMeC, OMeG	2'deoxy-2'-F RNA
2'-OMe	2'-O-Methyl modification
fA, fU, fC, fG	2' deoxy-2'-F RNA nucleotides
2'-F, 2'-fluoro, 2' fluoro	2'-fluoro modification
(ps)	phosphorothioate
(vp)	Vinyl-(E)-phosphonate
ivA, ivC, ivU, ivG	inverted RNA (3'-3')
FAM	6-Carboxyfluorescein
BHQ	Black Hole Quencher 1
ST23	
ST41/C4XLT	
ST43 (or C6XLT)	

ST43-phos/C6XLT-phos	
Long trebler/ltrb/STKS (phosphoramidite)	
Ser(GN)	
Ser(GN) (phosphoramidite)	
C3Am(GN)	
GlyC3Am(GN)	


C6Am(GN)
C7Am(GN)
PipAm(GN)
GalNAc
GalNAc
GalNAc



[ST23 (ps)]3 C4XLT (ps) = [ST23 (ps)]3 ST41 (ps) = L4


[ST23 (ps)]3 C6XLT (ps) = [ST23 (ps)]3 ST43
(ps) = L6

Claims

1. A nucleic acid for inhibiting expression of *LPA* in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from the *LPA* gene, wherein said first strand comprises, or preferably consists of, a nucleotide sequence selected from the following sequences: SEQ ID NO: 9, 5, 1, 3, 7, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, or 43,
wherein the nucleotides at positions 2 and 14 from the 5' end of the first strand are modified with a 2' fluoro modification, and the nucleotides on the second strand which correspond to positions 11-13 of the first strand are modified with a 2' fluoro modification.

2. The nucleic acid of claim 1, wherein all nucleotides of the nucleic acid are modified at the 2' position of the sugar.

3. The nucleic acid of any preceding claim, wherein the nucleic acid is modified on the first strand with alternating 2' O-methyl modifications and 2' fluoro modifications.

4. The nucleic acid of any preceding claim, wherein the remaining modifications of the second strand are naturally occurring modifications, preferably 2' O-methyl.

5. The nucleic acid of any preceding claim, wherein the nucleic acid comprises a phosphorothioate linkage between the terminal two or three 3' nucleotides and/or 5' nucleotides of one or both ends of the first and/or the second strand.

6. The nucleic acid of any preceding claim, wherein the first strand comprises, or preferably consists of SEQ ID NO: 165 and optionally wherein the second strand comprises, or preferably consists of SEQ ID NO: 163.

7. The nucleic acid of any of the preceding claims, wherein the nucleic acid is conjugated to a ligand.

8. The nucleic acid of claim 7, wherein the ligand comprises (i) one or more N-acetyl galactosamine (GalNAc) moieties or derivatives thereof, and (ii) a linker, wherein the

linker conjugates the at least one GalNAc moiety or derivative thereof to the nucleic acid.

9. The nucleic acid of any preceding claim, wherein the nucleic acid is conjugated to a ligand comprising a compound of formula (I):

$$[S\text{-}X^1\text{-}P\text{-}X^2]_3\text{-}A\text{-}X^3\text{-} \qquad (I)$$

wherein:

S represents a saccharide, preferably wherein the saccharide is N-acetyl galactosamine;

X^1 represents C_3-C_6 alkylene or $(\text{-}CH_2\text{-}CH_2\text{-}O)_m(\text{-}CH_2)_2\text{-}$ wherein m is 1, 2, or 3;

P is a phosphate or modified phosphate, preferably a thiophosphate;

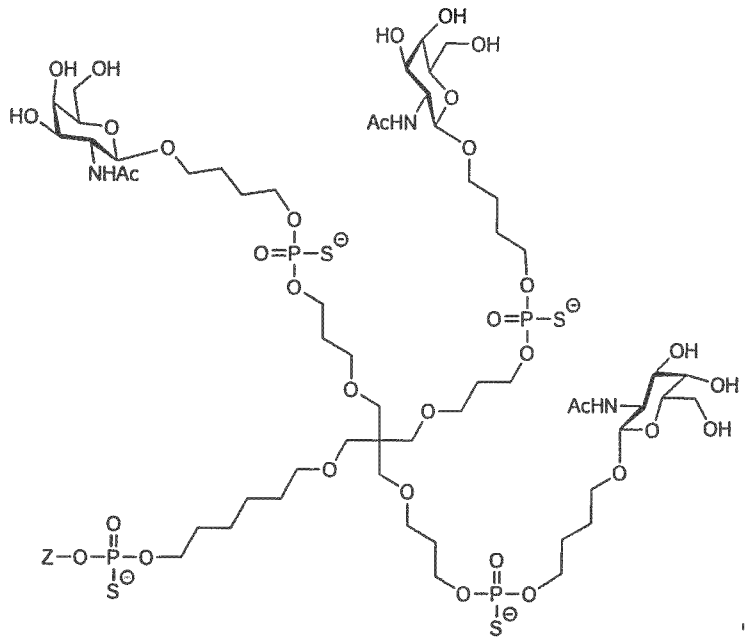
X^2 is alkylene or an alkylene ether of the formula $(\text{-}CH_2)_n\text{-}O\text{-}CH_2\text{-}$ where n = 1-6;

A is a branching unit;

X^3 represents a bridging unit;

wherein a nucleic acid as defined in any of claims 1 to 8 is conjugated to X^3 via a phosphate or modified phosphate, preferably a thiophosphate, and the nucleic acid is preferably conjugated to X^3 via the 5' end of the second strand.

10. The nucleic acid of any preceding claim, wherein the nucleic acid is conjugated to a ligand and has the following structure



wherein Z is a nucleic acid according any preceding claim and the ligand is preferably conjugated to the 5' end of the second strand.

11. The nucleic acid of any of claims 7-10, wherein the nucleic acid comprises two phosphorothioate linkages between each of the three terminal 3' and between each of the three terminal 5' nucleotides on the first strand, and two phosphorothioate linkages between the three terminal nucleotides of the 3' end of the second strand and wherein the ligand is conjugated to the 5' end of the second strand.

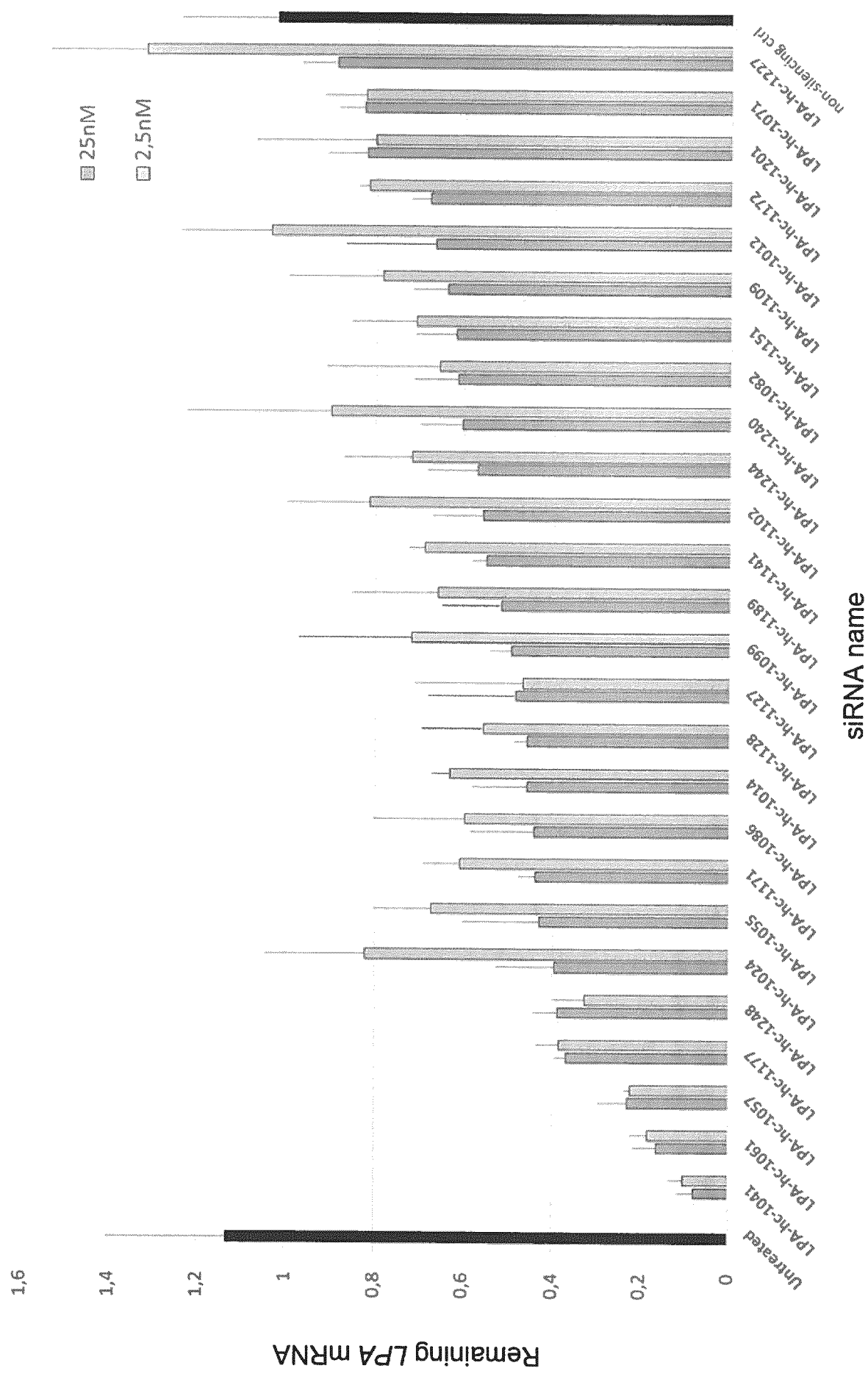
12. A composition comprising a nucleic acid of any of claims 1-11 and optionally a delivery vehicle and/or a physiologically acceptable excipient and/or a carrier and/or a diluent and/or a buffer and/or a preservative, for use as a medicament, preferably for the prevention or treatment or risk reduction of a disease or pathology, wherein the disease or pathology preferably is a cardiovascular disease, wherein the cardiovascular disease preferably is a stroke, atherosclerosis, thrombosis, a coronary heart disease or aortic stenosis and/or any other disease or pathology associated to elevated levels of Lp(a) particles.

13. A pharmaceutical composition comprising a nucleic acid of any of claims 1-11 and further comprising a delivery vehicle and/or a physiologically acceptable excipient and/or a carrier and/or a diluent.

14. Use of a nucleic acid of any of claims 1-11 or a pharmaceutical composition of claim 13 for the prevention or treatment or risk reduction of a disease or pathology, wherein the disease or pathology preferably is a cardiovascular disease, wherein the cardiovascular disease preferably is a stroke, atherosclerosis, thrombosis, a coronary heart disease or aortic stenosis and any other disease or pathology associated to elevated levels of Lp(a) particles.

15. A method of preventing or treating a disease, disorder or syndrome comprising administering a composition comprising a nucleic acid of any of claims 1-11 or a composition of any of claims 12-13 to an individual in need of treatment, preferably wherein the nucleic acid or composition is administered to the subject subcutaneously, intravenously or using any other application routes such as oral, rectal or intraperitoneal.

Figure 1


Remaining LPA mRNA
0
0,2
0,4
0,6
0,8
1
1,2
1,4
1,6
25nM
2,5nM
siRNA name
Untreated
LPA-hc-1041
LPA-hc-1061
LPA-hc-1057
LPA-hc-1177
LPA-hc-1248
LPA-hc-1024
LPA-hc-1055
LPA-hc-1171
LPA-hc-1086
LPA-hc-1014
LPA-hc-1128
LPA-hc-1127
LPA-hc-1099
LPA-hc-1189
LPA-hc-1141
LPA-hc-1102
LPA-hc-1244
LPA-hc-1240
LPA-hc-1082
LPA-hc-1151
LPA-hc-1109
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LPA-hc-1172
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LPA-hc-1071
LPA-hc-1227
non-silencing ctrl

Figure 2A

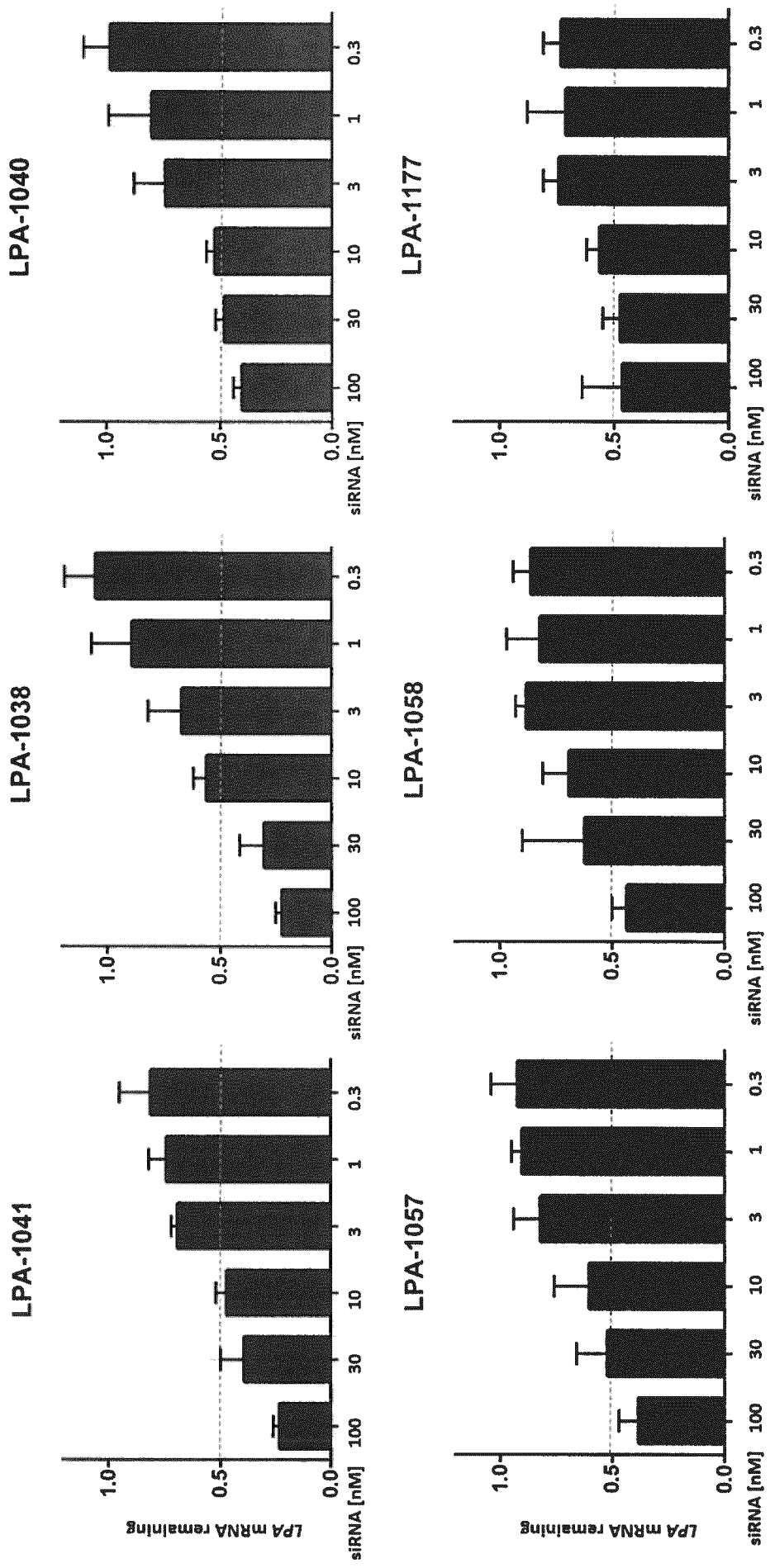

LPA-1040
LPA-1038
LPA-1041
LPA-1177
LPA-1058
LPA-1057
LPA mRNA remaining
siRNA [nM]
100
30
10
3
1
0.3
0.0
0.5
1.0

Figure 2B

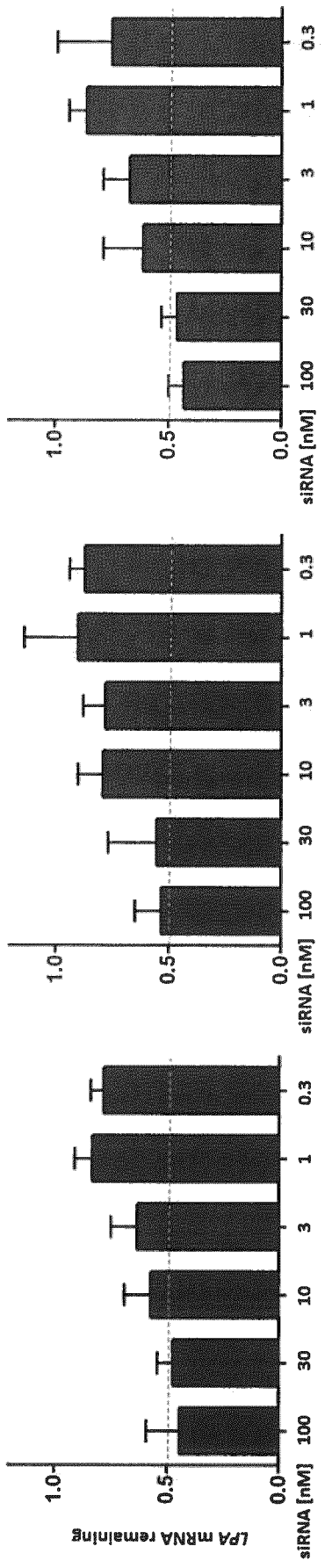


Figure 3

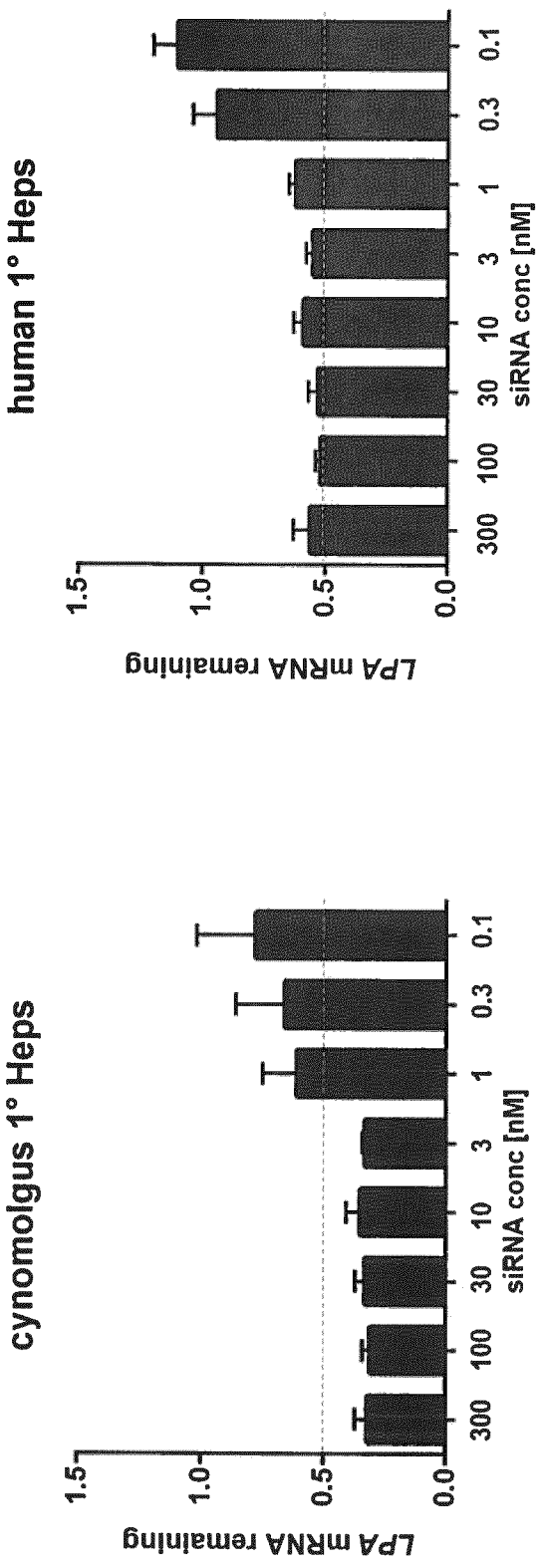


Figure 4

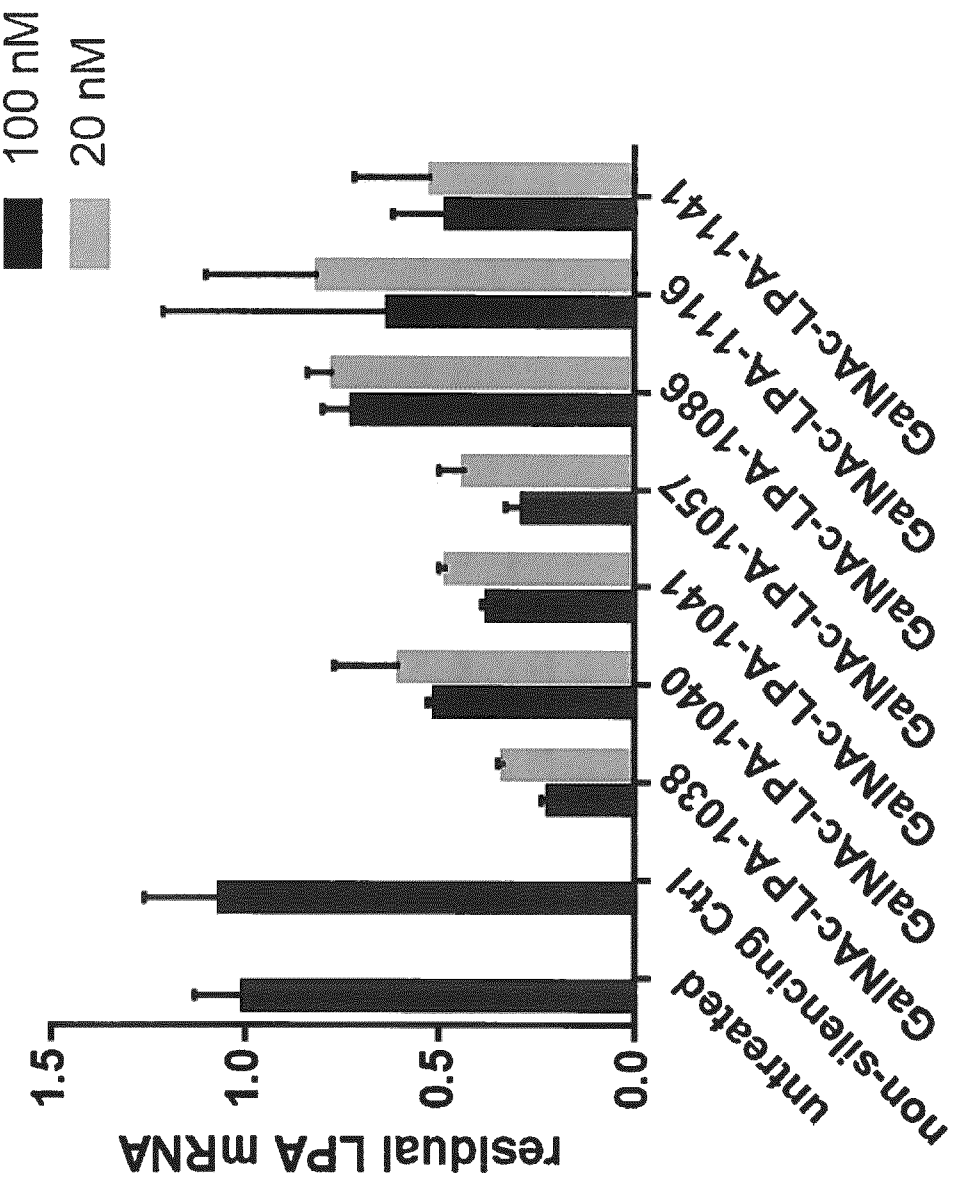

100 nM
20 nM
residual LPA mRNA
1.5
1.0
0.5
0.0
untreated
non-silencing Ctrl
GalNAc-LPA-1038
GalNAc-LPA-1040
GalNAc-LPA-1041
GalNAc-LPA-1057
GalNAc-LPA-1086
GalNAc-LPA-1116
GalNAc-LPA-1141

Figure 5

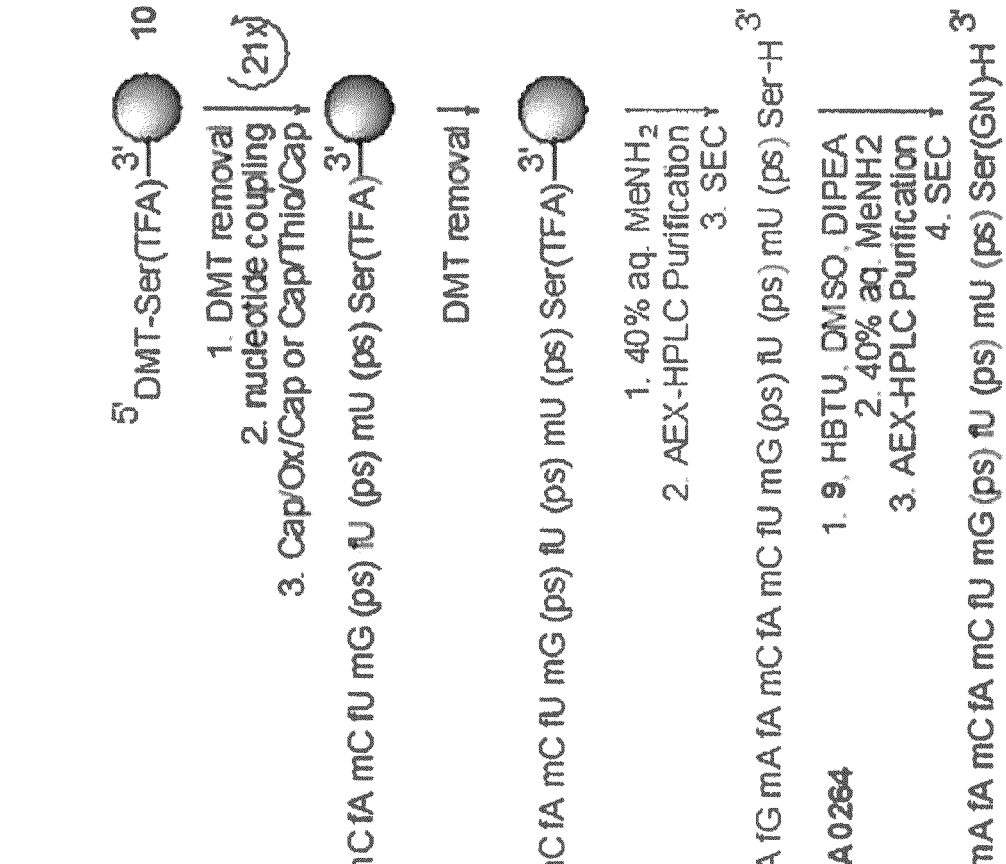

5' DMT-Ser(TFA) 3'
10
1. DMT removal
2. nucleotide coupling
3. Cap/Ox/Cap or Cap/Thio/Cap
(21x)
5' DMT-mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(TFA) 3'
DMT removal
5' mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(TFA) 3'
1. 40% aq. MeNH2
2. AEX-HPLC Purification
3. SEC
5' mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser-H 3'
A0264
1. 9, HBTU, DMSO, DIPEA
2. 40% aq. MeNH2
3. AEX-HPLC Purification
4. SEC
5' mU (ps) fU (ps) mA fU mA fG mA fG mC fA mA fG mA fA mC fA mC fU mG (ps) fU (ps) mU (ps) Ser(GN)-H 3'
A0268

Figure 6

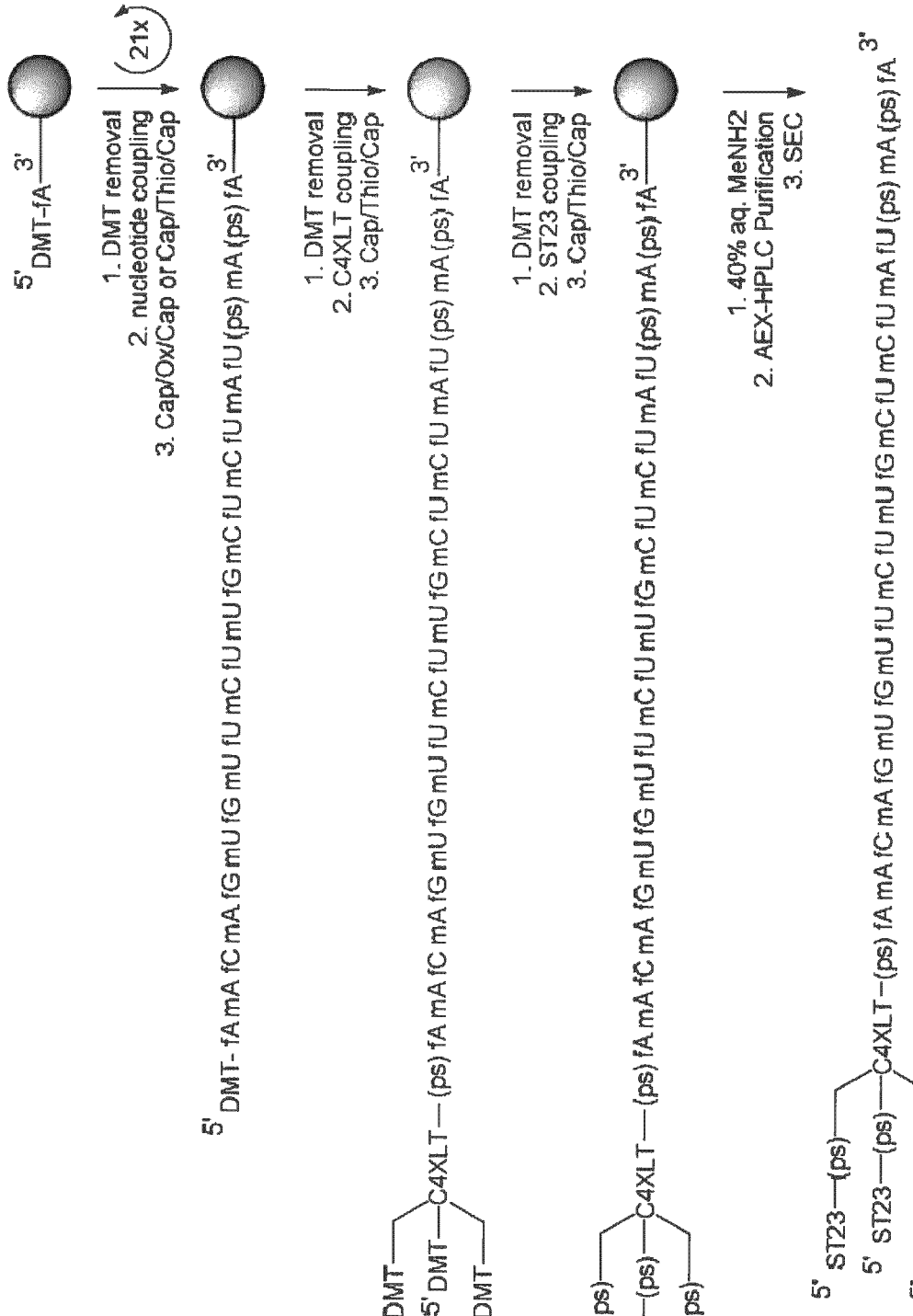

5' DMT-fA 3'
1. DMT removal
2. nucleotide coupling
3. Cap/Ox/Cap or Cap/Thio/Cap
21x
5' DMT- fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA 3'
1. DMT removal
2. C4XLT coupling
3. Cap/Thio/Cap
5' DMT
5' DMT
C4XLT — (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA 3'
5' DMT
1. DMT removal
2. ST23 coupling
3. Cap/Thio/Cap
5' ST23(Ac)3 (ps)
5' ST23(Ac)3 (ps)
5' ST23(Ac)3 (ps)
C4XLT — (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA 3'
1. 40% aq. MeNH2
2. AEX-HPLC Purification
3. SEC
5' ST23 (ps)
5' ST23 (ps)
5' ST23 (ps)
C4XLT – (ps) fA mA fC mA fG mU fG mU fU mC fU mU fG mC fU mC fU mA fU (ps) mA (ps) fA 3'
A0006

Figure 7a

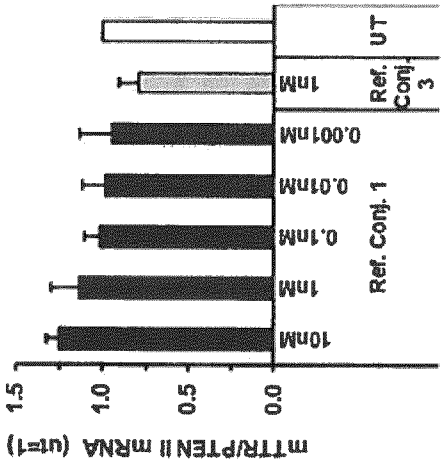


Figure 7b

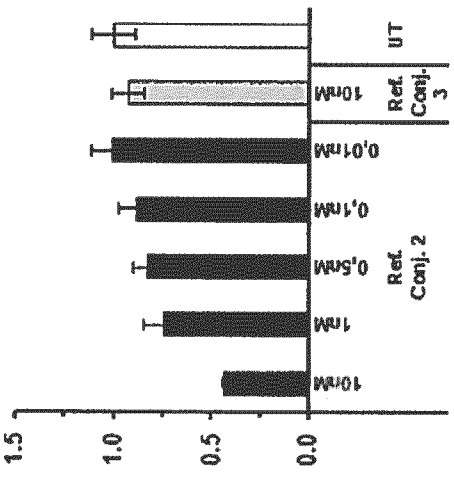


Figure 7c

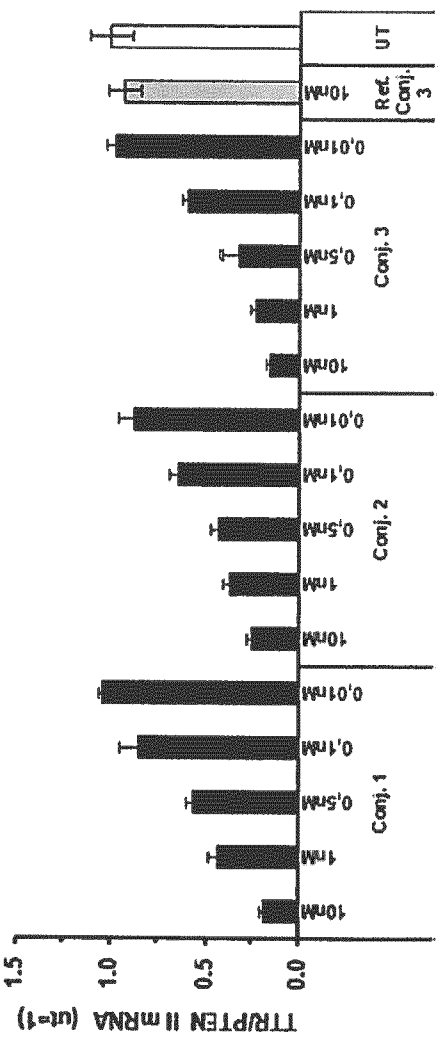


Figure 8

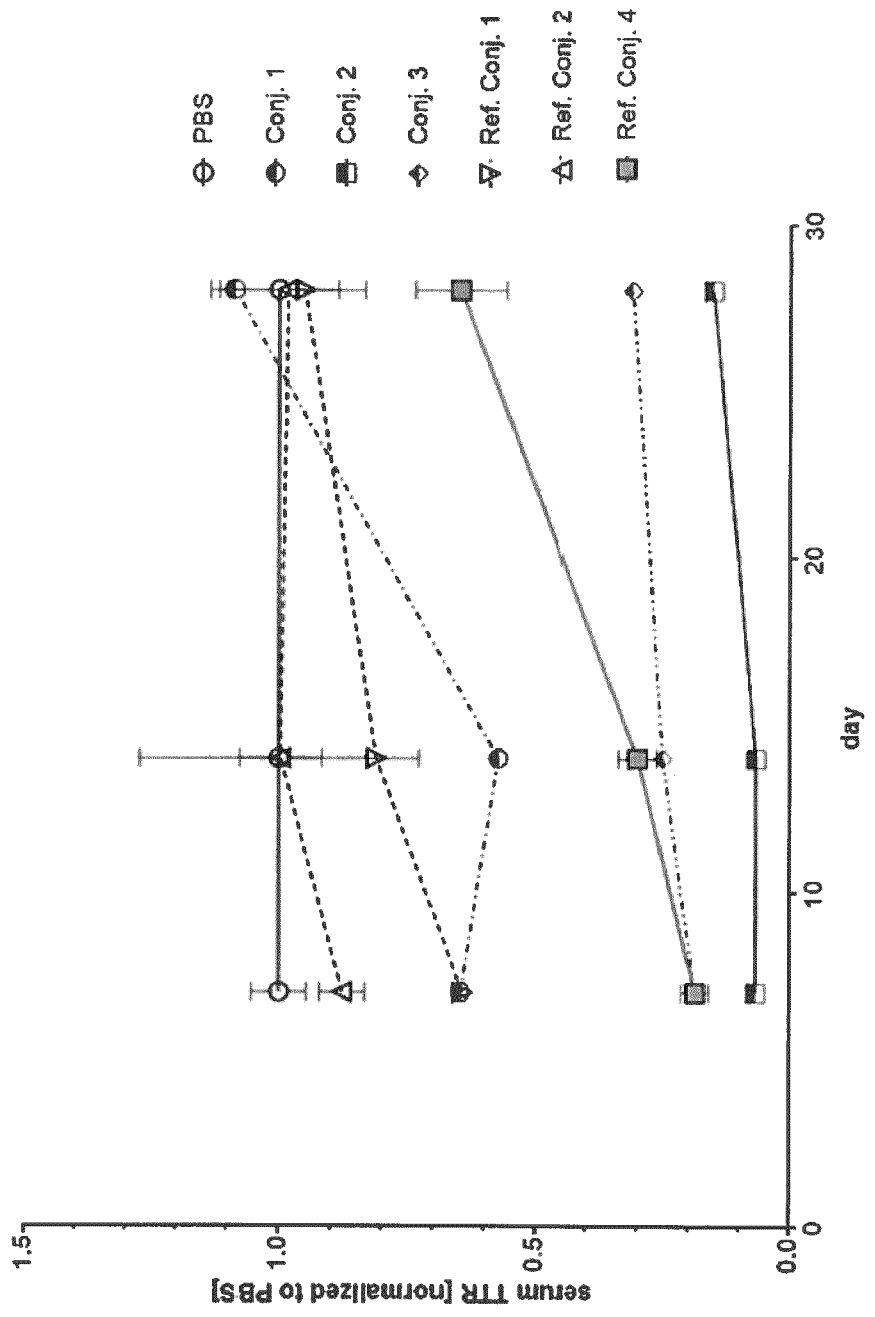

time course of serum TTR in C57BL/6 following
s.c. application of 1mg/kg siRNA-conjugate (mean ± SD, n=4)
PBS
Conj. 1
Conj. 2
Conj. 3
Ref. Conj. 1
Ref. Conj. 2
Ref. Conj. 4
serum TTR [normalized to PBS]
1.5
1.0
0.5
0.0
0
10
20
30
day

Figure 9

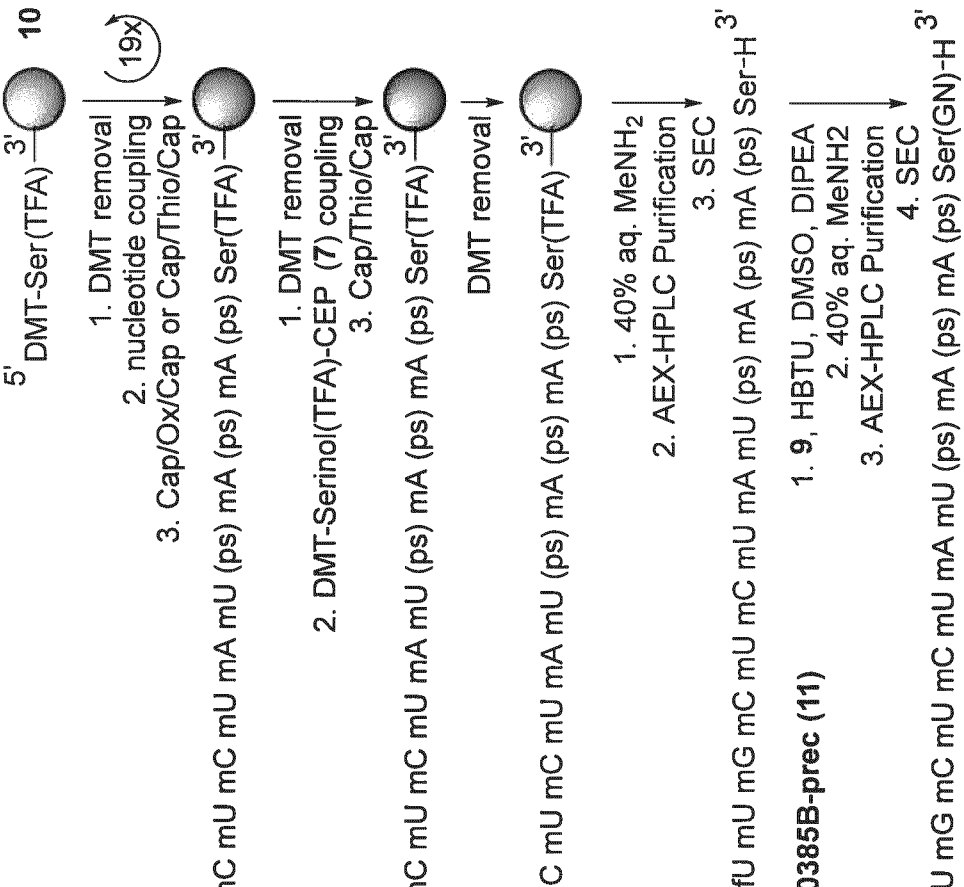
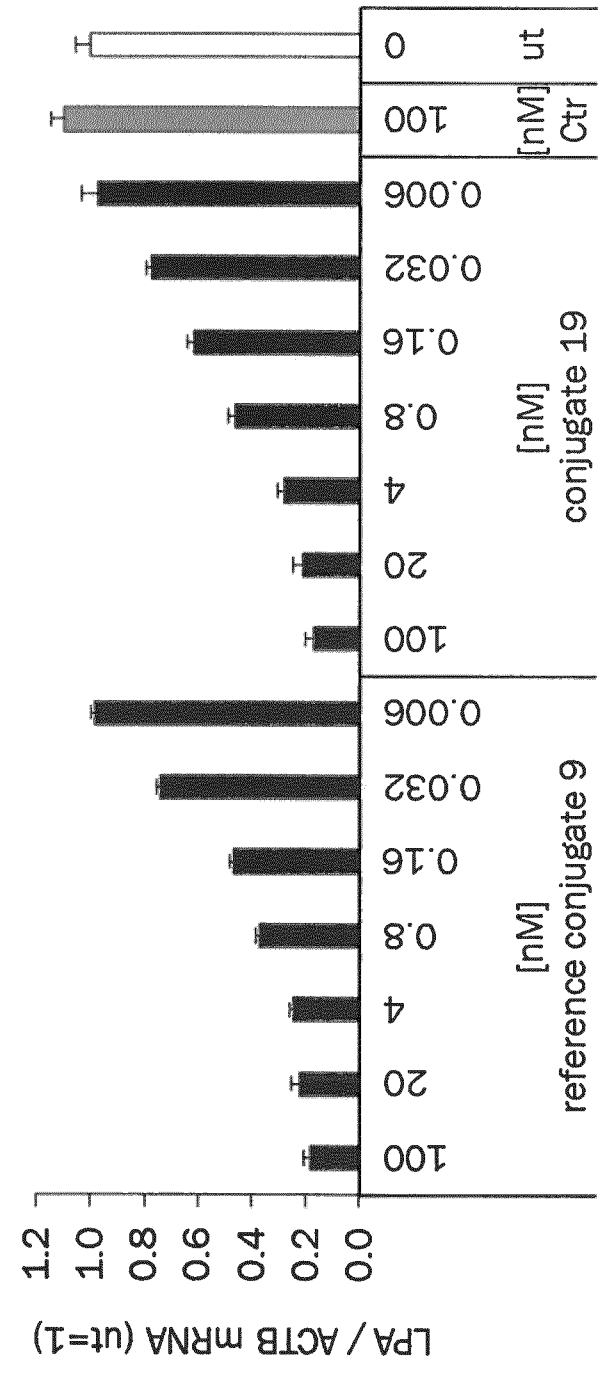

5' DMT-Ser(TFA) 3' 10
1. DMT removal
2. nucleotide coupling
3. Cap/Ox/Cap or Cap/Thio/Cap
19x
5' DMT-mC (ps) mA (ps) mG mU mG mU fU fC fU mU mG mC mU mC mU mA mU (ps) mA (ps) Ser(TFA) 3'
1. DMT removal
2. DMT-Serinol(TFA)-CEP (7) coupling
3. Cap/Thio/Cap
5' DMT-Ser(TFA) (ps) mC (ps) mA (ps) mG mU mG mU fU fC fU mU mG mC mU mC mU mA mU (ps) mA (ps) Ser(TFA) 3'
DMT removal
5' H-Ser(TFA) (ps) mC (ps) mA (ps) mG mU mG mU fU fC fU mU mG mC mU mC mU mA mU (ps) mA (ps) Ser(TFA) 3'
1. 40% aq. MeNH2
2. AEX-HPLC Purification
3. SEC
5' H-Ser (ps) mC (ps) mA (ps) mG mU mG mU fU fC fU mU mG mC mU mC mU mA mU (ps) mA (ps) Ser-H 3'
X0385B-prec (11)
1. 9, HBTU, DMSO, DIPEA
2. 40% aq. MeNH2
3. AEX-HPLC Purification
4. SEC
5' H-Ser(GN) (ps) mC (ps) mA (ps) mG mU mG mU fU fC fU mU mG mC mU mC mU mA mU (ps) mA (ps) Ser(GN)-H 3'
X0385B (12)

Figure 10


LPA / ACTB mRNA (ut=1)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
100
20
4
0.8
0.16
0.032
0.006
[nM]
reference conjugate 9
100
20
4
0.8
0.16
0.032
0.006
[nM]
conjugate 19
100
[nM]
Ctr
0
ut

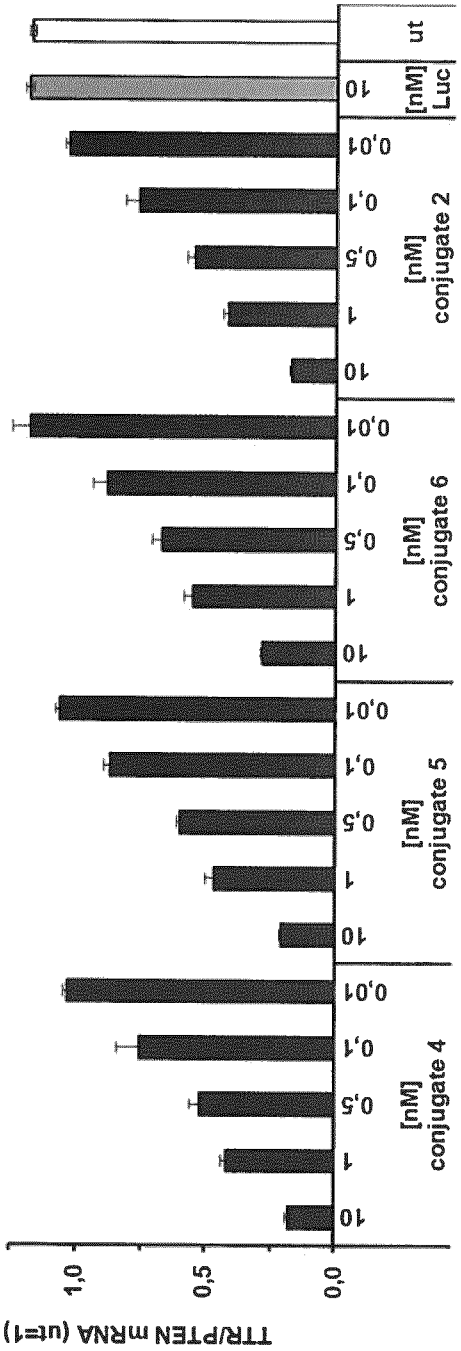


Figure 11A

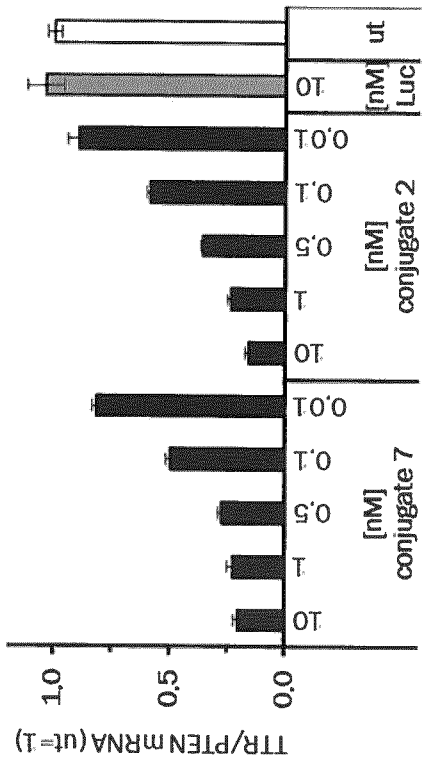


Figure 11B

Figure 12A

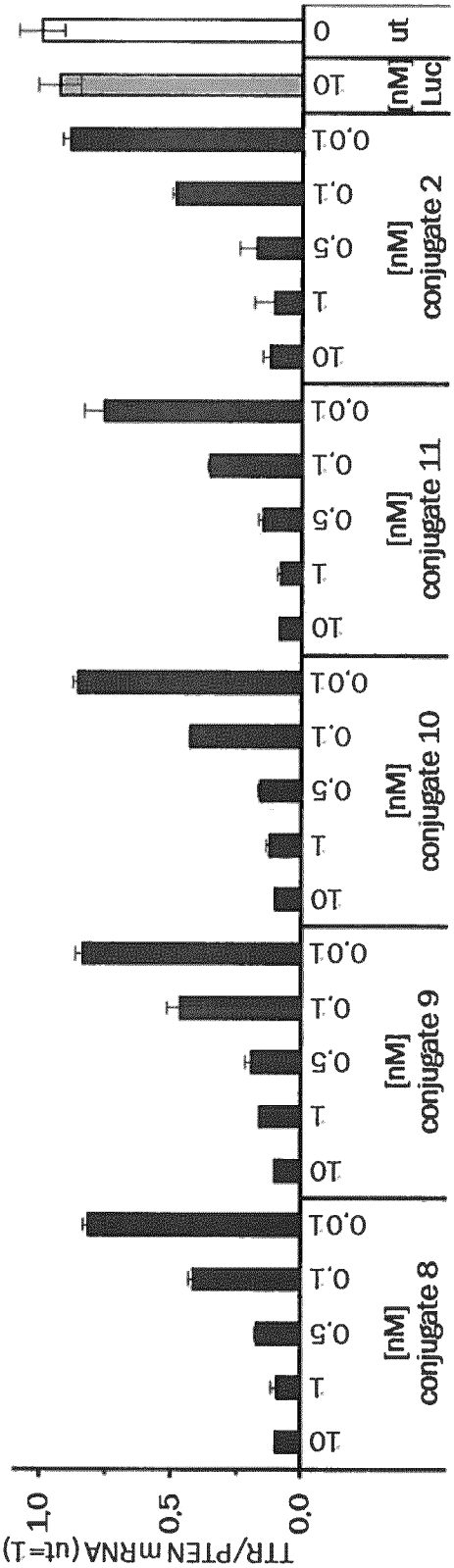
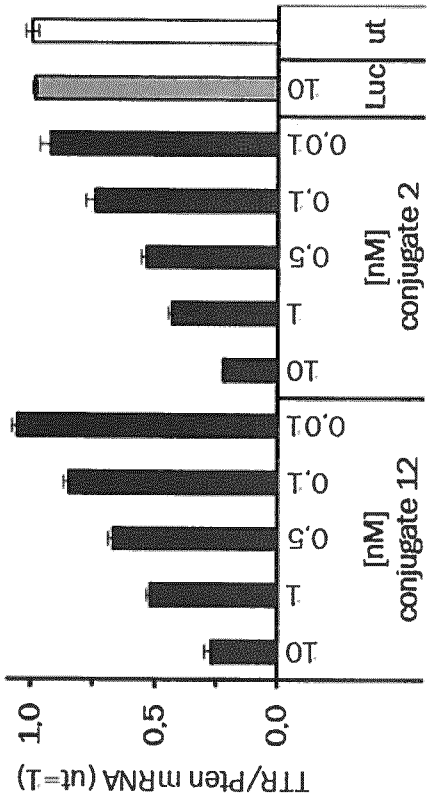


Figure 12B



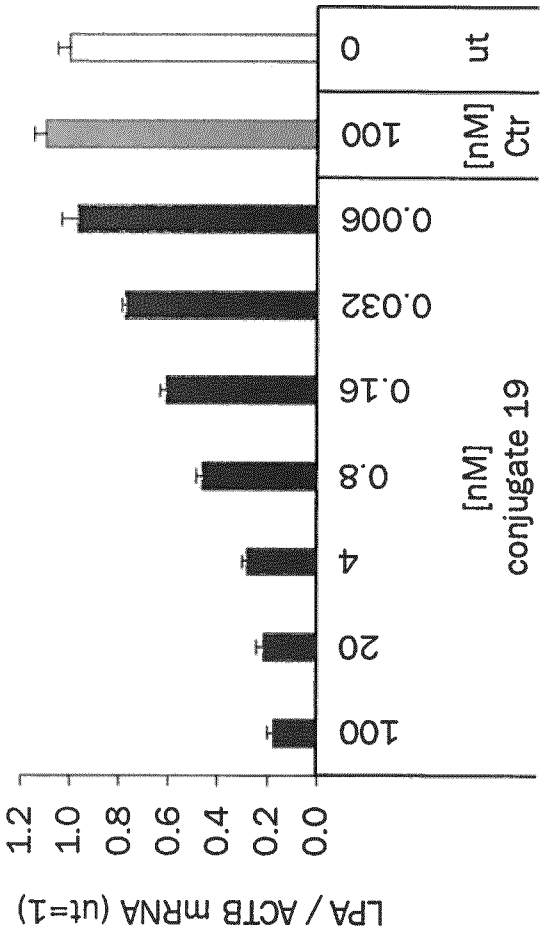

LPA / ACTB mRNA (ut=1)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
100
20
4
0.8
0.16
0.032
0.006
100
0
[nM]
conjugate 19
[nM]
Ctr
ut

Figure 13

Figure 14

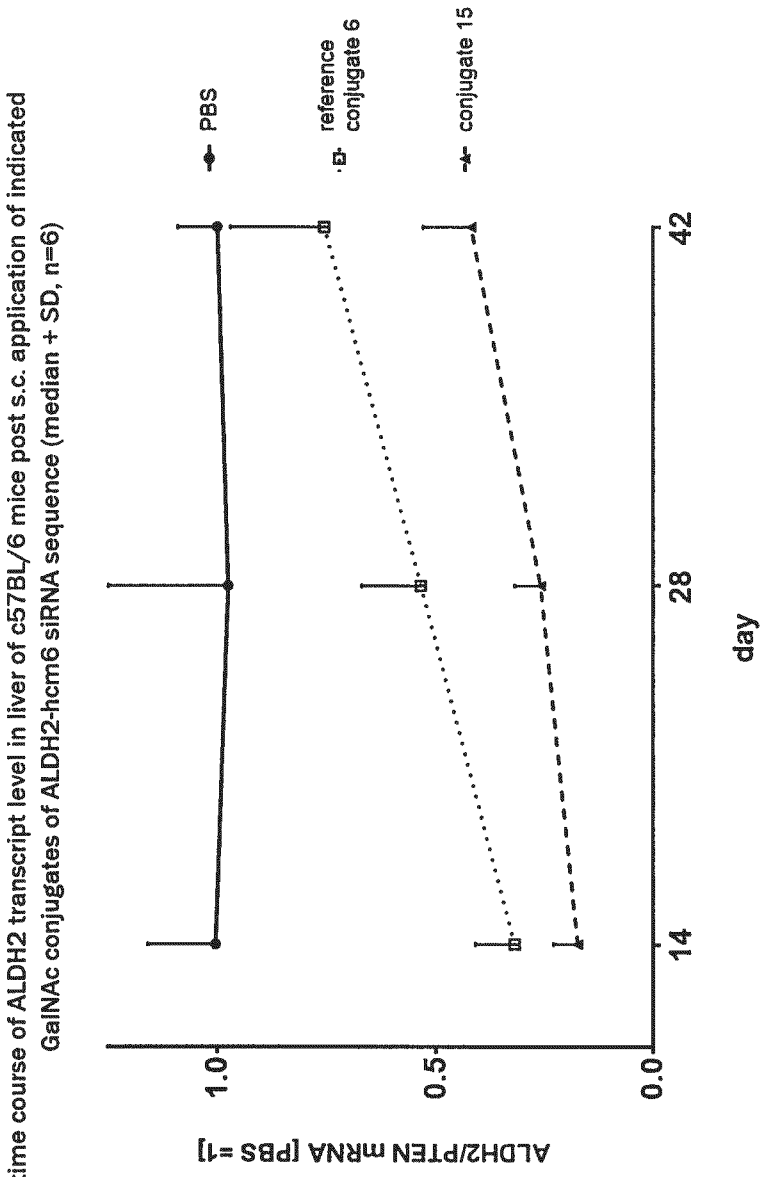

time course of ALDH2 transcript level in liver of c57BL/6 mice post s.c. application of indicated GalNAc conjugates of ALDH2-hcm6 siRNA sequence (median + SD, n=6)
PBS
reference conjugate 6
conjugate 15
ALDH2/PTEN mRNA [PBS =1]
1.0
0.5
0.0
14
28
42
day

Figure 15

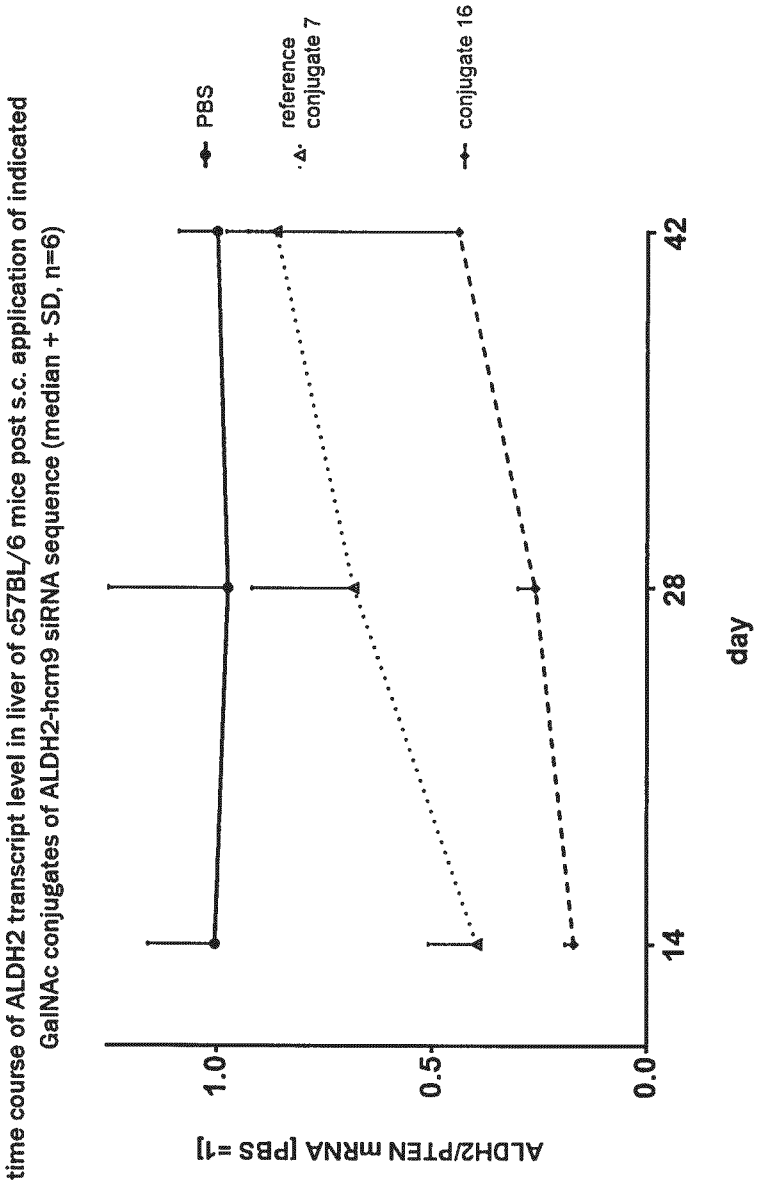

time course of ALDH2 transcript level in liver of c57BL/6 mice post s.c. application of indicated GalNAc conjugates of ALDH2-hcm9 siRNA sequence (median + SD, n=6)
PBS
reference conjugate 7
conjugate 16
ALDH2/PTEN mRNA [PBS =1]
1.0
0.5
0.0
14
28
42
day

Figure 16

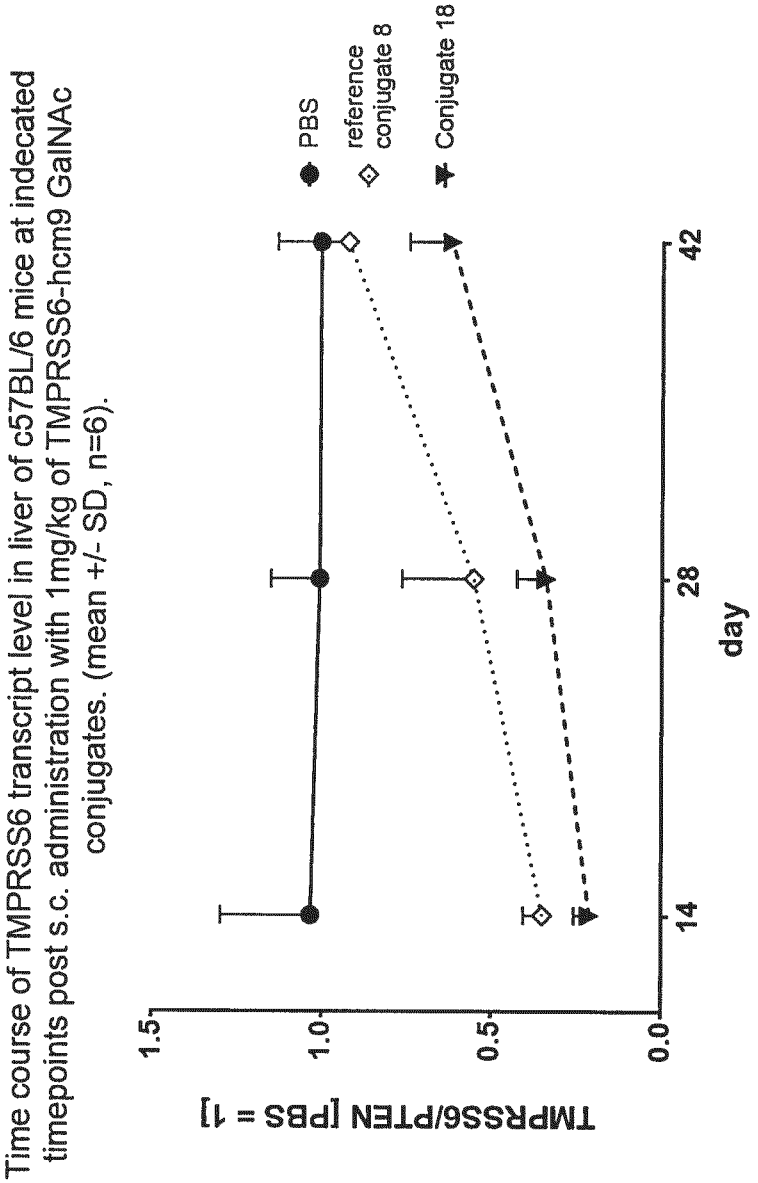

Time course of TMPRSS6 transcript level in liver of c57BL/6 mice at indecated timepoints post s.c. administration with 1mg/kg of TMPRSS6-hcm9 GalNAc conjugates. (mean +/- SD, n=6).
PBS
reference conjugate 8
Conjugate 18
TMPRSS6/PTEN [PBS = 1]
1.5
1.0
0.5
0.0
14
28
42
day

Figure 17

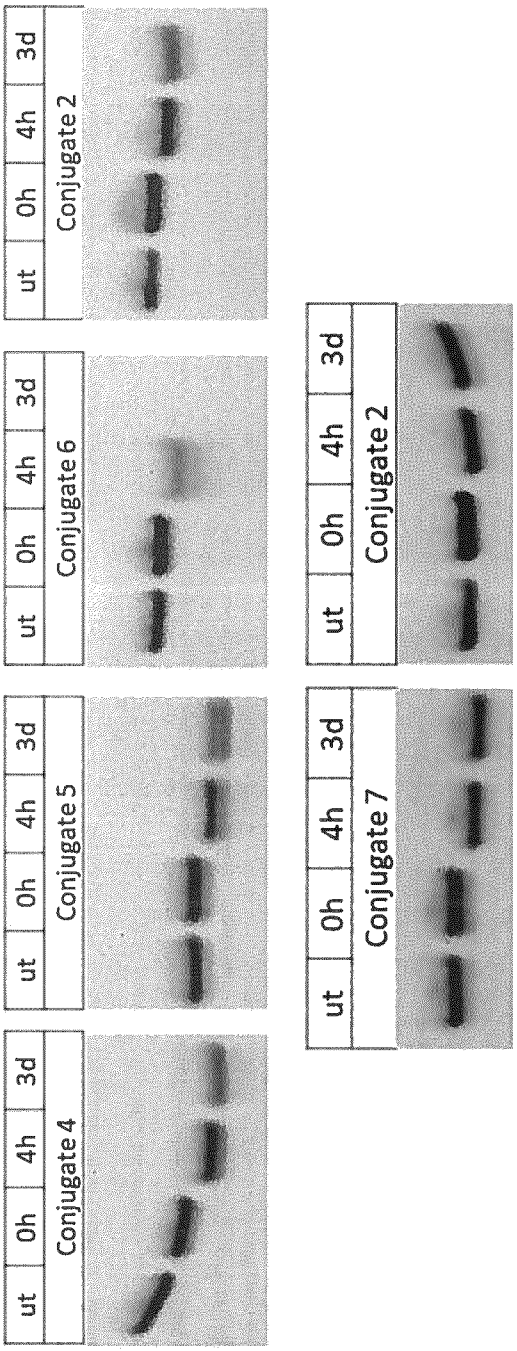


Figure 18

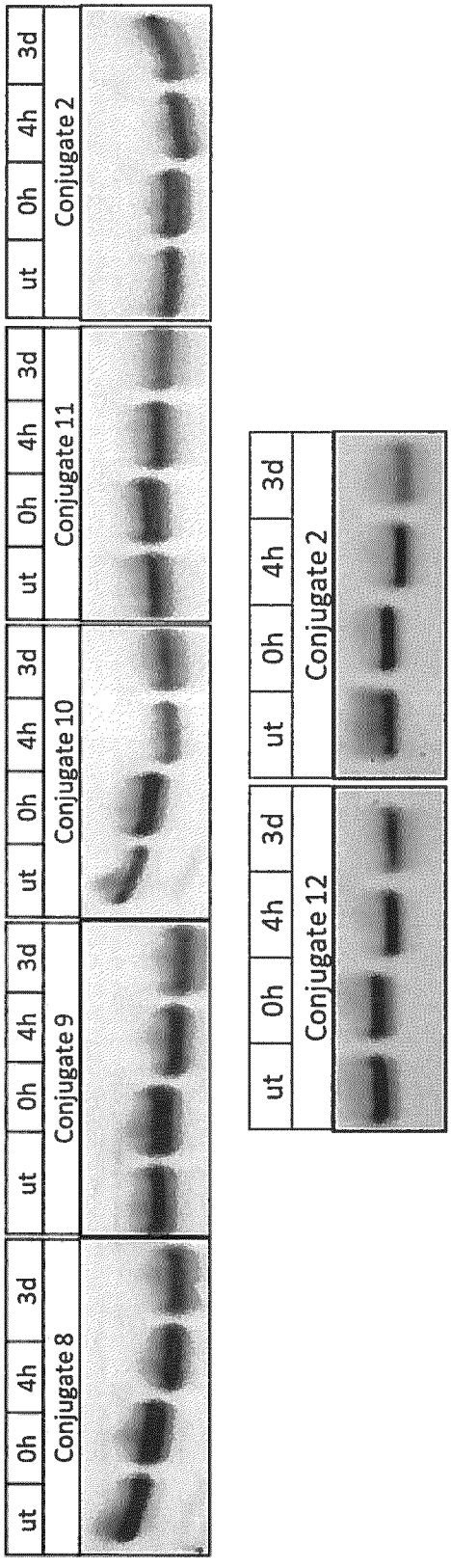


Figure 19

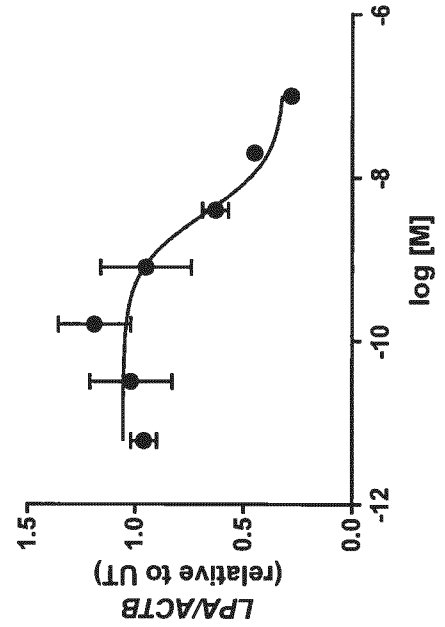


Figure 20

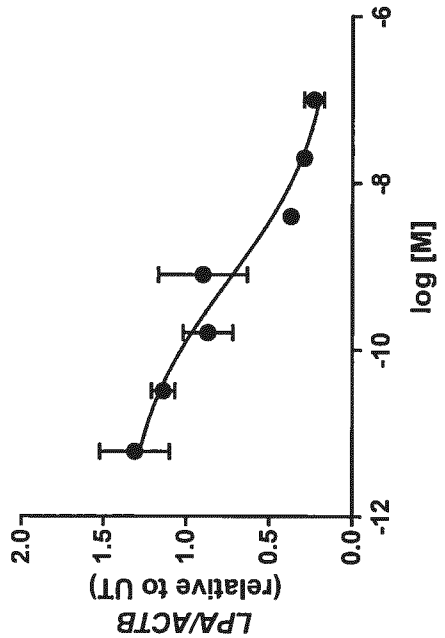


Figure 21

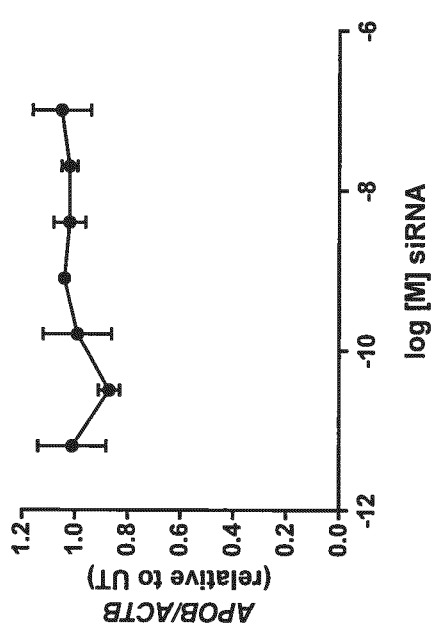


Figure 22

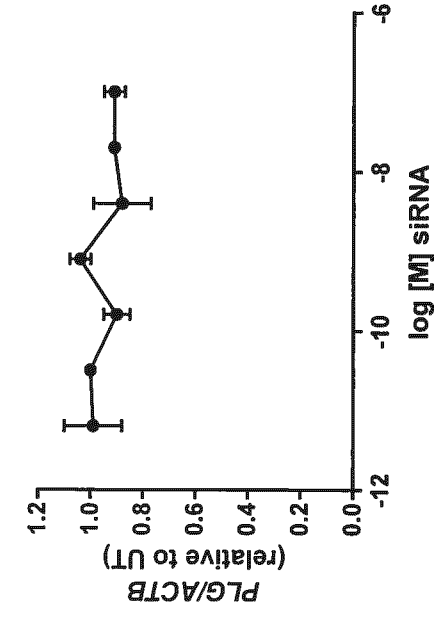


Figure 23

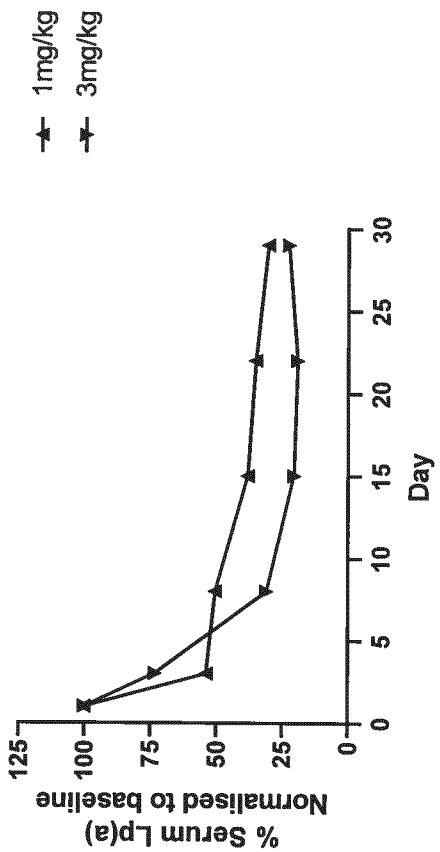
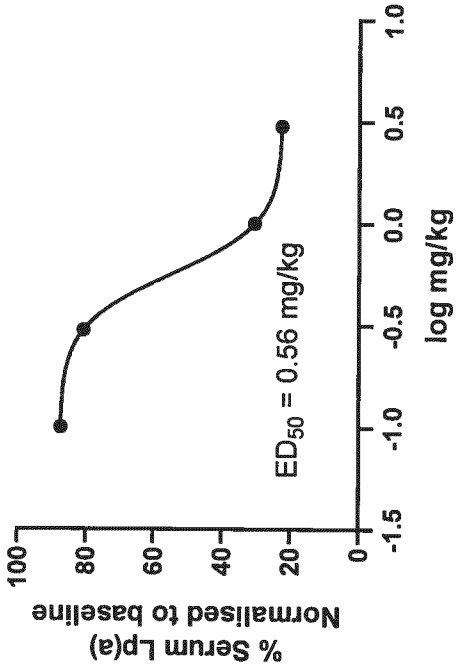


Figure 24



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2019/081158

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12N15/113 A61K31/713 A61P9/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, BIOSIS, Sequence Search, EMBASE, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2017/059223 A2 (ARROWHEAD PHARMACEUTICALS INC [US]) 6 April 2017 (2017-04-06) page 69 - page 82; claims 1,11; examples 2-5; tables 2A, 2B; sequences 186,195,796,1242,1243,1263,1271,1274,1277 ----- -/--	1-15

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
17 January 2020	19/03/2020

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Bucka, Alexander

1

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	TADIN-STRAPPS MARIJA ET AL: "Development of Lipoprotein(a) siRNAs for Mechanism of Action Studies in Non-Human Primate Models of Atherosclerosis", JOURNAL OF CARDIOVASCULAR TRANSLATIONAL RESEARCH, SPRINGER US, BOSTON, vol. 8, no. 1, 21 January 2015 (2015-01-21), pages 44-53, XP035461835, ISSN: 1937-5387, DOI: 10.1007/S12265-014-9605-1 [retrieved on 2015-01-21] tables 1-3	1-15
A	WO 2016/149020 A1 (ARROWHEAD RES CORP [US]) 22 September 2016 (2016-09-22) page 50; example 5; sequence 67	1-15
A	WO 2005/000201 A2 (ISIS PHARMACEUTICALS INC [US]; CROOKE ROSANNE M [US]; GRAHAM MARK J [U) 6 January 2005 (2005-01-06) the whole document	1-15
A	MARK J. GRAHAM ET AL: "Antisense inhibition of apolipoprotein (a) to lower plasma lipoprotein (a) levels in humans", JOURNAL OF LIPID RESEARCH, vol. 57, no. 3, 4 November 2015 (2015-11-04), pages 340-351, XP055502501, US ISSN: 0022-2275, DOI: 10.1194/jlr.R052258 figure 1; table 1	1-15
A	KURT B ET AL: "Lipoprotein(a) clinical aspects and future challenges", CLINICAL RESEARCH IN CARDIOLOGY SUPPLEMENTS2015SPRINGER VERLAGDEU,, vol. 10, no. 1, 3 March 2015 (2015-03-03), pages 26-32, XP009506615, ISSN: 1861-0706, DOI: 10.1007/S11789-015-0075-Z [retrieved on 2015-03-03] the whole document	1-15
A	KONRAD SCHMIDT ET AL: "Structure, function, and genetics of lipoprotein (a)", JOURNAL OF LIPID RESEARCH, vol. 57, no. 8, 13 April 2016 (2016-04-13) , pages 1339-1359, XP055502476, US ISSN: 0022-2275, DOI: 10.1194/jlr.R067314 the whole document	1-15

-/--

1

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	WO 2019/092283 A1 (SILENCE THERAPEUTICS GMBH [DE]) 16 May 2019 (2019-05-16) sequence 123	1-15
X,P	WO 2019/092282 A1 (SILENCE THERAPEUTICS GMBH [DE]) 16 May 2019 (2019-05-16) sequence 174	1-15

1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2019/081158

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

6(completely); 1-5, 7-15(partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 6(completely); 1-5, 7-15(partially)

A nucleic acid for inhibiting expression of LPA in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from the LPA gene, wherein said first strand comprises the nucleotide sequence of SEQ ID NO: 9 or 165, wherein positions 2 and 14 of the first strand are 2'-F modified and positions corresponding to positions 11-13 of the first strand are 2'-F modified in the second strand; related products and uses thereof.

2-22. claims: 1-5, 7-15(all partially)

A nucleic acid for inhibiting expression of LPA in a cell, comprising at least one duplex region that comprises at least a portion of a first strand and at least a portion of a second strand that is at least partially complementary to the first strand, wherein said first strand is at least partially complementary to at least a portion of RNA transcribed from the LPA gene, wherein in each separate invention said first strand comprises a nucleotide sequence selected from the following sequences: SEQ ID NOs: 5, 1, 3, 7, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41 or 43,
wherein positions 2 and 14 of the first strand are 2'-F modified and positions corresponding to positions 11-13 of the first strand are 2'-F modified in the second strand; related products and uses thereof.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2019/081158

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2017059223 A2	06-04-2017	AU 2016331084 A1	19-04-2018
		BR 112018006489 A2	09-10-2018
		CA 3000397 A1	06-04-2017
		CL 2018000803 A1	31-08-2018
		CN 108368506 A	03-08-2018
		CO 2018003678 A2	30-11-2018
		CR 20180231 A	31-05-2018
		EA 201890864 A1	28-09-2018
		EP 3356529 A2	08-08-2018
		JP 2018529732 A	11-10-2018
		KR 20180052703 A	18-05-2018
		PE 20181139 A1	17-07-2018
		PH 12018500713 A1	15-10-2018
		TW 201726918 A	01-08-2017
		US 2017096665 A1	06-04-2017
		US 2018195070 A1	12-07-2018
		UY 36926 A	28-04-2017
		WO 2017059223 A2	06-04-2017
WO 2016149020 A1	22-09-2016	TW 201639962 A	16-11-2016
		US 2016272970 A1	22-09-2016
		WO 2016149020 A1	22-09-2016
WO 2005000201 A2	06-01-2005	EP 1633302 A2	15-03-2006
		US 2004138164 A1	15-07-2004
		US 2006281698 A1	14-12-2006
		US 2009075924 A1	19-03-2009
		US 2010273860 A1	28-10-2010
		US 2011039910 A1	17-02-2011
		US 2012316219 A1	13-12-2012
		US 2014206750 A1	24-07-2014
		US 2015184156 A1	02-07-2015
		WO 2005000201 A2	06-01-2005
WO 2019092283 A1	16-05-2019	NONE	
WO 2019092282 A1	16-05-2019	NONE	