ANTISENSE OLIGONUCLEOTIDES FOR MODULATING HTRA1 EXPRESSION

FIELD OF INVENTION

The present invention relates to antisense oligonucleotides (oligomers) that are complementary to HTRA1, leading to modulation of the expression of HTRA1. Modulation of HTRA1 expression is beneficial for a range of medical disorders, such as macular degeneration, e.g. age-related macular degeneration.

BACKGROUND

The human high temperature requirement A (HTRA) family of serine proteases are ubiquitously expressed PDZ-proteases that are involved in maintaining protein homeostasis in extracellular compartments by combining the dual functions of a protease and a chaperone. HTRA housekeeping proteases are implicated in organization of the extracellular matrix, cell proliferation and ageing. Modulation of HTRA activity is connected with severe diseases, including Duchenne muscular dystrophy (Bakay et al. 2002, Neuromuscul. Disord. 12: 125-141), arthritis, such as osteoarthritis (Grau et al. 2006, JBC 281: 6124-6129), cancer, familial ischemic cerebral small-vessel disease and age-related macular degeneration, as well as Parkinson's disease and Alzheimer's disease. The human HTRA1 contains an insulin-like growth factor (IGF) binding domain. It has been proposed to regulate IGF availability and cell growth (Zumbrunn and Trueb, 1996, FEES Letters 398:189-192) and to exhibit tumor suppressor properties. HTRA1 expression is down-regulated in metastatic melanoma, and may thus indicate the degree of melanoma progression. Overexpression of HTRA1 in a metastatic melanoma cell line reduced proliferation and invasion in vitro, and reduced tumor growth in a xenograft mouse model (Baldi et al., 2002, Oncogene 21:6684-6688). HTRA1 expression is also down-regulated in ovarian cancer. In ovarian cancer cell lines, HTRA1 overexpression induces cell death, while antisense HTRA1 expression promoted anchorage-independent growth (Chien et al., 2004, Oncogene 23:1636-1644).

In addition to its effect on the IGF pathway, HTRA1 also inhibits signaling by the TGFβ family of growth factors (Oka et al., 2004, Development 131:1041-1053). HTRA1 can cleave amyloid precursor protein (APP), and HTRA1 inhibitors cause the accumulation of Aβ peptide in cultured cells. Thus, HTRA1 is also implicated in Alzheimer's disease (Grau et al.,2005, Proc. Nat. Acad. Sci. USA. 102:6021-6026).

On the other hand HTRA1 upregulation has been observed and seems to be associated to Duchenne muscular dystrophy (Bakay et al. 2002, Neuromuscul. Disord. 12: 125-141) and osteoarthritis (Grau et al. 2006, JBC 281: 6124-6129) and AMD (Fritsche, et al. Nat Gen 2013 45(4):433-9.)

A single nucleotide polymorphism (SNP) in the HTRA1 promoter region (rs11200638) is associated with a 10 fold increased the risk of developing age-related macular degeneration (AMD). Moreover the HTRA1 SNPs are in linkage disequilibrium with the ARMS2 SNP (rs10490924) associated with increased risk of developing age-related macular degeneration (AMD). The risk allele is associated with 2-3 fold increased HTRA1 mRNA and protein expression, and HTRA1 is present in drusen in patients with AMD (Dewan et al., 2006, Science 314:989-992; Yang et al., 2006, Science 314:992-993). Different animal models have confirmed that over-expression of HtrA1 Induces AMD-like phenotype in mice. The hHTRA transgenic mouse (Veierkottn, PlosOne 2011) reveals degradation of the elastic lamina of Bruch's membrane, determines choroidal vascular abnormalities (Jones, PNAS 2011) and increases the Polypoidal choroidal vasculopathy (PCV) lesions (Kumar, IOVS 2014). Additionally it has been reported Bruch's membrane damage in hHTRA1 Tg mice, which determines upon exposure to cigarette smoke 3 fold increases CNV (Nakayama, IOVS 2014)

Age-related macular degeneration (AMD) is the leading cause of irreversible loss of vision in people over the age of 65. With onset of AMD there is gradual loss of the light sensitive photoreceptor cells in the back of the eye, the underlying pigment epithelial cells that support them metabolically, and the sharp central vision they provide. Age is the major risk factor for the onset of AMD: the likelihood of developing AMD triples after age 55. Smoking, light iris color, gender (women are at greater risk), obesity, and repeated exposure to UV radiation also increase the risk of AMD. There are two forms of AMD: dry AMD and wet AMD. In dry AMD, drusen appear in the macula of the eye, the cells in the macula die, and vision becomes blurry. Dry AMD can progress in three stages: 1) early, 2) intermediate, and 3) advanced dry AMD. Dry AMD can also progress into wet AMD during any of these stages. Wet AMD (also known as exudative AMD), is associated with pathologic posterior segment neovascularization. The posterior segment neovascularization (PSNV) found in exudative AMD is characterized as pathologic choroidal neovascularization. Leakage from abnormal blood vessels forming in this process damages the macula and impairs vision, eventually leading to blindness. Treatment strategies for wet AMD are few and palliative at best. There is therefore an unmet medical need in the provision of effective drugs to treat macular degenerative conditions such as wet and dry AMD. WO 2008/013893 claims a composition for treating a subject suffering from age related macular degeneration comprising a nucleic acid molecules comprising an antisense sequence that hybridizes to HTRA1 gene or mRNA: No antisense molecules are disclosed. WO2009/006460 provides siRNAs targeting HTRA1 and their use in treating AMD.

OBJECTIVE OF THE INVENTION

The present invention provides antisense oligonucleotides which modulate HTRA1 *in vivo* or *in vitro*. The invention identified cryptic target sequence motifs present in the human HTRA1 mRNA (including pre-mRNA) which may be targeted by antisense oligonucleotides to give

effective HTRA1 inhibition. The invention also provides effective antisense oligonucleotide sequences and compounds which are capable of inhibiting HTRA1, and their use in treatment of diseases or disorders where HTRA1 is indicated.

SUMMARY

The present disclosure relates to oligonucleotides targeting a mammalian HTRA1 nucleic acid, *i.e.* are capable of inhibiting the expression of HTRA1 and to treat or prevent diseases related to the functioning of the HTRA1. The oligonucleotides targeting HTRA1 are antisense oligonucleotides, *i.e.* are complementary to their HTRA1 nucleic acid target.

The oligonucleotide of the disclosure may be in the form of a pharmaceutically acceptable salt, such as a sodium salt or a potassium salt.

Accordingly, the disclosure provides antisense oligonucleotides which comprise a contiguous nucleotide sequence of 10 - 30 nucleotides in length with at least 90% complementarity, such as fully complementary to a mammalian HTRA1 nucleic acid, such as SEQ ID NO 1, SEQ ID NO 2, SEQ ID NO 3 or SEQ ID NO 4.

The disclosure provides pharmaceutical compositions comprising the oligonucleotides of the disclosure and pharmaceutically acceptable diluents, carriers, salts and/or adjuvants.

The disclosure provides LNA antisense oligonucleotides, such as LNA gapmer oligonucleotides, which comprise a contiguous nucleotide sequence of 10 - 30 nucleotides in length with at least 90% complementarity, such as fully complementary to a HTRA1 nucleic acid, such as a sequence selected from the group consisting of SEQ ID NO 1, SEQ ID NO 2, SEQ ID NO 3 or SEQ ID NO 4.

In one aspect, the disclosure provides for an antisense oligonucleotide of formula $T_sA_sT_st_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT_sT$ (SEQ ID NO 143), wherein a capital letter represents an LNA nucleoside unit, a lower case letter represents a DNA nucleoside unit, subscript s represents a phosphorothioate internucleoside linkage.

The disclosure provides for an antisense oligonucleotide comprising a contiguous nucleotide region of 10 – 22, such as 12 - 22 nucleotides which are at least 90% such as 100% complementarity to SEQ ID NO 147:

SEQ ID NO 147: 5' CCAACAACCAGGTAAATATTTG 3'

The disclosure provides for an antisense oligonucleotide comprising a contiguous nucleotide region of 10 – 17, such as 11, 12, 13, 14, 15, 16, such as 12 – 16 or 12 - 17 nucleotides which are complementarity to a sequence selected from the group consisting of SEQ ID NO 148 - 155.

The disclosure provides for an antisense oligonucleotide comprising a contiguous nucleotide region of 10 – 17, such as 11, 12, 13, 14, 15, 16, such as 12 – 16 or 12 - 17 nucleotides which are complementarity to SEQ ID NO 148 or 155.

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The disclosure provides for an antisense oligonucleotide of 10 – 30 nucleotides in length, wherein said antisense oligonucleotide comprises a contiguous nucleotide region of 10 – 22 nucleotides which are at least 90% such as 100% complementarity to SEQ ID NO 147:

SEQ ID NO 147: 5' CCAACAACCAGGTAAATATTTG 3'

The disclosure provides for an antisense oligonucleotide of 10 – 30 nucleotides in length, wherein said antisense oligonucleotide comprises a contiguous nucleotide region of at least 10, such as at least 12 contiguous nucleotides which are complementary to a sequence present in a sequence selected from SEQ ID NO 148 – 155.

The disclosure provides for an antisense oligonucleotide of at least 12 nucleotides in length, wherein said antisense oligonucleotide comprises the contiguous sequence of SEQ ID NO 146 SEQ ID NO 146: 5' TTTACCTGGTT 3'.

The disclosure provides for the oligonucleotides provided in the examples. The disclosure provides for the oligonucleotide, such as an antisense oligonucleotide, which comprises at least 10, such as at least 12, present in a sequence selected from the group consisting of SEQ ID NO 5 – 145.

The disclosure provides for a conjugate comprising the oligonucleotide according to the disclosure, and at least one conjugate moiety covalently attached to said oligonucleotide.

The disclosure provides for a pharmaceutically acceptable salt of the oligonucleotide or conjugate of the disclosure. In another aspect, the disclosure provides for a pharmaceutically acceptable salt of the antisense oligonucleotide as defined herein.

In another aspect, the disclosure provides for a pharmaceutical composition comprising the antisense oligonucleotide as defined herein; and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant

The disclosure provides methods for *in vivo* or *in vitro* method for modulation of HTRA1 expression in a cell which is expressing HTRA1, by administering an oligonucleotide, conjugate or composition of the disclosure in an effective amount to said cell. In another aspect, the disclosure provides for an in vitro method for modulating HTRA1 expression in a target cell which is expressing HTRA1, said method comprising administering the antisense oligonucleotide, pharmaceutically acceptable salt, or pharmaceutical composition as defined herein in an effective amount to said cell.

The disclosure provides methods for treating or preventing a disease, disorder or dysfunction associated with *in vivo* activity of HTRA1 comprising administering a therapeutically or prophylactically effective amount of the oligonucleotide of the disclosure, or conjugate thereof, to a subject suffering from or susceptible to the disease, disorder or dysfunction.

The oligonucleotide or composition of the disclosure is used for the treatment or prevention of macular degeneration, and other disorders where HTRA1 is implicated.

In another aspect, the disclosure provides for the antisense oligonucleotide as defined herein, or the pharmaceutically acceptable salt as defined herein, or the pharmaceutical composition as defined herein, for use in medicine.

The disclosure provides for the oligonucleotide or conjugate of the disclosure, for use in the treatment of a disease or disorder selected from the list comprising of Duchenne muscular dystrophy, arthritis, such as osteoarthritis, familial ischemic cerebral small-vessel disease, Alzhiemer's disease and Parkinson's disease.

In another aspect, the disclosure provides for the antisense oligonucleotide as defined herein, or the pharmaceutically acceptable salt as defined herein, or the pharmaceutical composition as defined herein, for use in the treatment or prevention of macular degeneration.

The disclosure provides for the oligonucleotide or conjugate of the disclosure, for use in the treatment of macular degeneration, such as wet or dry age related macular degeneration (e.g. wAMD, dAMD, geographic atrophy, intermediate dAMD) or diabetic retinopathy.

The disclosure provides for the use of the oligonucleotide, conjugate or composition of the disclosure, for the manufacture of a medicament for the treatment of macular degeneration, such as wet or dry age related macular degeneration (*e.g.* wAMD, dAMD, geographic atrophy, intermediate dAMD) or diabetic retinopathy.

In another aspect, the disclosure provides for use of the antisense oligonucleotide as defined herein, or the pharmaceutically acceptable salt as defined herein, or the pharmaceutical composition as defined herein, for the preparation of a medicament for treatment or prevention of macular degeneration.

The disclosure provides for the use of the oligonucleotide, conjugate or composition of the disclosure, for the manufacture of a medicament for the treatment of a disease or disorder selected from the group consisting of Duchenne muscular dystrophy, arthritis, such as osteoarthritis, familial ischemic cerebral small-vessel disease, Alzhiemer's disease and Parkinson's disease.

The disclosure provides for a method of treatment of a subject suffering from a disease or disorder selected from the group consisting of Duchenne muscular dystrophy, arthritis, such as osteoarthritis, familial ischemic cerebral small-vessel disease, Alzhiemer's disease and Parkinson's disease, said method comprising the step of administering an effective amount of the oligonucleotide, conjugate or composition of the disclosure to the subject.

The disclosure provides for a method of treatment of a subject suffering from an ocular disease, such as macular degeneration, such as wet or dry age related macular degeneration (*e.g.* wAMD, dAMD, geographic atrophy, intermediate dAMD) or diabetic retinopathy, said method comprising the step of administering an effective amount of the oligonucleotide, conjugate or composition of the disclosure to the subject.

The disclosure provides for a method of treatment of a subject suffering from an ocular disease, such as macular degeneration, such as wet or dry age related macular degeneration (*e.g.* wAMD, dAMD, geographic atrophy, intermediate dAMD) or diabetic retinopathy, said method comprising administering at least two dosages of the oligonucleotide of the disclosure, or pharmaceutically acceptable salt thereof, in an intraocular injection in a dosage of from about 10µg - 200 µg, wherein the dosage interval between administration consecutive is at least 4 weeks or at least monthly.

BRIEF DESCRIPTION OF FIGURES

Figure 1. A library of n=129 HTRA1 LNA oligonucleotides were screened in U251 and ARPE19 cell lines at 25 µM. Read out: HTRA1 qPCR. n=6 oligos located between position 33042 – 33064 were relatively active.

Figure 2. A library of n=116 HTRA1 LNA oligonucleotides in the 33042 – 33064 hot spot were screened in U251 and ARPE19 cell lines at 5 and 25 µM, respectively. n=7 oligos were selected for further analysis. Read out: HTRA1 qPCR.

Figure 3. Dose response of HTRA1 mRNA level upon treatment of human primary RPE cells with LNA oligonucleotide 139,1 and 143,1.

Figure 5. Rat *in vivo* efficacy study, 7 days of treatment, IVT administration, dose response. Retina samples from rat eyes treated with PBS, 140.1 or 143.1 were analyzed. Htra1 ISH RNAscope was performed, in A) representative samples and in B) an overview table of results are shown. GFAP IHC was also performed, GFAP is a marker for reactive gliosis and reticular fibrosis. C) Retina samples subjected to Htra1 qPCR. RE: right eye, LE: left eye. D) Oligo content bioanalysis was performed and dose response curves for bioanalysis plotted versus relative mRNA expression is shown. EC_{50} determinations was made in Graph Pad Prims. For PBS treated samples, the oligo content were set to 0.01µg/g tissue.

Figure 6. Poc study, Blue light-induced retinal degeneration in albino rats A) Recovery of electroretinogram a-wave and b-wave amplitudes 14 days after blue light exposure (%).The bars indicate group means and 95% CI. Each data point indicates mean of right and left eye values for each study animal. B) ISH RNA scope, examples from 2 different areas of the retina. C) Htra1 qPCR of retina samples. D) PK PD correlation.

Figure 7. Rat *in vivo* efficacy kinetic study, IVT administration, 50µg/eye, 3, 7, 14 days of treatment. A) HTRA1 mRNA level measured in the retina by qPCR. B) HTRA1 mRNA level quantified by ISH. The residual HTRA1 mRNA expression level is shown as % of control (PBS-treated cells) in A and B & C) Dose response curves of oligo content vs. qPCR data for individual time points.

Figure 8. Non Human Primate (NHP) PK/PD study, IVT administration, 25µg/eye. A) HTRA1 mRNA level measured in the retina by qPCR. B) HTRA1 mRNA level illustrated by ISH. C-D) Quantification of HTRA1 protein level in retina and vitreous, respectively, by IP-MS. Dots show data for individual animals. Error bars show standard deviations for technical replicates (n=3).

Figure 9. A Compound of the invention (Compound ID NO 143,1). The compound may be in the form of a pharmaceutical salt, such as a sodium salt or a potassium salt.

Figure 10. A Compound of the invention (Compound ID No 145,3). The compound may be in the form of a pharmaceutical salt, such as a sodium salt or a potassium salt.

Figure 11. An example of a pharmaceutical salt of compound 143.1. M+ is a suitable cation, typically a positive metal ion, such as a sodium or potassium ion. The stoichiometric ratio of the cation to the oligonucleotide anion will depend on the charge of the cation used. Suitably, cations with one, two or three positive charge (M^+, M^{++}, or M^{+++}, may be used). For illustrative purpose, twice as many single + charged cations (monovalent), such as Na^+ or K^+ are needed as compared to a divalent cation such as Ca^{2+}.

Figure 12. An example of a pharmaceutical salt of compound 145.3. See the figure legend for figure 11 for the description of the cation M^+.

DEFINITIONS

Oligonucleotide

The term "oligonucleotide" as used herein is defined as it is generally understood by the skilled person as a molecule comprising two or more covalently linked nucleosides. Such covalently bound nucleosides may also be referred to as nucleic acid molecules or oligomers. Oligonucleotides are commonly made in the laboratory by solid-phase chemical synthesis followed by purification. When referring to a sequence of the oligonucleotide, reference is made to the sequence or order of nucleobase moieties, or modifications thereof, of the covalently linked nucleotides or nucleosides. The oligonucleotide of the invention is man-made, and is chemically synthesized, and is typically purified or isolated. The oligonucleotide of the invention may comprise one or more modified nucleosides or nucleotides.

Antisense oligonucleotides

The term "Antisense oligonucleotide" as used herein is defined as oligonucleotides capable of modulating expression of a target gene by hybridizing to a target nucleic acid, in particular to a contiguous sequence on a target nucleic acid. The antisense oligonucleotides are not essentially double stranded and are therefore not siRNAs. Preferably, the antisense oligonucleotides of the present invention are single stranded.

Contiguous Nucleotide Region

The term "contiguous nucleotide region" refers to the region of the oligonucleotide which is complementary to the target nucleic acid. The term may be used interchangeably herein with the term "contiguous nucleotide sequence" or "contiguous nucleobase sequence" and the term "oligonucleotide motif sequence". In some embodiments all the nucleotides of the oligonucleotide are present in the contiguous nucleotide region. In some embodiments the oligonucleotide comprises the contiguous nucleotide region and may, optionally comprise further nucleotide(s), for example a nucleotide linker region which may be used to attach a functional group to the contiguous nucleotide sequence. The nucleotide linker region may or

may not be complementary to the target nucleic acid. In some embodiments the internucleoside linkages present between the nucleotides of the contiguous nucleotide region are all phosphorothioate internucleoside linkages. In some embodiments, the contiguous nucleotide region comprises one or more sugar modified nucleosides.

Nucleotides

Nucleotides are the building blocks of oligonucleotides and polynucleotides, and for the purposes of the present invention include both naturally occurring and non-naturally occurring nucleotides. In nature, nucleotides, such as DNA and RNA nucleotides comprise a ribose sugar moiety, a nucleobase moiety and one or more phosphate groups (which is absent in nucleosides). Nucleosides and nucleotides may also interchangeably be referred to as "units" or "monomers".

Modified nucleoside

The term "modified nucleoside" or "nucleoside modification" as used herein refers to nucleosides modified as compared to the equivalent DNA or RNA nucleoside by the introduction of one or more modifications of the sugar moiety or the (nucleo)base moiety. In a preferred embodiment the modified nucleoside comprise a modified sugar moiety. The term modified nucleoside may also be used herein interchangeably with the term "nucleoside analogue" or modified "units" or modified "monomers".

Modified internucleoside linkage

The term "modified internucleoside linkage" is defined as generally understood by the skilled person as linkages other than phosphodiester (PO) linkages, that covalently couples two nucleosides together. Nucleotides with modified internucleoside linkage are also termed "modified nucleotides". In some embodiments, the modified internucleoside linkage increases the nuclease resistance of the oligonucleotide compared to a phosphodiester linkage. For naturally occurring oligonucleotides, the internucleoside linkage includes phosphate groups creating a phosphodiester bond between adjacent nucleosides. Modified internucleoside linkages are particularly useful in stabilizing oligonucleotides for in vivo use, and may serve to protect against nuclease cleavage at regions of DNA or RNA nucleosides in the oligonucleotide of the invention, for example within the gap region of a gapmer oligonucleotide, as well as in regions of modified nucleosides.

In an embodiment, the oligonucleotide comprises one or more internucleoside linkages modified from the natural phosphodiester to a linkage that is for example more resistant to nuclease attack. Nuclease resistance may be determined by incubating the oligonucleotide in blood serum or by using a nuclease resistance assay (e.g. snake venom phosphodiesterase (SVPD)), both are well known in the art. Internucleoside linkages which are capable of enhancing the nuclease resistance of an oligonucleotide are referred to as nuclease resistant internucleoside

linkages. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are modified. It will be recognized that, in some embodiments the nucleosides which link the oligonucleotide of the invention to a non-nucleotide functional group, such as a conjugate, may be phosphodiester. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages.

In some embodiments the modified internucleoside linkages may be phosphorothioate internucleoside linkages. In some embodiments, the modified internucleoside linkages are compatible with the RNaseH recruitment of the oligonucleotide of the invention, for example phosphorothioate.

In some embodiments the internucleoside linkage comprises sulphur (S), such as a phosphorothioate internucleoside linkage.

A phosphorothioate internucleoside linkage is particularly useful due to nuclease resistance, beneficial pharmakokinetics and ease of manufacture. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate.

Nucleobase

The term nucleobase includes the purine (e.g. adenine and guanine) and pyrimidine (e.g. uracil, thymine and cytosine) moiety present in nucleosides and nucleotides which form hydrogen bonds in nucleic acid hybridization. In the context of the present invention the term nucleobase also encompasses modified nucleobases which may differ from naturally occurring nucleobases, but are functional during nucleic acid hybridization. In this context “nucleobase” refers to both naturally occurring nucleobases such as adenine, guanine, cytosine, thymidine, uracil, xanthine and hypoxanthine, as well as non-naturally occurring variants. Such variants are for example described in Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1.

In a some embodiments the nucleobase moiety is modified by changing the purine or pyrimidine into a modified purine or pyrimidine, such as substituted purine or substituted pyrimidine, such as a nucleobased selected from isocytosine, pseudoisocytosine, 5-methyl cytosine, 5-thiozolo-cytosine, 5-propynyl-cytosine, 5-propynyl-uracil, 5-bromouracil 5-thiazolo-uracil, 2-thio-uracil, 2’thio-thymine, inosine, diaminopurine, 6-aminopurine, 2-aminopurine, 2,6-diaminopurine and 2-chloro-6-aminopurine.

The nucleobase moieties may be indicated by the letter code for each corresponding nucleobase, e.g. A, T, G, C or U, wherein each letter may optionally include modified nucleobases of equivalent function. For example, in the exemplified oligonucleotides, the

nucleobase moieties are selected from A, T, G, C, and 5-methyl cytosine. Optionally, for LNA gapmers, 5-methyl cytosine LNA nucleosides may be used. In some embodiments, the cytosine nucleobases in a 5'cg3' motif is 5-methyl cytosine.

Modified oligonucleotide

The term modified oligonucleotide describes an oligonucleotide comprising one or more sugar-modified nucleosides and/or modified internucleoside linkages. The term chimeric" oligonucleotide is a term that has been used in the literature to describe oligonucleotides with modified nucleosides.

Complementarity

The term complementarity describes the capacity for Watson-Crick base-pairing of nucleosides/nucleotides. Watson-Crick base pairs are guanine (G)-cytosine (C) and adenine (A) - thymine (T)/uracil (U). It will be understood that oligonucleotides may comprise nucleosides with modified nucleobases, for example 5-methyl cytosine is often used in place of cytosine, and as such the term complementarity encompasses Watson Crick base-paring between non-modified and modified nucleobases (see for example Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1).

The term "% complementary" as used herein, refers to the number of nucleotides in percent of a contiguous nucleotide region or sequence in a nucleic acid molecule (e.g. oligonucleotide) which, at a given position, are complementary to (*i.e.* form Watson Crick base pairs with) a contiguous nucleotide sequence, at a given position of a separate nucleic acid molecule (e.g. the target nucleic acid). The percentage is calculated by counting the number of aligned bases that form pairs between the two sequences, dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. In such a comparison a nucleobase/nucleotide which does not align (form a base pair) is termed a mismatch.

It will be understood that when referring to complementarity between two sequences, the determination of complementarity is measured across the length of the shorter of the two sequences, such as the length of the contiguous nucleotide region or sequence.

The term "fully complementary", refers to 100% complementarity. In the absence of a % term value or indication of a mismatch, complementary means fully complementary.

Identity

The term "Identity" as used herein, refers to the number of nucleotides in percent of a contiguous nucleotide sequence in a nucleic acid molecule (e.g. oligonucleotide) which, at a given position, are identical to (*i.e.* in their ability to form Watson Crick base pairs with the complementary nucleoside) a contiguous nucleotide sequence, at a given position of a separate

nucleic acid molecule (e.g. the target nucleic acid). The percentage is calculated by counting the number of aligned bases that are identical between the two sequences, including gaps, dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. Percent Identity = (Matches x 100)/Length of aligned region (with gaps).

When determining the identity of the contiguous nucleotide region of an oligonucleotide, the identity is calculated across the length of the contiguous nucleotide region. In embodiments where the entire contiguous nucleotide sequence of the oligonucleotide is the contiguous nucleotide region, identity is therefore calculated across the length of the nucleotide sequence of the oligonucleotide. In this respect the contiguous nucleotide region may be identical to a region of the reference nucleic acid sequence, or in some embodiments may be identical to the entire reference nucleic acid. Unless otherwise indicated a sequence which has 100% identity to a reference sequence is referred to as being identical. For example, the reference sequence may be selected from the group consisting of any one of SEQ ID NOs 5 – 146 and 156. However, if the oligonucleotide comprises additional nucleotide(s) flanking the contiguous nucleotide region, for example region D' or D'', these additional flanking nucleotides may be disregarded when determining identity. In some embodiments, identity may be calculated across the entire oligonucleotide sequence.

In some embodiments, the antisense oligonucleotide oligonucleotide of the invention comprises a contiguous nucleotide region of 10 – 22 contiguous nucleotides which are identical to SEQ ID NO 156:

SEQ ID NO 156: 5' CAAATATTTACCTGGTTGTTGG 3'

In some embodiments, the contiguous nucleotide region consists or comprises of at least 10 contiguous nucleotides, such as 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, contiguous nucleotides, such as from 12-22, such as from 14-18 contiguous nucleotides of SEQ ID NO 156. In some embodiments, the entire contiguous sequence of the oligonucleotide consists or comprises of at least 10 contiguous nucleotides, such as 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, contiguous nucleotides, such as from 12-22, such as from 14-18 contiguous nucleotides of SEQ ID NO 156.

In some embodiments, the contiguous nucleotide region is at least 12 contiguous nucleotides of SEQ ID NO 156. In some embodiments, the contiguous nucleotide region is at least 14 contiguous nucleotides of SEQ ID NO 156. In some embodiments, the contiguous nucleotide region is at least 16 contiguous nucleotides SEQ ID NO 156.

In some embodiments, the contiguous nucleotide region is at least 10, 12, 14 or 16 contiguous nucleotides which are identical to SEQ ID NO 143.

In some embodiments, the contiguous nucleotide region is at least 10, 12, 14 or 16 contiguous nucleotides which are identical to SEQ ID NO 145.

In some embodiments, the contiguous nucleotide region is at least 10, 11, 12, 13, 14, 15 or 16 contiguous nucleotides which are identical to SEQ ID NO 143.

In some embodiments, the contiguous nucleotide region is at least 10, 11, 12, 13, 14, 15, 16 or 17 contiguous nucleotides which are identical to SEQ ID NO 145.

In some embodiments, the contiguous nucleotide consists or comprises SEQ ID NO 143.

In some embodiments, the contiguous nucleotide region consists or comprises SEQ ID NO 145.

In some embodiments, the contiguous nucleotide region is at least 10, 12, 14 or 16 contiguous nucleotides which are identical to a sequence selected from the group consisting of SEQ ID NO 138, 139, 140, 141, 142, 143, 144 and 145. In some embodiments, the contiguous nucleotide region comprises or consists of a sequence selected from the group consisting of SEQ ID NO 138, 139, 140, 141, 142, 143, 144 and 145.

In some embodiments the contiguous nucleotide region comprises the sequence SEQ ID NO 146: TTTACCTGGTT.

The invention provides for an antisense oligonucleotide 11 – 30 nucleotides in length, such as 12 – 20 nucleotides in length, which comprises the sequence SEQ ID NO 146: TTTACCTGGTT.

Hybridization

The term “hybridizing” or “hybridizes” as used herein is to be understood as two nucleic acid strands (e.g. an oligonucleotide and a target nucleic acid) forming hydrogen bonds between base pairs on opposite strands thereby forming a duplex. The affinity of the binding between two nucleic acid strands is the strength of the hybridization. It is often described in terms of the melting temperature (T_m) defined as the temperature at which half of the oligonucleotides are duplexed with the target nucleic acid. At physiological conditions T_m is not strictly proportional to the affinity (Mergny and Lacroix, 2003,*Oligonucleotides* 13:515–537). The standard state Gibbs free energy ΔG° is a more accurate representation of binding affinity and is related to the dissociation constant (K_d) of the reaction by $\Delta G° = -RT\ln(K_d)$, where R is the gas constant and T is the absolute temperature. Therefore, a very low ΔG° of the reaction between an oligonucleotide and the target nucleic acid reflects a strong hybridization between the oligonucleotide and target nucleic acid. ΔG° is the energy associated with a reaction where aqueous concentrations are 1M, the pH is 7, and the temperature is 37°C. The hybridization of oligonucleotides to a target nucleic acid is a spontaneous reaction and for spontaneous reactions ΔG° is less than zero. ΔG° can be measured experimentally, for example, by use of the isothermal titration calorimetry (ITC) method as described in Hansen et al., 1965,*Chem. Comm.* 36–38 and Holdgate et al., 2005, *Drug Discov Today*. The skilled person will know that commercial equipment is available for ΔG° measurements. ΔG° can also be estimated numerically by using the nearest neighbor model as described by SantaLucia, 1998, *Proc Natl*

Acad Sci USA. 95: 1460–1465 using appropriately derived thermodynamic parameters described by Sugimoto et al., 1995, *Biochemistry* 34:11211–11216 and McTigue et al., 2004, *Biochemistry* 43:5388–5405. In order to have the possibility of modulating its intended nucleic acid target by hybridization, oligonucleotides of the present invention hybridize to a target nucleic acid with estimated ΔG° values below -10 kcal for oligonucleotides that are 10-30 nucleotides in length. In some embodiments the degree or strength of hybridization is measured by the standard state Gibbs free energy ΔG°. The oligonucleotides may hybridize to a target nucleic acid with estimated ΔG° values below the range of -10 kcal, such as below -15 kcal, such as below -20 kcal and such as below -25 kcal for oligonucleotides that are 8-30 nucleotides in length. In some embodiments the oligonucleotides hybridize to a target nucleic acid with an estimated ΔG° value of -10 to -60 kcal, such as -12 to -40, such as from -15 to -30 kcal or-16 to -27 kcal such as -18 to -25 kcal.

Target Sequence

The oligonucleotide comprises a contiguous nucleotide region which is complementary to or hybridizes to a sub-sequence of the target nucleic acid molecule. The term "target sequence" as used herein refers to a sequence of nucleotides present in the target nucleic acid which comprises the nucleobase sequence which is complementary to the contiguous nucleotide region or sequence of the oligonucleotide of the invention. In some embodiments, the target sequence consists of a region on the target nucleic acid which is complementary to the contiguous nucleotide region or sequence of the oligonucleotide of the invention. In some embodiments the target sequence is longer than the complementary sequence of a single oligonucleotide, and may, for example represent a preferred region of the target nucleic acid which may be targeted by several oligonucleotides of the invention.

The oligonucleotide of the invention comprises a contiguous nucleotide region which is complementary to the target nucleic acid, such as a target sequence.

The oligonucleotide comprises a contiguous nucleotide region of at least 10 nucleotides which is complementary to or hybridizes to a target sequence present in the target nucleic acid molecule. The contiguous nucleotide region (and therefore the target sequence) comprises of at least 10 contiguous nucleotides, such as 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, contiguous nucleotides, such as from 12-22, such as from 14-18 contiguous nucleotides.

In some embodiments the target sequence is, or is present within SEQ ID NO 147.

In some embodiments the target sequence is selected from the group consisting of

SEQ ID NO 148, 149, 150, 151, 152, 153, 154 and 155:

SEQ ID NO 148: AACAACCAGGTAAATA

SEQ ID NO 149: CAACCAGGTAAATATTTG

SEQ ID NO 150: CCAACAACCAGGTAAA
SEQ ID NO 151: AACCAGGTAAATATTTGG
SEQ ID NO 152: ACAACCAGGTAAATATTTGG
SEQ ID NO 153: CAACAACCAGGTAAATAT
SEQ ID NO 154: ACAACCAGGTAAATAT
SEQ ID NO 155: AACAACCAGGTAAATAT

The invention provides for an antisense oligonucleotide of 10 – 30 nucleotides in length, wherein said antisense oligonucleotide comprises a contiguous nucleotide region of at least 10, contiguous nucleotides which are complementary to a sequence present in a sequence selected from SEQ ID NO 147 & 148 – 155.

The invention provides for an antisense oligonucleotide of 12 – 30 nucleotides in length, wherein said antisense oligonucleotide comprises a contiguous nucleotide region of at least 12 contiguous nucleotides which are complementary to a sequence present in a sequence selected from SEQ ID NO 147 & 148 – 155.

The invention provides for an antisense oligonucleotide of 14 – 30 nucleotides in length, wherein said antisense oligonucleotide comprises a contiguous nucleotide region of at least 14 contiguous nucleotides which are complementary to a sequence present in a sequence selected from SEQ ID NO 147 & 148 – 155.

The invention provides for an antisense oligonucleotide which consists or comprises a contiguous nucleotide region which is complementary to a sequence selected from SEQ ID NO 148 – 155.

The target sequence may be a sub-sequence of the target nucleic acid. In some embodiments the oligonucleotide or contiguous nucleotide region is fully complementary to, or only comprises one or two mismatches to an HTRA1 sub-sequence, such as a sequence selected from the group consisting of SEQ ID NO 148 - 154. In some embodiments the oligonucleotide or contiguous nucleotide region is fully complementary to, or only comprises one or two mismatches to an HTRA1 sub-sequence SEQ ID NO 147.

Target Cell

The term a target cell as used herein refers to a cell which is expressing the target nucleic acid. In some embodiments the target cell may be *in vivo* or *in vitro*. In some embodiments the target cell is a mammalian cell such as a rodent cell, such as a mouse cell, or a rat cell, or a primate

cell such as a monkey cell or a human cell. In some embodiments, the cell may be a pig cell, a dog cell or a rabbit cell. In some embodiments the target cell may be a retinal cell, such as a retinal pigment epithelium (PRE) cell. In some embodiments the cell is selected from the group consisting of RPE cells, Bipolar Cell, Amacrine cells, Endothelial cells, Ganglion cells and Microglia cells. For *in vitro* assessment, the target cell may be a primary cell or an established cell line, such as U251, ARPE19, HEK293, or rat C6 cells.

Target nucleic acid

According to the present invention, the target nucleic acid is a nucleic acid which encodes mammalian HTRA1 and may for example be a gene, a RNA, a mRNA, and pre-mRNA, a mature mRNA or a cDNA sequence. The target may therefore be referred to as an HTRA1 target nucleic acid.

Suitably, the target nucleic acid encodes an HTRA1 protein, in particular mammalian HTRA1, such as human HTRA1 (See for example tables 1 & 2 which provides the mRNA and pre-mRNA sequences for human and rat HTRA1).

In some embodiments, the target nucleic acid is selected from the group consisting of SEQ ID NO: 1, 2, 3, and 4, or naturally occurring variants thereof (e.g. sequences encoding a mammalian HTRA1 protein.

A target cell is a cell which is expressing the HTRA1 target nucleic acid. In preferred embodiments the target nucleic acid is the HTRA1 mRNA, such as the HTRA1 pre-mRNA or HTRA1 mature mRNA. The poly A tail of HTRA1 mRNA is typically disregarded for antisense oligonucleotide targeting.

If employing the oligonucleotide of the invention in research or diagnostics the target nucleic acid may be a cDNA or a synthetic nucleic acid derived from DNA or RNA.

The target sequence may be a sub-sequence of the target nucleic acid. In some embodiments the oligonucleotide or contiguous nucleotide region is fully complementary to, or only comprises one or two mismatches to an HTRA1 sub-sequence, such as a sequence selected from the group consisting of SEQ ID NO 148, 149, 150, 151, 152, 153, 154 and 155.

Complementarity to the target or sub-sequence thereof is measured over the length of the oligonucleotide, or contiguous nucleotide region thereof.

For *in vivo* or *in vitro* application, the oligonucleotide of the invention is typically capable of inhibiting the expression of the HTRA1 target nucleic acid in a cell which is expressing the HTRA1 target nucleic acid. The contiguous sequence of nucleobases of the oligonucleotide of the invention is typically complementary to the HTRA1 target nucleic acid, as measured across the length of the oligonucleotide, optionally with the exception of one or two mismatches, and optionally excluding nucleotide based linker regions which may link the oligonucleotide to an

optional functional group such as a conjugate, or other non-complementary terminal nucleotides (e.g. region D). The target nucleic acid may, in some embodiments, be a RNA or DNA, such as a messenger RNA, such as a mature mRNA or a pre-mRNA. In some embodiments the target nucleic acid is a RNA or DNA which encodes mammalian HTRA1 protein, such as human HTRA1, e.g. the human HTRA1 mRNA sequence, such as that disclosed as SEQ ID NO 1 (NM_002775.4, GI:190014575). Further information on exemplary target nucleic acids is provided in tables 1 & 2.

Table 1. Genome and assembly information for human and rat HTRA1.

Species	Chr.	Strand	Genomic coordinates Start	End	Assembly	NCBI reference sequence* accession number for mRNA
Human	10	fwd	122461525	122514908	GRCh38.p2 release 107	NM_002775.4
Rat	1	fwd	201499067	201548508	Rnor_6.0 release 105	NM_031721.1

Fwd = forward strand. The genome coordinates provide the pre-mRNA sequence (genomic sequence). The NCBI reference provides the mRNA sequence (cDNA sequence).

*The National Center for Biotechnology Information reference sequence database is a comprehensive, integrated, non-redundant, well-annotated set of reference sequences including genomic, transcript, and protein. It is hosted at www.ncbi.nlm.nih.gov/refseq.

Table 2. Sequence details for human and rat HTRA1.

Species	RNA type	Length (nt)	SEQ ID NO
Human	mRNA	2138	1
Human	premRNA	53384	2
Rat	mRNA	2012	3
Rat	premRNA	49442	4

Naturally occurring variant

The term “naturally occurring variant” refers to variants of HTRA1 gene or transcripts which originate from the same genetic loci as the target nucleic acid, but may differ for example, by virtue of degeneracy of the genetic code causing a multiplicity of codons encoding the same amino acid, or due to alternative splicing of pre-mRNA, or the presence of polymorphisms, such as single nucleotide polymorphisms, and allelic variants. Based on the presence of the sufficient complementary sequence to the oligonucleotide, the oligonucleotide of the invention may therefore target the target nucleic acid and naturally occurring variants thereof. In some embodiments, the naturally occurring variants have at least 95% such as at least 98% or at least 99% homology to a mammalian HTRA1 target nucleic acid, such as a target nucleic acid selected form the group consisting of SEQ ID NO 1, 2, 3, or 4.

Modulation of expression

The term "modulation of expression" as used herein is to be understood as an overall term for an oligonucleotide's ability to alter the amount of HTRA1 when compared to the amount of HTRA1 before administration of the oligonucleotide. Alternatively modulation of expression may be determined by reference to a control experiment where the oligonucleotide of the invention is not administered. One type of modulation is an oligonucleotide's ability to inhibit, down-regulate, reduce, suppress, remove, stop, block, prevent, lessen, lower, avoid or terminate expression of HTRA1, e.g. by degradation of mRNA or blockage of transcription. The antisense oligonucleotide of the invention are capable of inhibiting, down-regulating, reduce, suppress, remove, stop, block, prevent, lessen, lower, avoid or terminate expression of HTRA1.

High affinity modified nucleosides

A high affinity modified nucleoside is a modified nucleotide which, when incorporated into the oligonucleotide enhances the affinity of the oligonucleotide for its complementary target, for example as measured by the melting temperature (T^m). A high affinity modified nucleoside of the present invention preferably result in an increase in melting temperature between +0.5 to +12°C, more preferably between +1.5 to +10°C and most preferably between+3 to +8°C per modified nucleoside. Numerous high affinity modified nucleosides are known in the art and include for example, many 2' substituted nucleosides as well as locked nucleic acids (LNA) (see e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213).

Sugar modifications

The oligomer of the invention may comprise one or more nucleosides which have a modified sugar moiety, *i.e.* a modification of the sugar moiety when compared to the ribose sugar moiety found in DNA and RNA.

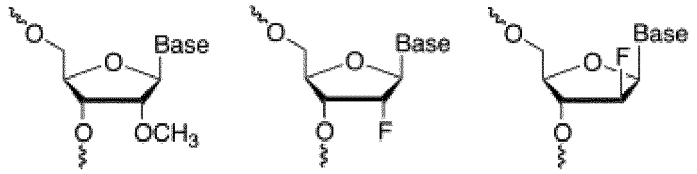
Numerous nucleosides with modification of the ribose sugar moiety have been made, primarily with the aim of improving certain properties of oligonucleotides, such as affinity and/or nuclease resistance.

Such modifications include those where the ribose ring structure is modified, *e.g.* by replacement with a hexose ring (HNA), or a bicyclic ring, which typically have a biradicle bridge between the C2 and C4 carbons on the ribose ring (LNA), or an unlinked ribose ring which typically lacks a bond between the C2 and C3 carbons (e.g. UNA). Other sugar modified nucleosides include, for example, bicyclohexose nucleic acids (WO2011/017521) or tricyclic nucleic acids (WO2013/154798). Modified nucleosides also include nucleosides where the sugar moiety is replaced with a non-sugar moiety, for example in the case of peptide nucleic acids (PNA), or morpholino nucleic acids.

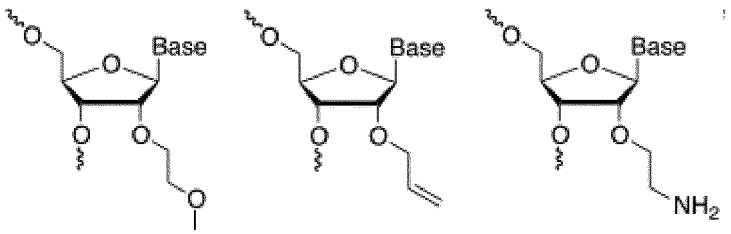
Sugar modifications also include modifications made via altering the substituent groups on the ribose ring to groups other than hydrogen, or the 2'-OH group naturally found in DNA and RNA nucleosides. Substituents may, for example be introduced at the 2', 3', 4' or 5' positions. Nucleosides with modified sugar moieties also include 2' modified nucleosides, such as 2' substituted nucleosides. Indeed, much focus has been spent on developing 2' substituted nucleosides, and numerous 2' substituted nucleosides have been found to have beneficial properties when incorporated into oligonucleotides, such as enhanced nucleoside resistance and enhanced affinity.

2' modified nucleosides.

A 2' sugar modified nucleoside is a nucleoside which has a substituent other than H or –OH at the 2' position (2' substituted nucleoside) or comprises a 2' linked biradicle, and includes 2' substituted nucleosides and LNA (2' – 4' biradicle bridged) nucleosides. For example, the 2' modified sugar may provide enhanced binding affinity and/or increased nuclease resistance to the oligonucleotide. Examples of 2' substituted modified nucleosides are 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-F-ANA nucleoside. For further examples, please see e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213, and Deleavey and Damha, Chemistry and Biology 2012, 19, 937. Below are illustrations of some 2' substituted modified nucleosides.



2′-*O*-Me 2′F-RNA 2′F-ANA

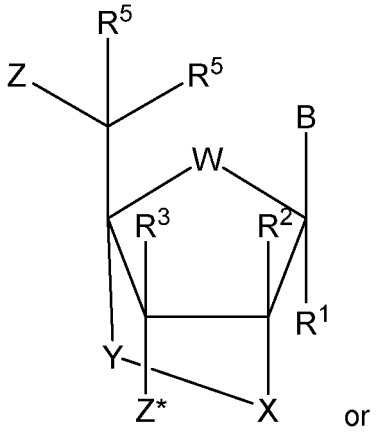


2′-*O*-MOE 2′-*O*-Allyl 2′-*O*-Ethylamine

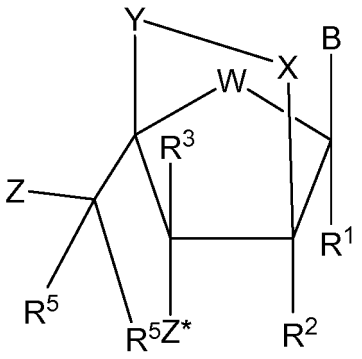
Locked Nucleic Acid Nucleosides (LNA).

LNA nucleosides are modified nucleosides which comprise a linker group (referred to as a biradicle or a bridge) between C2' and C4' of the ribose sugar ring of a nucleotide. These nucleosides are also termed bridged nucleic acid or bicyclic nucleic acid (BNA) in the literature.

In some embodiments, the modified nucleoside or the LNA nucleosides of the oligomer of the invention has a general structure of the formula I or II:



or



beta-D alpha-L

Formula I Formula II

wherein W is selected from -O-, -S-, -N(R^a)-, -C(R^aR^b)-, such as, in some embodiments –O-;

B designates a nucleobase moiety;

Z designates an internucleoside linkage to an adjacent nucleoside, or a 5'-terminal group;

Z* designates an internucleoside linkage to an adjacent nucleoside, or a 3'-terminal group;

X designates a group selected from the list consisting of -C(R^aR^b)-, -C(R^a)=C(R^b)-, -C(R^a)=N-, -O-, -Si(R^a)$_2$-, -S-, -SO_2-, -N(R^a)-, and >C=Z

In some embodiments, X is selected from the group consisting of: –O-, -S-, NH-, NR^aR^b, -CH_2-, CR^aR^b, -C(=CH_2)-, and -C(=CR^aR^b)-

In some embodiments, X is -O-

Y designates a group selected from the group consisting of -C(R^aR^b)-, -C(R^a)=C(R^b)-, -C(R^a)=N-, -O-, -Si(R^a)$_2$-, -S-, -SO_2-, -N(R^a)-, and >C=Z

In some embodiments, Y is selected from the group consisting of: –CH_2-, -C(R^aR^b)-, –CH_2CH_2-, -C(R^aR^b)-C(R^aR^b)-, –$CH_2CH_2CH_2$-, -C(R^aR^b)C(R^aR^b)C(R^aR^b)-, -C(R^a)=C(R^b)-, and -C(R^a)=N-

In some embodiments, Y is selected from the group consisting of: -CH_2-, -CHR^a-, -$CHCH_3$-, CR^aR^b-

or -X-Y- together designate a bivalent linker group (also referred to as a radicle) together designate a bivalent linker group consisting of 1, 2, or 3 groups/atoms selected from the group consisting of -C(R^aR^b)-, -C(R^a)=C(R^b)-, -C(R^a)=N-, -O-, -Si(R^a)$_2$-, -S-, -SO_2-, -N(R^a)-, and >C=Z,

In some embodiments, -X-Y- designates a biradicle selected from the groups consisting of: -X-CH_2-, -X-CR^aR^b-, -X-CHR^a-, -X-C(HCH_3)-, -O-Y-, -O-CH_2-, -S-CH_2-, -NH-CH_2-, -O-$CHCH_3$-, -CH_2-

O-CH_2, -O-CH(CH_3CH_3)-, -O-CH_2-CH_2-, OCH_2-CH_2-CH_2-,-O-CH_2OCH_2-, -O-NCH_2-, -C(=CH_2)-CH_2-, -NR^a-CH_2-, N-O-CH_2, -S-CR^aR^b- and -S-CHR^a-.

In some embodiments –X-Y- designates –O-CH_2- or –O-CH(CH_3)-.

wherein Z is selected from -O-, -S-, and -N(R^a)-,

and R^a and, when present R^b, each is independently selected from hydrogen, optionally substituted C_{1-6}-alkyl, optionally substituted C_{2-6}-alkenyl, optionally substituted C_{2-6}-alkynyl, hydroxy, optionally substituted C_{1-6}-alkoxy, C_{2-6}-alkoxyalkyl, C_{2-6}-alkenyloxy, carboxy, C_{1-6}-alkoxycarbonyl, C_{1-6}-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, mono- and di(C_{1-6}-alkyl)amino, carbamoyl, mono- and di(C_{1-6}-alkyl)-amino-carbonyl, amino-C_{1-6}-alkyl-aminocarbonyl, mono- and di(C_{1-6}-alkyl)amino-C_{1-6}-alkyl-aminocarbonyl, C_{1-6}-alkyl-carbonylamino, carbamido, C_{1-6}-alkanoyloxy, sulphono, C_{1-6}-alkylsulphonyloxy, nitro, azido, sulphanyl, C_{1-6}-alkylthio, halogen, where aryl and heteroaryl may be optionally substituted and where two geminal substituents R^a and R^b together may designate optionally substituted methylene (=CH_2), wherein for all chiral centers, asymmetric groups may be found in either *R* or *S* orientation.

wherein R^1, R^2, R^3, R^5 and R^{5*} are independently selected from the group consisting of: hydrogen, optionally substituted C_{1-6}-alkyl, optionally substituted C_{2-6}-alkenyl, optionally substituted C_{2-6}-alkynyl, hydroxy, C_{1-6}-alkoxy, C_{2-6}-alkoxyalkyl, C_{2-6}-alkenyloxy, carboxy, C_{1-6}-alkoxycarbonyl, C_{1-6}-alkylcarbonyl, formyl, aryl, aryloxy-carbonyl, aryloxy, arylcarbonyl, heteroaryl, heteroaryloxy-carbonyl, heteroaryloxy, heteroarylcarbonyl, amino, mono- and di(C_{1-6}-alkyl)amino, carbamoyl, mono- and di(C_{1-6}-alkyl)-amino-carbonyl, amino-C_{1-6}-alkyl-aminocarbonyl, mono- and di(C_{1-6}-alkyl)amino-C_{1-6}-alkyl-aminocarbonyl, C_{1-6}-alkyl-carbonylamino, carbamido, C_{1-6}-alkanoyloxy, sulphono, C_{1-6}-alkylsulphonyloxy, nitro, azido, sulphanyl, C_{1-6}-alkylthio, halogen, where aryl and heteroaryl may be optionally substituted, and where two geminal substituents together may designate oxo, thioxo, imino, or optionally substituted methylene.

In some embodiments R^1, R^2, R^3, R^5 and R^{5*} are independently selected from C_{1-6} alkyl, such as methyl, and hydrogen.

In some embodiments R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen.

In some embodiments R^1, R^2, R^3, are all hydrogen, and either R^5 and R^{5*} is also hydrogen and the other of R^5 and $R^{5*}$is other than hydrogen, such as C_{1-6} alkyl such as methyl.

In some embodiments, R^a is either hydrogen or methyl. In some embodiments, when present, R^b is either hydrogen or methyl.

In some embodiments, one or both of R^a and R^b is hydrogen

In some embodiments, one of R^a and R^b is hydrogen and the other is other than hydrogen

In some embodiments, one of R^a and R^b is methyl and the other is hydrogen

In some embodiments, both of R^a and R^b are methyl.

In some embodiments, the biradicle –X-Y- is –O-CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such LNA nucleosides are disclosed in WO99/014226, WO00/66604, WO98/039352 and WO2004/046160 which are all hereby incorporated by reference, and include what are commonly known as beta-D-oxy LNA and alpha-L-oxy LNA nucleosides.

In some embodiments, the biradicle –X-Y- is –S-CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such thio LNA nucleosides are disclosed in WO99/014226 and WO2004/046160 which are hereby incorporated by reference.

In some embodiments, the biradicle –X-Y- is –NH-CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such amino LNA nucleosides are disclosed in WO99/014226 and WO2004/046160 which are hereby incorporated by reference.

In some embodiments, the biradicle –X-Y- is –O-CH_2-CH_2- or –O-CH_2-CH_2- CH_2-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such LNA nucleosides are disclosed in WO00/047599 and Morita et al, Bioorganic & Med.Chem. Lett. 12 73-76, which are hereby incorporated by reference, and include what are commonly known as 2'-O-4'C-ethylene bridged nucleic acids (ENA).

In some embodiments, the biradicle –X-Y- is –O-CH_2-, W is O, and all of R^1, R^2, R^3, and one of R^5 and R^{5*} are hydrogen, and the other of R^5 and R^{5*} is other than hydrogen such as C_{1-6} alkyl, such as methyl. Such 5' substituted LNA nucleosides are disclosed in WO2007/134181 which is hereby incorporated by reference.

In some embodiments, the biradicle –X-Y- is –O-CR^aR^b-, wherein one or both of R^a and R^b are other than hydrogen, such as methyl, W is O, and all of R^1, R^2, R^3, and one of R^5 and R^{5*} are hydrogen, and the other of R^5 and R^{5*} is other than hydrogen such as C_{1-6} alkyl, such as methyl. Such bis modified LNA nucleosides are disclosed in WO2010/077578 which is hereby incorporated by reference.

In some embodiments, the biradicle –X-Y- designate the bivalent linker group –O-$CH(CH_2OCH_3)$- (2' O-methoxyethyl bicyclic nucleic acid - Seth at al., 2010, J. Org. Chem. Vol 75(5) pp. 1569-81). In some embodiments, the biradicle –X-Y- designate the bivalent linker group –O-$CH(CH_2CH_3)$- (2'O-ethyl bicyclic nucleic acid - Seth at al., 2010, J. Org. Chem. Vol 75(5) pp. 1569-81). In some embodiments, the biradicle –X-Y- is –O-CHR^a-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such 6' substituted LNA nucleosides are disclosed in WO10036698 and WO07090071 which are both hereby incorporated by reference.

In some embodiments, the biradicle –X-Y- is –O-CH(CH_2OCH_3)-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such LNA nucleosides are also known as cyclic MOEs in the art (cMOE) and are disclosed in WO07090071.

In some embodiments, the biradicle –X-Y- designate the bivalent linker group –O-CH(CH_3)-. – in either the R- or S- configuration. In some embodiments, the biradicle –X-Y- together designate the bivalent linker group –O-CH_2-O-CH_2- (Seth at al., 2010, J. Org. Chem). In some embodiments, the biradicle –X-Y- is –O-CH(CH_3)-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such 6' methyl LNA nucleosides are also known as cET nucleosides in the art, and may be either (S)cET or (R)cET stereoisomers, as disclosed in WO07090071 (beta-D) and WO2010/036698 (alpha-L) which are both hereby incorporated by reference).

In some embodiments, the biradicle –X-Y- is –O-CR^aR^b-, wherein in neither R^a or R^b is hydrogen, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments, R^a and R^b are both methyl. Such 6' di-substituted LNA nucleosides are disclosed in WO 2009006478 which is hereby incorporated by reference.

In some embodiments, the biradicle –X-Y- is –S-CHR^a-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such 6' substituted thio LNA nucleosides are disclosed in WO11156202 which is hereby incorporated by reference. In some 6' substituted thio LNA embodiments R^a is methyl.

In some embodiments, the biradicle –X-Y- is –C(=CH2)-C(R^aR^b)-, such as –C(=CH_2)-CH_2- , or –C(=CH_2)-CH(CH_3)-W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. Such vinyl carbo LNA nucleosides are disclosed in WO08154401 and WO09067647 which are both hereby incorporated by reference.

In some embodiments the biradicle –X-Y- is –N(-OR^a)-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl. Such LNA nucleosides are also known as N substituted LNAs and are disclosed in WO2008/150729 which is hereby incorporated by reference. In some embodiments, the biradicle –X-Y- together designate the bivalent linker group –O-NR^a-CH_3- (Seth at al., 2010, J. Org. Chem). In some embodiments the biradicle –X-Y- is –N(R^a)-, W is O, and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl.

In some embodiments, one or both of R^5 and R^{5*} is hydrogen and, when substituted the other of R^5 and R^{5*} is C_{1-6} alkyl such as methyl. In such an embodiment, R^1, R^2, R^3, may all be hydrogen, and the biradicle –X-Y- may be selected from –O-CH2- or –O-C(HCR^a)-, such as –O-C(HCH3)-.

In some embodiments, the biradicle is –CR^aR^b-O-CR^aR^b-, such as CH_2-O-CH_2-, W is O and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl.

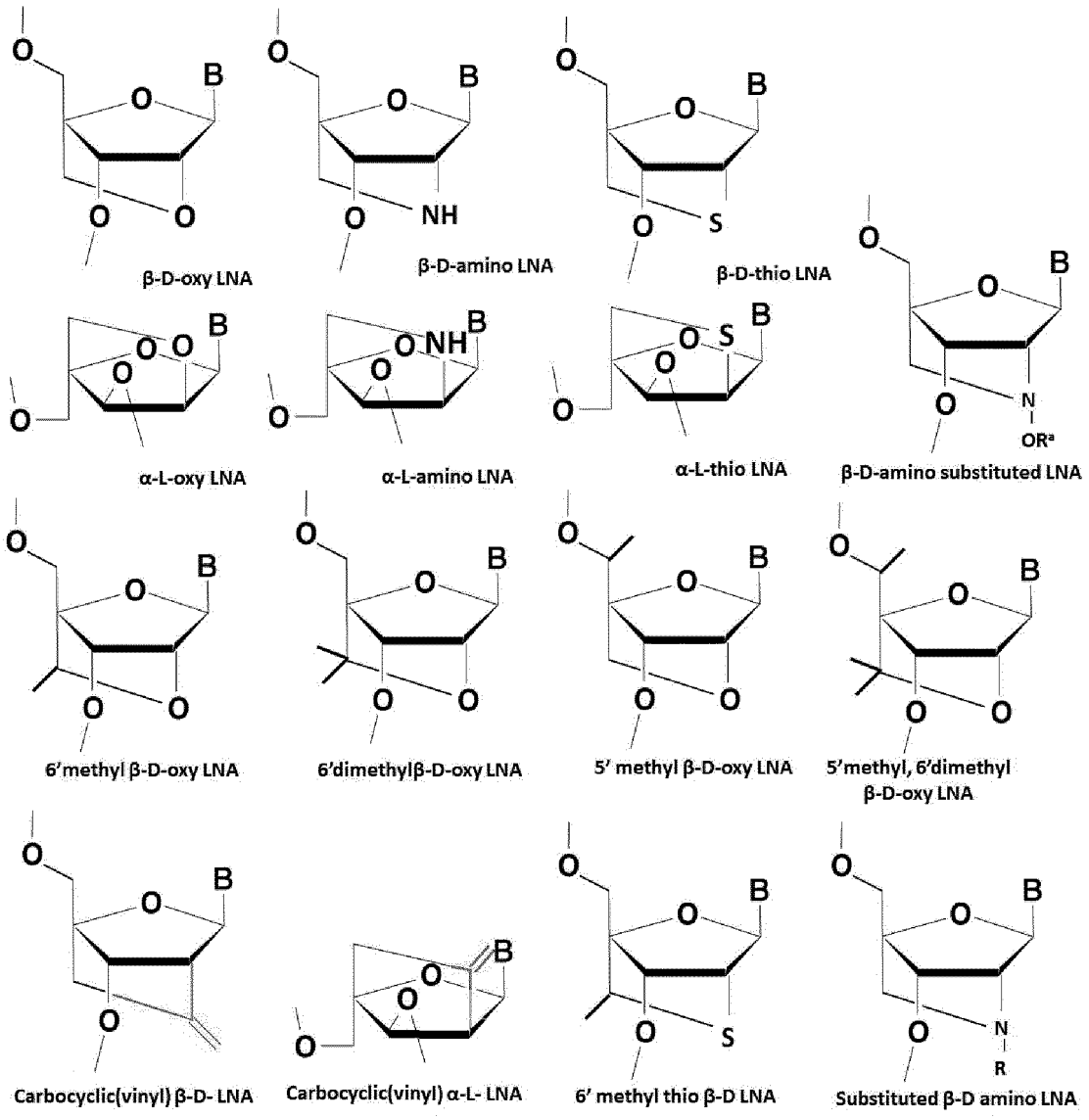
Such LNA nucleosides are also known as conformationally restricted nucleotides (CRNs) and are disclosed in WO2013036868 which is hereby incorporated by reference.

In some embodiments, the biradicle is $–O-CR^aR^b-O-CR^aR^b-$, such as $O-CH_2-O-CH_2-$, W is O and all of R^1, R^2, R^3, R^5 and R^{5*} are all hydrogen. In some embodiments R^a is C_{1-6} alkyl such as methyl. Such LNA nucleosides are also known as COC nucleotides and are disclosed in Mitsuoka et al., Nucleic Acids Research 2009 37(4), 1225-1238, which is hereby incorporated by reference.

It will be recognized than, unless specified, the LNA nucleosides may be in the beta-D or alpha-L stereoisoform.

Examples of LNA nucleosides are presented in Scheme 1.

Scheme 1



As illustrated in the examples, in some embodiments of the invention the LNA nucleosides in the oligonucleotides are beta-D-oxy-LNA nucleosides.

Nuclease mediated degradation

Nuclease mediated degradation refers to an oligonucleotide capable of mediating degradation of a complementary nucleotide sequence when forming a duplex with such a sequence.

In some embodiments, the oligonucleotide may function via nuclease mediated degradation of the target nucleic acid, where the oligonucleotides of the invention are capable of recruiting a nuclease, particularly and endonuclease, preferably endoribonuclease (RNase), such as RNase H. Examples of oligonucleotide designs which operate via nuclease mediated mechanisms are oligonucleotides which typically comprise a region of at least 5 or 6 DNA nucleosides and are flanked on one side or both sides by affinity enhancing nucleosides, for example gapmers, headmers and tailmers.

RNase H Activity and Recruitment

The RNase H activity of an antisense oligonucleotide refers to its ability to recruit RNase H when in a duplex with a complementary RNA molecule. WO01/23613 provides *in vitro* methods for determining RNaseH activity, which may be used to determine the ability to recruit RNaseH. Typically an oligonucleotide is deemed capable of recruiting RNase H if it, when provided with a complementary target nucleic acid sequence, has an initial rate, as measured in pmol/l/min, of at least 5%, such as at least 10% or more than 20% of the of the initial rate determined when using a oligonucleotide having the same base sequence as the modified oligonucleotide being tested, but containing only DNA monomers, with phosphorothioate linkages between all monomers in the oligonucleotide, and using the methodology provided by Example 91 - 95 of WO01/23613 (hereby incorporated by reference).

Gapmer

The term gapmer as used herein refers to an antisense oligonucleotide which comprises a region of RNase H recruiting oligonucleotides (gap) which is flanked 5' and 3' by regions which comprise one or more affinity enhancing modified nucleosides (flanks or wings). Various gapmer designs are described herein. Headmers and tailmers are oligonucleotides capable of recruiting RNase H where one of the flanks is missing, *i.e.* only one of the ends of the oligonucleotide comprises affinity enhancing modified nucleosides. For headmers the 3' flank is missing (i.e. the 5' flank comprises affinity enhancing modified nucleosides) and for tailmers the 5' flank is missing (i.e. the 3' flank comprises affinity enhancing modified nucleosides).

LNA Gapmer

The term LNA gapmer is a gapmer oligonucleotide wherein at least one of the affinity enhancing modified nucleosides is an LNA nucleoside.

Mixed Wing Gapmer

The term mixed wing gapmer refers to a LNA gapmer wherein the flank regions comprise at least one LNA nucleoside and at least one non-LNA modified nucleoside, such as at least one DNA nucleoside or at least one 2' substituted modified nucleoside, such as, for example, 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA and 2'-F-ANA nucleoside(s). In some embodiments the mixed wing gapmer has one flank which comprises LNA nucleosides (e.g. 5' or 3') and the other flank (3' or 5' respectfully) comprises 2' substituted modified nucleoside(s).

Conjugate

The term conjugate as used herein refers to an oligonucleotide which is covalently linked to a non-nucleotide moiety (conjugate moiety or region C or third region).

The term conjugate as used herein refers to an oligonucleotide which is covalently linked to a non-nucleotide moiety (conjugate moiety or region C or third region).

In some embodiments, the non-nucleotide moiety selected from the group consisting of a protein, such as an enzyme, an antibody or an antibody fragment or a peptide; a lipophilic moiety such as a lipid, a phospholipid, a sterol; a polymer, such as polyethyleneglycol or polypropylene glycol; a receptor ligand; a small molecule; a reporter molecule; and a non-nucleosidic carbohydrate.

Linkers

A linkage or linker is a connection between two atoms that links one chemical group or segment of interest to another chemical group or segment of interest via one or more covalent bonds. Conjugate moieties can be attached to the oligonucleotide directly or through a linking moiety (e.g. linker or tether). Linkers serve to covalently connect a third region, e.g. a conjugate moiety to an oligonucleotide (e.g. the termini of region A or C).

In some embodiments of the invention the conjugate or oligonucleotide conjugate of the invention may optionally, comprise a linker region which is positioned between the oligonucleotide and the conjugate moiety. In some embodiments, the linker between the conjugate and oligonucleotide is biocleavable.

Biocleavable linkers comprising or consisting of a physiologically labile bond that is cleavable under conditions normally encountered or analogous to those encountered within a mammalian body. Conditions under which physiologically labile linkers undergo chemical transformation (e.g., cleavage) include chemical conditions such as pH, temperature, oxidative or reductive conditions or agents, and salt concentration found in or analogous to those encountered in mammalian cells. Mammalian intracellular conditions also include the presence of enzymatic activity normally present in a mammalian cell such as from proteolytic enzymes or hydrolytic enzymes or nucleases. In one embodiment the biocleavable linker is susceptible to S1 nuclease

cleavage. In a preferred embodiment the nuclease susceptible linker comprises between 1 and 10 nucleosides, such as 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 nucleosides, more preferably between 2 and 6 nucleosides and most preferably between 2 and 4 linked nucleosides comprising at least two consecutive phosphodiester linkages, such as at least 3 or 4 or 5 consecutive phosphodiester linkages. Preferably the nucleosides are DNA or RNA. Phosphodiester containing biocleavable linkers are described in more detail in WO 2014/076195 (hereby incorporated by reference), and may be refered to as region D herein.

Conjugates may also be linked to the oligonucleotide via non biocleavable linkers, or in some embodiments the conjugate may comprise a non-cleavable linker which is covalently attached to the biocleavable linker. Linkers that are not necessarily biocleavable but primarily serve to covalently connect a conjugate moiety to an oligonucleotide or biocleavable linker. Such linkers may comprise a chain structure or an oligomer of repeating units such as ethylene glycol, amino acid units or amino alkyl groups. In some embodiments the linker (region Y) is an amino alkyl, such as a C_2 – C_{36} amino alkyl group, including, for example C_6 to C_{12} amino alkyl groups. In some embodiments the linker (region Y) is a C_6 amino alkyl group. Conjugate linker groups may be routinely attached to an oligonucleotide via use of an amino modified oligonucleotide, and an activated ester group on the conjugate group.

Treatment

The term 'treatment' as used herein refers to both treatment of an existing disease (*e.g.* a disease or disorder as herein referred to), or prevention of a disease, *i.e.* prophylaxis. It will therefore be recognized that treatment as referred to herein may, in some embodiments, be prophylactic.

DETAILED DESCRIPTION OF THE INVENTION

The Oligonucleotides of the Invention

The invention relates to oligonucleotides capable of inhibiting the expression of HTRA1. The modulation is may achieved by hybridizing to a target nucleic acid encoding HTRA1 or which is involved in the regulation of HTRA1. The target nucleic acid may be a mammalian HTRA 1 sequence, such as a sequence selected from the group consisting of SEQ ID 1, 2, 3 or 4.

The oligonucleotide of the invention is an antisense oligonucleotide which targets HTRA1, such as a mammalian HTRA1.

In some embodiments the antisense oligonucleotide of the invention is capable of modulating the expression of the target by inhibiting or down-regulating it. Preferably, such modulation produces an inhibition of expression of at least 20% compared to the normal expression level of the target, such as at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% inhibition compared to the

normal expression level of the target. In some embodiments compounds of the invention may be capable of inhibiting expression levels of HTRA1 mRNA by at least 60% or 70% in vitro using ARPE-19 cells. In some embodiments compounds of the invention may be capable of inhibiting expression levels of *HTRA1* mRNA by at least 60% or 70% *in vitro* using ARPE-19 cells. In some embodiments compounds of the invention may be capable of inhibiting expression levels of HTRA1 protein by at least 50% in vitro using ARPE-19 cells. Suitably, the examples provide assays which may be used to measure HTRA1 RNA or protein inhibition (e.g. example 3). The target modulation is triggered by the hybridization between a contiguous nucleotide sequence of the oligonucleotide and the target nucleic acid. In some embodiments the oligonucleotide of the invention comprises mismatches between the oligonucleotide and the target nucleic acid. Despite mismatches hybridization to the target nucleic acid may still be sufficient to show a desired modulation of HTRA1 expression. Reduced binding affinity resulting from mismatches may advantageously be compensated by increased number of nucleotides in the oligonucleotide and/or an increased number of modified nucleosides capable of increasing the binding affinity to the target, such as 2' modified nucleosides, including LNA, present within the oligonucleotide sequence.

An aspect of the present invention relates to an antisense oligonucleotide which comprises a contiguous nucleotide region of 10 to 30 nucleotides in length with at least 90% complementarity to HTRA1 target sequence, such as fully complementary to an HTRA1 target sequence, e.g. a nucleic acid selected from the group consisting SEQ ID NO 1, 2, 3 & 4.

In some embodiments, the oligonucleotide comprises a contiguous sequence which is at least 90% complementary, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, or 100% complementary with a region of the target nucleic acid.

In some embodiments, the oligonucleotide of the invention, or a contiguous nucleotide sequence thereof is fully complementary (100% complementary) to a region of the target nucleic acid, or in some embodiments may comprise one or two mismatches between the oligonucleotide and the target nucleic acid.

In some embodiments the oligonucleotide, or a contiguous nucleotide sequence of at least 12 nucleotides thereof, is at least 90% complementary, such as fully (or 100%) complementary to a region of SEQ ID NO 147.

In some embodiments the oligonucleotide, or a contiguous nucleotide sequence of at least 12 nucleotides thereof, is at least 90% complementary, such as fully (or 100%) complementary to a region of a sequence selected from the group consisting of SEQ ID NOs 148, 149, 150, 151, 152, 153, 154 and 155.

In some embodiments the oligonucleotide, or a contiguous nucleotide sequence of at least 14 nucleotides thereof, is fully (or 100%) complementary to SEQ ID 147, or a sequence selected from the group consisting of SEQ ID NOs 148, 149, 150, 151, 152, 153, 154 and 155.

In some embodiments the oligonucleotide, or a contiguous nucleotide sequence of at least 16 nucleotides thereof, is fully (or 100%) complementary to SEQ ID 147, or a sequence selected from the group consisting of SEQ ID NOs 148, 149, 150, 151, 152, 153, 154 and 155.

In some embodiments the oligonucleotide, or contiguous nucleotide region thereof is fully (or 100%) complementary to a sequence selected from the group consisting of SEQ ID NOs 148, 149, 150, 151, 152, 153, 154 and 155.

In some embodiments, the oligonucleotide or contiguous nucleotide region thereof comprises or consists of a sequence selected from the group consisting of SEQ ID NOs 143, 138, 139, 140, 141, 142, 144 and 145:

SEQ ID NO 143: TATTTACCTGGTTGTT
SEQ ID NO 138: CAAATATTTACCTGGTTG
SEQ ID NO 139: TTTACCTGGTTGTTGG
SEQ ID NO 140: CCAAATATTTACCTGGTT
SEQ ID NO 141: CCAAATATTTACCTGGTTGT
SEQ ID NO 142: ATATTTACCTGGTTGTTG
SEQ ID NO 144: ATATTTACCTGGTTGT
SEQ ID NO 145: ATATTTACCTGGTTGTT

It is understood that the oligonucleotide motif sequences can be modified to for example increase nuclease resistance and/or binding affinity to the target nucleic acid. Modifications are described in the definitions and in the “Oligonucleotide design” section.

In some embodiments, the oligonucleotide of the invention, or contiguous nucleotide region thereof is fully complementary (100% complementary) to a region of the target nucleic acid, or in some embodiments may comprise one or two mismatches between the oligonucleotide and the target nucleic acid. In some embodiments the oligonucleotide, or contiguous nucleotide sequence of at least 12 nucleotides thereof, is at least 90% complementary, such as fully (or 100%) complementary to the target nucleic acid sequence.

In some embodiments the oligonucleotide, or a contiguous nucleotide sequence of at least 12 nucleotides thereof, has 100% identity to a sequence selected from the group consisting of SEQ ID NOs 5 – 107, or SEQ ID NOs 108 – 137.

In some embodiments the oligonucleotide, or a contiguous nucleotide sequence of at least 14 nucleotides thereof, has 100% identity to a sequence selected from the group consisting of SEQ ID NOs 5 – 107, or SEQ ID NOs 108 – 137.

In some embodiments the oligonucleotide, or contiguous nucleotide sequence of at least 16 nucleotides thereof, has 100% identity to a sequence selected from the group consisting of SEQ ID NOs 5 – 107, or SEQ ID NOs 108 – 137.

In some embodiments the oligonucleotide, or contiguous nucleotide region thereof, comprises or consists of a sequence selected from SEQ ID NOs 5 – 107, or SEQ ID NOs 108 – 137.

In some embodiments the compound of the invention is selected from the group consisting of:

SEQ ID NO	Compound ID #	
138	138,1	$^{m}C_sA_sA_sA_st_sa_st_st_st_sa_sc_sc_st_sg_sG_sT_sT_sG$
139	139,1	$T_sT_st_sa_sc_sc_st_sg_sg_st_st_sg_st_sT_sG_sG$
140	140,1	$^{m}C_s{}^{m}C_sA_sA_sa_st_sa_st_st_st_sa_sc_sc_st_sg_sG_sT_sT$
141	141,1	$^{m}C_s{}^{m}C_sA_sa_sa_st_sa_st_st_st_sa_sc_sc_st_sg_sg_st_st_sG_sT$
142	142,1	$A_sT_sA_st_st_st_sa_sc_sc_st_sg_sg_st_st_sg_sT_sT_sG$
143	143,1	$T_sA_sT_st_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT_sT$
143	143,2	$T_sA_st_st_st_sa_sc_sc_st_sg_sG_st_sT_sg_sT_sT$
143	143,3	$T_sA_sT_st_st_sa_sc_sc_st_sg_sg_sT_sT_sg_sT_sT$
144	144,1	$A_sT_sA_sT_st_st_sa_sc_sc_st_sg_sg_sT_sT_sG_sT$
144	144,2	$A_st_sA_sT_sT_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT$
145	145,1	$A_st_sA_sT_st_st_sa_sc_sc_st_sg_sG_sT_sT_sg_sT_sT$
145	145,2	$A_sT_sA_st_st_st_sa_sc_sc_st_sg_sG_st_sT_sg_sT_sT$
145	145,3	$A_st_sA_sT_st_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT_sT$

Wherein capital letters represent beta-D-oxy LNA nucleosides, all LNA cytosines are 5-methyl cytosine (as indicated by the superscript ^{m}), lower case letters represent DNA nucleosides. All internucleoside linkages are phosphorothioate internucleoside linkages (as indicated by the subscript $_s$).

Oligonucleotide design

Oligonucleotide design refers to the pattern of nucleoside sugar modifications in the oligonucleotide sequence. The oligonucleotides of the invention comprise sugar-modified nucleosides and may also comprise DNA or RNA nucleosides. In some embodiments, the oligonucleotide comprises sugar-modified nucleosides and DNA nucleosides. Incorporation of modified nucleosides into the oligonucleotide of the invention may enhance the affinity of the oligonucleotide for the target nucleic acid. In that case, the modified nucleosides can be referred to as affinity enhancing modified nucleotides.

In an embodiment, the oligonucleotide comprises at least 1 modified nucleoside, such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15 or at least 16 modified nucleosides. In

an embodiment the oligonucleotide comprises from 1 to 10 modified nucleosides, such as from 2 to 9 modified nucleosides, such as from 3 to 8 modified nucleosides, such as from 4 to 7 modified nucleosides, such as 6 or 7 modified nucleosides. In an embodiment, the oligonucleotide of the invention may comprise modifications, which are independently selected from these three types of modifications (modified sugar, modified nucleobase and modified internucleoside linkage) or a combination thereof. Preferably the oligonucleotide comprises one or more sugar modified nucleosides, such as 2' sugar modified nucleosides. Preferably the oligonucleotide of the invention comprise the one or more 2' sugar modified nucleoside independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides. Even more preferably the the one or more modified nucleoside is LNA.

In some embodiments, at least 1 of the modified nucleosides is a locked nucleic acid (LNA), such as at least 2, such as at least 3, at least 4, at least 5, at least 6, at least 7, or at least 8 of the modified nucleosides are LNA. In a still further embodiment all the modified nucleosides are LNA.

In a further embodiment the oligonucleotide comprises at least one modified internucleoside linkage. In a preferred embodiment the the internucleoside linkages within the contiguous nucleotide sequence are phosphorothioate or boranophosphate internucleoside linkages. In some embodiments all the internucleotide linkages in the contiguous sequence of the oligonucleotide are phosphorothioate linkages.

In some embodiments, the oligonucleotide of the invention comprise at least one modified nucleoside which is a 2'-MOE-RNA, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 2'-MOE-RNA nucleoside units. In some embodiments, at least one of said modified nucleoside is 2'-fluoro DNA, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 2'-fluoro-DNA nucleoside units.

In some embodiments, the oligonucleotide of the invention comprises at least one LNA unit, such as 1, 2, 3, 4, 5, 6, 7, or 8 LNA units, such as from 2 to 6 LNA units, such as from 3 to 7 LNA units, 4 to 8 LNA units or 3, 4, 5, 6 or 7 LNA units. In some embodiments, all the modified nucleosides are LNA nucleosides. In some embodiments, all LNA cytosine units are 5-methyl-cytosine. In some embodiments the oligonucleotide or contiguous nucleotide region thereof has at least 1 LNA unit at the 5' end and at least 2 LNA units at the 3' end of the nucleotide sequence. In some embodiments all cytosine nucleobases present in the oligonucleotide of the invention are 5-methyl-cytosine.

In some embodiments, the oligonucleotide of the invention comprises at least one LNA unit and at least one 2' substituted modified nucleoside.

In some embodiments of the invention, the oligonucleotide comprise both 2' sugar modified nucleosides and DNA units.

In an embodiment of the invention the oligonucleotide of the invention is capable of recruiting RNase H.

In some embodiments, the oligonucleotide of the invention or contiguous nucleotide region thereof is a gapmers oligonucleotide.

Gapmer design

In some embodiments the oligonucleotide of the invention, or contiguous nucleotide region thereof, has a gapmer design or structure also referred herein merely as "Gapmer". In a gapmer structure the oligonucleotide comprises at least three distinct structural regions a 5'-flank, a gap and a 3'-flank, F-G-F' in '5 -> 3' orientation. In this design, flanking regions F and F' (also termed wing regions) comprise at least one sugar modified nucleoside which is adjacent to region G, and may in some embodiments comprise a contiguous stretch of 2 – 7 sugar modified nucleoside, or a contiguous stretch of sugar modified and DNA nucleosides (mixed wings comprising both sugar modified and DNA nucleosides). Consequently, the nucleosides of the 5' flanking region and the 3' flanking region which are adjacent to the gap region are sugar modified nucleosides, such as 2' modified nucleosides. The gap region, G, comprises a contiguous stretch of nucleotides which are capable of recruiting RNase H, when the oligonucleotide is in duplex with the HTRA1target nucleic acid. In some embodiments, region G comprises a contiguous stretch of 5 – 16 DNA nucleosides. The gapmer region F-G-F' is complementary to the HTRA1 target nucleic acid, and may therefore be the contiguous nucleotide region of the oligonucleotide.

Regions F and F', flanking the 5' and 3' ends of region G, may comprise one or more affinity enhancing modified nucleosides. In some embodiments, the 3' flank comprises at least one LNA nucleoside, preferably at least 2 LNA nucleosides. In some embodiments, the 5' flank comprises at least one LNA nucleoside. In some embodiments both the 5' and 3' flanking regions comprise a LNA nucleoside. In some embodiments all the nucleosides in the flanking regions are LNA nucleosides. In other embodiments, the flanking regions may comprise both LNA nucleosides and other nucleosides (mixed flanks), such as DNA nucleosides and/or non-LNA modified nucleosides, such as 2' substituted nucleosides. In this case the gap is defined as a contiguous sequence of at least 5 RNase H recruiting nucleosides (such as 5 – 16 DNA nucleosides) flanked at the 5' and 3' end by an affinity enhancing modified nucleoside, such as an LNA, such as beta-D-oxy-LNA.

Region F

Region F (5' flank or 5' wing) attached to the '5 end of region G comprises, contains or consists of at least one sugar modified nucleoside such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7 modified nucleosides. In some embodiments region F comprises or consists of from 1 to 7 modified nucleosides, such as from 2 to 6 modified nucleosides, such as from 2 to 5 modified nucleosides, such as from 2 to 4 modified nucleosides, such as from 1 to 3 modified nucleosides, such as 1, 2, 3 or 4 modified nucleosides.

In an embodiment, one or more or all of the modified nucleosides in region F are 2' modified nucleosides.

In a further embodiment one or more of the 2' modified nucleosides in region F are selected from 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, LNA units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units.

In one embodiment of the invention all the modified nucleosides in region F are LNA nucleosides. In a further embodiment the LNA nucleosides in region F are independently selected from the group consisting of oxy-LNA, thio-LNA, amino-LNA, cET, and/or ENA, in either the beta-D or alpha-L configurations or combinations thereof. In a preferred embodiment region F has at least 1 beta-D-oxy LNA unit, at the 5' end of the contiguous sequence.

Region G

Region G (gap region) may comprise, contain or consist of at 5 - 16 consecutive DNA nucleosides capable of recruiting RNaseH. In a further embodiment region G comprise, contain or consist of from 5 to 12, or from 6 to 10 or from 7 to 9, such as 8 consecutive nucleotide units capable of recruiting RNaseH.

In a still further embodiment at least one nucleoside unit in region G is a DNA nucleoside unit, such as from 4 to 20 or or 6 to 18 DNA units, such as 5 to 16, In some embodiments, all of the nucleosides of region G are DNA units.

In further embodiments the region G may consist of a mixture of DNA and other nucleosides capable of mediating RNase H cleavage. In some embodiments, at least 50% of the nucleosides of region G are DNA, such as at least 60 %, at least 70% or at least 80 %, or at least 90% DNA.

Region F'

Region F' (3' flank or 3' wing) attached to the '3 end of region G comprises, contains or consists of at least one sugar modified nucleoside such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7 modified nucleosides. In some embodiments region F' comprises or consists of from 1 to 7 modified nucleosides, such as from 2 to 6 modified nucleosides, such as from 2 to

5 modified nucleosides, such as from 2 to 4 modified nucleosides, such as from 1 to 3 modified nucleosides, such as 1, 2, 3 or 4 modified nucleosides.

In an embodiment, one or more or all of the modified nucleosides in region F' are 2' modified nucleosides.

In a further embodiment one or more of the 2' modified nucleosides in region F' are selected from 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, LNA units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units.

In one embodiment of the invention all the modified nucleosides in region F' are LNA nucleosides. In a further embodiment the LNA nucleosides in region F' are independently selected from the group consisting of oxy-LNA, thio-LNA, amino-LNA, cET, and/or ENA, in either the beta-D or alpha-L configurations or combinations thereof. In a preferred embodiment region F' has at least 1 beta-D-oxy LNA unit, at the 5' end of the contiguous sequence.

Region D, D' and D''

The oligonucleotide of the invention ncomprises a contiguous nucleotide region which is complementary to the target nucleic acid. In some embodiments, the oligonucleotide may further comprise additional nucleotides positioned 5' and/or 3' to the contiguous nucleotide region, which are referred to as region D herein. Region D' and D'' can be attached to the 5' end of region F or the 3' end of region F', respectively. The D regions (region D' or D'') may in some embodiments form part of the contiguous nucleotide sequence which is complementary to the target nucleic acid, or in other embodiments the D region(s) may be non-complementary to the target nucleic acid.

In some embodiments the oligonucleotide of the invention consists or comprises of the contiguous nucleotide region and optionally 1 – 5 additional 5' nucleotides (region D').

In some embodiments the oligonucleotide of the invention consists or comprises of the contiguous nucleotide region and optionally 1 – 5 additional 3' nucleotides (region D'').

Region D' or D'' may independently comprise 1, 2, 3, 4 or 5 additional nucleotides, which may be complementary or non-complementary to the target nucleic acid. In this respect the oligonucleotide of the invention, may in some embodiments comprise a contiguous nucleotide sequence capable of modulating the target which is flanked at the 5' and/or 3' end by additional nucleotides. Such additional nucleotides may serve as a nuclease susceptible biocleavable linker, and may therefore be used to attach a functional group such as a conjugate moiety to the oligonucleotide of the invention. In some embodiments the additional 5' and/or 3' end nucleotides are linked with phosphodiester linkages, and may be DNA or RNA. In another embodiment, the additional 5' and/or 3' end nucleotides are modified nucleotides which may for example be included to enhance nuclease stability or for ease of synthesis. In some

embodiments the oligonucleotide of the invention comprises a region D' and/or D'' in addition to the contiguous nucleotide region.

In some embodiments, the gapmer oligonucleotide of the present invention can be represented by the following formulae:

F-G-F'; in particular F_{1-7}-G_{4-12}-F'_{1-7}

D'-F-G-F', in particular D'_{1-3}-F_{1-7}-G_{4-12}-F'_{1-7}

F-G-F'-D'', in particular F_{1-7}-G_{4-12}-F'_{1-7}-D''_{1-3}

D'-F-G-F'-D'', in particular D'_{1-3}-F_{1-7}-G_{4-12}-F'_{1-7}-D''_{1-3}

Method of manufacture

In a further aspect, the invention provides methods for manufacturing the oligonucleotides of the invention comprising reacting nucleotide units and thereby forming covalently linked contiguous nucleotide units comprised in the oligonucleotide. Preferably, the method uses phophoramidite chemistry (see for example Caruthers et al, 1987, Methods in Enzymology vol. 154, pages 287-313). In a further embodiment the method further comprises reacting the contiguous nucleotide sequence with a conjugating moiety (ligand). In a further aspect a method is provided for manufacturing the composition of the invention, comprising mixing the oligonucleotide or conjugated oligonucleotide of the invention with a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

Pharmaceutical Salts

For use as a therapeutic, the oligonucleotide of the invention may be provided as a suitable pharmaceutical salt, such as a sodium or potassium salt. In some embodiments the oligonucleotide of the invention is a sodium salt.

Pharmaceutical Composition

In a further aspect, the invention provides pharmaceutical compositions comprising any of the aforementioned oligonucleotides and/or oligonucleotide conjugates and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant. A pharmaceutically acceptable diluent includes phosphate-buffered saline (PBS) and pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts. In some embodiments the pharmaceutically acceptable diluent is sterile phosphate buffered saline. In some embodiments the oligonucleotide is used in the pharmaceutically acceptable diluent at a concentration of 50 - 300µM solution. In some embodiments, the oligonucleotide of the invention is administered at a dose of 10 - 1000µg.

WO 2007/031091 provides suitable and preferred examples of pharmaceutically acceptable diluents, carriers and adjuvants (hereby incorporated by reference). Suitable dosages, formulations, administration routes, compositions, dosage forms, combinations with other therapeutic agents, pro-drug formulations are also provided in WO2007/031091.

Oligonucleotides or oligonucleotide conjugates of the invention may be mixed with pharmaceutically acceptable active or inert substances for the preparation of pharmaceutical compositions or formulations. Compositions and methods for the formulation of pharmaceutical compositions are dependent upon a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

In some embodiments, the oligonucleotide or oligonucleotide conjugate of the invention is a prodrug. In particular with respect to oligonucleotide conjugates the conjugate moiety is cleaved of the oligonucleotide once the prodrug is delivered to the site of action, e.g. the target cell.

Applications

The oligonucleotides of the invention may be utilized as research reagents for, for example, diagnostics, therapeutics and prophylaxis.

In research, such oligonucleotides may be used to specifically modulate the synthesis of HTRA1 protein in cells (e.g. *in vitro* cell cultures) and experimental animals thereby facilitating functional analysis of the target or an appraisal of its usefulness as a target for therapeutic intervention. Typically the target modulation is achieved by degrading or inhibiting the mRNA producing the protein, thereby prevent protein formation or by degrading or inhibiting a modulator of the gene or mRNA producing the protein.

In diagnostics the oligonucleotides may be used to detect and quantitate HTRA1 expression in cell and tissues by northern blotting, *in-situ* hybridisation or similar techniques.

For therapeutics, an animal or a human, suspected of having a disease or disorder, which can be treated by modulating the expression of HTRA1.

The invention provides methods for treating or preventing a disease, comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide, an oligonucleotide conjugate or a pharmaceutical composition of the invention to a subject suffering from or susceptible to the disease.

The invention also relates to an oligonucleotide, a composition or a conjugate as defined herein for use as a medicament.

The oligonucleotide, oligonucleotide conjugate or a pharmaceutical composition according to the invention is typically administered in an effective amount.

The invention also provides for the use of the oligonucleotide or oligonucleotide conjugate of the invention as described for the manufacture of a medicament for the treatment of a disorder as referred to herein, or for a method of the treatment of as a disorder as referred to herein.

The disease or disorder, as referred to herein, is associated with expression of HTRA1. In some embodiments disease or disorder may be associated with a mutation in the HTRA1 gene or a

gene whose protein product is associated with or interacts with HTRA1. Therefore, in some embodiments, the target nucleic acid is a mutated form of the HTRA1 sequence and in other embodiments, the target nucleic acid is a regulator of the HTRA1 sequence.

The methods of the invention are preferably employed for treatment or prophylaxis against diseases caused by abnormal levels and/or activity of HTRA1.

The invention further relates to use of an oligonucleotide, oligonucleotide conjugate or a pharmaceutical composition as defined herein for the manufacture of a medicament for the treatment of abnormal levels and/or activity of HTRA1.

In one embodiment, the invention relates to oligonucleotides, oligonucleotide conjugates or pharmaceutical compositions for use in the treatment of diseases or disorders selected from eye disorders, such as macular degeneration, including age related macular degeneration (AMD), such as dry AMD or wet AMD, and diabetic retinopathy. In some embodiments the oligonucleotide conjugates or pharmaceutical compositions of the invention may be for use in the treatment of geographic atrophy or intermediate dAMD. HTRA1 has also been indicated in Alzheimer's and Parkinson's disease, and therefore in some embodiments, the oligonucleotide conjugates or pharmaceutical compositions of the invention may be for use in the treatment of Alzheimer's or Parkinson's. HTRA1 has also been indicated in Duchenne muscular dystrophy, arthritis, such as osteoarthritis, familial ischemic cerebral small-vessel disease, and therefore in some embodiments, the oligonucleotide conjugates or pharmaceutical compositions of the invention may be for use in the treatment of Duchenne muscular dystrophy, arthritis, such as osteoarthritis, or familial ischemic cerebral small-vessel disease.

Administration

The oligonucleotides or pharmaceutical compositions of the present invention may be administered topical (such as, to the skin, inhalation, ophthalmic or otic) or enteral (such as, orally or through the gastrointestinal tract) or parenteral (such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular or intrathecal).

In some embodiments the oligonucleotide, conjugate or pharmaceutical compositions of the present invention are administered by a parenteral route including intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion, intrathecal or intracranial, e.g. intracerebral or intraventricular, administration. In some embodiments the active oligonucleotide or oligonucleotide conjugate is administered intravenously. In another embodiment the active oligonucleotide or oligonucleotide conjugate is administered subcutaneously.

For use in treating eye disorders, such as macular degeneration, e.g. AMD (wet or dry), intraocular injection may be used.

In some embodiments, the compound of the invention, or pharmaceutically acceptable salt thereof, is administered via an intraocular injection in a dose from about 10µg to about 200µg per eye, such as about 50µg to about 150 µg per eye, such as about 100µg per eye. In some embodiments, the dosage interval, *i.e.* the period of time between consecutive dosings is at least monthy, such as at least bi monthly or at least once every three months.

Combination therapies

In some embodiments the oligonucleotide, oligonucleotide conjugate or pharmaceutical composition of the invention is for use in a combination treatment with another therapeutic agent. The therapeutic agent can for example be the standard of care for the diseases or disorders described above

Embodiments of the Invention

1. An antisense oligonucleotide of 10 – 30 nucleotides in length, wherein said antisense oligonucleotide comprises a contiguous nucleotide region of 10 – 22 nucleotides which are at least 90% such as 100% complementarity to SEQ ID NO 147:

SEQ ID NO 147: 5' CCAACAACCAGGTAAATATTTG 3'

2. The antisense oligonucleotide according to embodiment 1, wherein the antisense oligonucleotide is capable of inhibiting the expression of HTRA1 mRNA.

3. The antisense oligonucleotide according to embodiment 1 or 2, wherein the contiguous nucleotide region is identical to a sequence present in a sequence selected from the group consisting of SEQ ID NO 138, 139, 140, 141, 142, 143, 144 and 145:

SEQ ID NO 138: CAAATATTTACCTGGTTG
SEQ ID NO 139: TTTACCTGGTTGTTGG
SEQ ID NO 140: CCAAATATTTACCTGGTT
SEQ ID NO 141: CCAAATATTTACCTGGTTGT
SEQ ID NO 142: ATATTTACCTGGTTGTTG
SEQ ID NO 143: TATTTACCTGGTTGTT
SEQ ID NO 144: ATATTTACCTGGTTGT
SEQ ID NO 145: ATATTTACCTGGTTGTT

4. The antisense oligonucleotide according to any one of embodiments 1 - 3, wherein the contiguous nucleotide region comprises the sequence SEQ ID NO 146:

SEQ ID NO 146: TTTACCTGGTT

5. The antisense oligonucleotide according to any one of embodiments 1 – 4, wherein the contiguous nucleotide region of the oligonucleotide consists or comprises of a sequence selected from any one of SEQ ID NO 138, 139, 140, 141, 142, 143, 144 and 145.

6. The antisense oligonucleotide according to any one of embodiments 1 – 5 wherein the contiguous nucleotide region of the oligonucleotide comprises one or more 2' sugar modified nucleosides.

7. The antisense oligonucleotide according to embodiment 6, wherein the one or more 2' sugar modified nucleoside is independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.

8. The antisense oligonucleotide according to any one of embodiments 5 - 7, wherein the one or more modified nucleoside is a LNA nucleoside.

9. The antisense oligonucleotide according to any one of embodiments 1 - 8, where the contiguous nucleotide region of the oligonucleotide comprises at least one modified internucleoside linkage, such as one or more phosphorothioate internucleoside linkages.

10. The antisense oligonucleotide according to embodiment 9, wherein all the internucleoside linkages within the contiguous nucleotide region are phosphorothioate internucleoside linkages.

11. The antisense oligonucleotide according to any one of embodiments 1 – 10, wherein the oligonucleotide is capable of recruiting RNase H.

12. The antisense oligonucleotide according to any one of embodiments 1 - 11, wherein the oligonucleotide or contiguous nucleotide sequence thereof is or comprises a gapmer.

13. The antisense oligonucleotide of embodiment 11 or 12, wherein the oligonucleotide or contiguous nucleotide sequence thereof is a gapmer of formula 5'-F-G-F'-3', where region F and F' independently comprise 1 - 7 sugar modified nucleosides and G is a region 6 - 16 nucleosides which is capable of recruiting RNaseH, wherein the nucleosides of regions F and F' which are adjacent to region G are sugar modified nucleosides.

14. The antisense oligonucleotide according to embodiment 13, wherein region G consists or comprises 6 – 16 DNA nucleosides.

15. The antisense oligonucleotide according to embodiment 13 or 14, wherein region F and F' each comprise at least one LNA nucleoside.

16. The antisense oligonucleotide according to any one of embodiments 1 – 15, selected from the group selected from:

$C_sA_sA_sA_st_sa_st_st_st_sa_sc_sc_st_sg_sG_sT_sT_sG$ (SEQ ID NO 138, Comp # 138,1)
$T_sT_st_sa_sc_sc_st_sg_sg_st_st_sg_st_sT_sG_sG$ (SEQ ID NO 139, Comp # 139,1)
$C_sC_sA_sA_sa_st_sa_st_st_st_sa_sc_sc_st_sg_sG_sT_sT$ (SEQ ID NO 140, Comp # 140,1)
$C_sC_sA_sa_sa_st_sa_st_st_st_sa_sc_sc_st_sg_sg_st_st_sG_sT$ (SEQ ID NO 141, Comp # 141,1)

$A_sT_sA_st_st_st_sa_sc_sc_st_sg_sg_st_st_sg_sT_sT_sG$ (SEQ ID NO 142, Comp # 142,1)

$T_sA_sT_st_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT_sT$ (SEQ ID NO 143, Comp # 143,1)

$T_sA_st_st_st_sa_sc_sc_st_sg_sG_st_sT_sg_sT_sT$ (SEQ ID NO 143, Comp # 143,2)

$T_sA_sT_st_st_sa_sc_sc_st_sg_sg_sT_sT_sg_sT_sT$ (SEQ ID NO 143, Comp # 143,3)

$A_sT_sA_sT_st_st_sa_sc_sc_st_sg_sg_sT_sT_sG_sT$ (SEQ ID NO 144, Comp # 144,1)

$A_st_sA_sT_sT_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT$ (SEQ ID NO 144, Comp # 144,2)

$A_st_sA_sT_st_st_sa_sc_sc_st_sg_sG_sT_sT_sg_sT_sT$ (SEQ ID NO 145, Comp # 145,1)

$A_sT_sA_st_st_st_sa_sc_sc_st_sg_sG_st_sT_sg_sT_sT$ (SEQ ID NO 145, Comp # 145,2)

$A_st_sA_sT_st_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT_sT$ (SEQ ID NO 145, Comp # 145,3)

Wherein a capital letter represents an LNA nucleoside unit, a lowe case letter represents a DNA nucleoside unit, subscript s represents a phosphorothioate internucleoside linkage, wherein all LNA cytosines are 5-methyl cytosine.

17. The antisense oligonucleotide according to embodiment 16, wherein the LNA nucleosides are all beta-D-oxy LNA nucleosides.

18. A conjugate comprising the oligonucleotide according to any one of embodiments 1 – 17, and at least one conjugate moiety covalently attached to said oligonucleotide.

19. A pharmaceutical composition comprising the oligonucleotide of embodiment 1 – 17 or the conjugate of embodiment 18 and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

20. An *in vivo* or *in vitro* method for modulating HTRA1 expression in a target cell which is expressing HTRA1, said method comprising administering an oligonucleotide of any one of embodiments 1 – 17 or the conjugate according to embodiment 18 or the pharmaceutical composition of embodiment 19 in an effective amount to said cell.

21. A method for treating or preventing a disease comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide of any one of embodiments 1 – 17 or the conjugate according to embodiment 18 or the pharmaceutical composition of embodiment 19 to a subject suffering from or susceptible to the disease.

22. The method of embodiment 21, wherein the disease is selected from the group consisting of macular degeneration (such as wetAMD, dryAMD, geographic atrophy, intermediate dAMD, diabetic retinopathy), Parkinson's disease, Alzhiemer's disease, Duchenne muscular dystrophy, arthritis, such as osteoarthritis, and familial ischemic cerebral small-vessel disease.

23. The oligonucleotide of any one of embodiments 1 – 17 or the conjugate according to embodiment 18 or the pharmaceutical composition of embodiment 19 for use in medicine.

24. The oligonucleotide of any one of embodiments 1 – 17 or the conjugate according to embodiment 18 or the pharmaceutical composition of embodiment 19 for use in the treatment or prevention of a disease is selected from the group consisting of macular degeneration (such as wetAMD, dryAMD, geographic atrophy, intermediate dAMD, diabetic retinopathy), Parkinson's disease, Alzhiemer's disease, Duchenne muscular dystrophy, arthritis, such as osteoarthritis, and familial ischemic cerebral small-vessel disease.

25. Use of the oligonucleotide of embodiment 1 – 17 or the conjugate according to embodiment 18 or the pharmaceutical composition of embodiment 19, for the preparation of a medicament for treatment or prevention of a disease is selected from the group consisting of macular degeneration (such as wetAMD, dryAMD, geographic atrophy, intermediate dAMD, diabetic retinopathy), Parkinson's disease, Alzhiemer's disease, Duchenne muscular dystrophy, arthritis, such as osteoarthritis, and familial ischemic cerebral small-vessel disease.

EXAMPLES

Materials and methods

Oligonucleotide synthesis

Oligonucleotide synthesis is generally known in the art. Below is a protocol which may be applied. The oligonucleotides of the present invention may have been produced by slightly varying methods in terms of apparatus, support and concentrations used.

Oligonucleotides are synthesized on uridine universal supports using the phosphoramidite approach on an Oligomaker 48 at 1 µmol scale. At the end of the synthesis, the oligonucleotides are cleaved from the solid support using aqueous ammonia for 5-16hours at 60˚C. The oligonucleotides are purified by reverse phase HPLC (RP-HPLC) or by solid phase extractions and characterized by UPLC, and the molecular mass is further confirmed by ESI-MS.

Elongation of the oligonucleotide:

The coupling of β-cyanoethyl- phosphoramidites (DNA-A(Bz), DNA- G(ibu), DNA- C(Bz), DNA-T, LNA-5-methyl-C(Bz), LNA-A(Bz), LNA- G(dmf), LNA-T) is performed by using a solution of 0.1 M of the 5'-O-DMT-protected amidite in acetonitrile and DCI (4,5–dicyanoimidazole) in acetonitrile (0.25 M) as activator. For the final cycle a phosphoramidite with desired modifications can be used, e.g. a C6 linker for attaching a conjugate group or a conjugate group as such. Thiolation for introduction of phosphorthioate linkages is carried out by using xanthane hydride (0.01 M in acetonitrile/pyridine 9:1). Phosphordiester linkages can be introduced using 0.02 M iodine in THF/Pyridine/water 7:2:1. The rest of the reagents are the ones typically used for oligonucleotide synthesis.

For post solid phase synthesis conjugation a commercially available C6 aminolinker phorphoramidite can be used in the last cycle of the solid phase synthesis and after

deprotection and cleavage from the solid support the aminolinked deprotected oligonucleotide is isolated. The conjugates are introduced via activation of the functional group using standard synthesis methods.

Purification by RP-HPLC:

The crude compounds are purified by preparative RP-HPLC on a Phenomenex Jupiter C18 10µ 150x10 mm column. 0.1 M ammonium acetate pH 8 and acetonitrile is used as buffers at a flow rate of 5 mL/min. The collected fractions are lyophilized to give the purified compound typically as a white solid.

Abbreviations:

DCI: 4,5-Dicyanoimidazole
DCM: Dichloromethane
DMF: Dimethylformamide
DMT: 4,4'-Dimethoxytrityl
THF: Tetrahydrofurane
Bz: Benzoyl
Ibu: Isobutyryl
RP-HPLC: Reverse phase high performance liquid chromatography

T_m Assay:

Oligonucleotide and RNA target (phosphate linked, PO) duplexes are diluted to 3 mM in 500 ml RNase-free water and mixed with 500 ml 2x T_m-buffer (200mM NaCl, 0.2mM EDTA, 20mM Naphosphate, pH 7.0). The solution is heated to 95ºC for 3 min and then allowed to anneal in room temperature for 30 min. The duplex melting temperatures (T_m) is measured on a Lambda 40 UV/VIS Spectrophotometer equipped with a Peltier temperature programmer PTP6 using PE Templab software (Perkin Elmer). The temperature is ramped up from 20ºC to 95ºC and then down to 25ºC, recording absorption at 260 nm. First derivative and the local maximums of both the melting and annealing are used to assess the duplex T_m.

Example 1: Testing *in vitro* efficacy of antisense oligonucleotides targeting rat Htra1 in C6 cell lines at single dose concentration.

Rat C6 cell line was purchased from ATCC and maintained as recommended by the supplier in a humidified incubator at 37°C with 5% CO_2. For assays, 1500 C6 cells/well were seeded in a 96 multi well plate in culture media. Cells were incubated for 2 hours before addition of oligonucleotides dissolved in PBS. Concentration of oligonucleotides: 25 µM. 4 days after addition of oligonucleotides, the cells were harvested. RNA was extracted using the PureLink Pro 96 RNA Purification kit (Ambion, according to the manufacturer's instructions). cDNA was then synthesized using M-MLT Reverse Transcriptase, random decamers RETROscript, RNase inhibitor (Ambion, according the manufacturer's instruction) with 100mM dNTP set PCR Grade

(Invitrogen) and DNase/RNase free Water (Gibco). For gene expressions analysis, qPCR was performed using TagMan Fast Advanced Master Mix (2X) (Ambion) in a doublex set up. Following TaqMan primer assays were used for qPCR: Htra1, Rn00581870_m1 (FAM-MGB) and house keeping gene, Tbp, Rn01455646_m1 (VIC-MGB). All primer sets were purchase from Life Technologies. The relative Htra1 mRNA expression level in the table is shown as % of control (PBS-treated cells).

Oligonucleotides used:

SEQ ID NO	Motif	CMP ID NO	Compound	mRNA level
5	gaaagggaaatatggg	5,1	GAAagggaaatatGGG	51
6	gatgaggtataaagtg	6,1	GATgaggtataaaGTG	54
7	ggtgtgttaataatca	7,1	GGTgtgttaataaTCA	60
8	cttatgacgcaaactg	8,1	CTTatgacgcaaaCTG	26
9	tttgtctcctttcctc	9,1	TTtgtctcctttccTC	70
10	gaatggaaagatgtaa	10,1	GAATggaaagatGTAA	27
11	gttctttggctttgct	11,1	GTtctttggctttgCT	63
12	ttcaatgatatatgct	12,1	TTCaatgatatatGCT	15
13	agtatgaagaagtatt	13,1	AGTatgaagaagtATT	27
14	cccaatcacctcgcca	14,1	CCCaatcacct^{m}cgCCA	72
15	gcagtagcaaagacagg	15,1	GCagtagcaaagacAGG	28
16	aagttgaaatcagtggt	16,1	AAGttgaaatcagTGGT	12
17	tctggtagtaagaatata	17,1	TCTGgtagtaagaaTATA	73
18	aacagtaagagctacttt	18,1	AACAgtaagagctaCTTT	62
19	tcagacacgatacagag	19,1	TCAgaca^{m}cgatacAGAG	39
20	tggtcagtgataagtaa	20,1	TGGtcagtgataaGTAA	34
21	gcactgtagatgagaaac	21,1	GCACtgtagatgagAAAC	37
22	ataaagtaaacttaatgcc	22,1	ATAAagtaaacttaaTGCC	32
23	attggttcttaggagtgggc	23,1	AttggttcttaggagtggGC	56
24	attattgttttactcgtga	24,1	ATTattgttttact^{m}cgTGA	32
25	atgctggggtaatgattg	25,1	ATGctggggtaatgaTTG	58
26	agtctaaattattgcacaa	26,1	AGTCtaaattattgcACAA	72
27	ccaattagaacagtagtgg	27,1	CCAAttagaacagtagtGG	58
28	agtgtctagttaaacagcac	28,1	AGtgtctagttaaacagCAC	84
29	taccagagtcaagcatatg	29,1	TACcagagtcaagcataTG	33
30	atctaaacttcatgtcagaa	30,1	ATCtaaacttcatgtcAGAA	86
31	ttcatacgactgagcatc	31,1	TTCAta^{m}cgactgagcATC	26
32	gtacagttttagatcatc	32,1	GTAcagttttagatCATC	18
33	atcctaaaagagttcaaca	33,1	ATCCtaaaagagttcaACA	77
34	cattctttgtcatatact	34,1	CATtctttgtcataTACT	49

35	ttcaaagtgactttcaag	35,1	TTCAaagtgactttCAAG	11
36	tcctttctataattacaaa	36,1	TCCTttctataattaCAAA	35
37	ctaattctgtagttttgg	37,1	CTaattctgtagttTTGG	31
38	actgagtgtgtaatgttga	38,1	ACtgagtgtgtaatgtTGA	59
39	agagaaatctgtagggc	39,1	AGAgaaatctgtaggGC	56
40	ttatcaaatcaactagcac	40,1	TTAtcaaatcaactaGCAC	84
41	ttatatttgatagtgtgatc	41,1	TTATatttgatagtgtgATC	55
42	aagagaagctgttatctaaa	42,1	AAGAgaagctgttatcTAAA	42
43	aagtcatgctagagttcc	43,1	AAgtcatgctagagtTCC	37
44	acacagtgtattcgaggg	44,1	ACAcagtgtatt^{m}cgagGG	38
45	gacacagtgtattcgaggg	45,1	GAcacagtgtatt^{m}cgagGG	52
46	gacacagtgtattcgagg	46,1	GACacagtgtatt^{m}cgaGG	26
47	aggacacagtgtattcgagg	47,1	AGgacacagtgtatt^{m}cgaGG	38
48	aggacacagtgtattcgag	48,1	AGgacacagtgtatt^{m}cgAG	32
49	caggacacagtgtattcgag	49,1	CAggacacagtgtatt^{m}cgAG	53
50	aggacacagtgtattcg	50,1	AGgacacagtgtaTTCG	11
51	aacaggacacagtgtattcg	51,1	AAcaggacacagtgtaTTCG	28
52	tgaatctatacagcaggaa	52,1	TGAAtctatacagcagGAA	46
53	cttaagttattcatatcca	53,1	CTTaagttattcatatCCA	39
54	taggtggtagcagatag	54,1	TAGgtggtagcagatAG	48
55	gtagtaataattctggga	55,1	GTAgtaataattctgGGA	7
56	agtggtaaggtgaagtgaa	56,1	AGtggtaaggtgaagTGAA	45
57	ttttgctgtgataaatagc	57,1	TTttgctgtgataaaTAGC	65
58	tttcttatcgttttatga	58,1	TTTCttat^{m}cgttttATGA	24
59	ggaaaacattaacaaggttg	59,1	GGAAaacattaacaagGTTG	38
60	tgggtagagtctaggag	60,1	TGggtagagtctaggAG	58
61	agggagtgactattagag	61,1	AGggagtgactattaGAG	45
62	cagagtagggaaagtggttc	62,1	CAgagtagggaaagtggtTC	76
63	accatgttatatttggg	63,1	ACCAtgttatatttgGG	54
64	tttattactgaggggaaagg	64,1	TTTAttactgaggggaaaGG	67
65	acttgagtgtagtacag	65,1	ACTtgagtgtagtACAG	21
66	catactagttttgcagaga	66,1	CAtactagttttgcagAGA	54
67	ggactagaagtagttac	67,1	GGActagaagtagTTAC	58
68	agggagtcaaaggttcaa	68,1	AGggagtcaaaggtTCAA	13
69	tctgtgtattagagaacg	69,1	TCTGtgtattagagAACG	44
70	tcaaaagctacatcagtc	70,1	TCAaaagctacatcAGTC	7
71	accgttgaattagtcac	71,1	ACCGttgaattagtCAC	39
72	tttccattaaaatgtttaca	72,1	TTTCcattaaaatgttTACA	28
73	gagatggtaaggagtaggag	73,1	GAgatggtaaggagtaggAG	60
74	agttttagactattctg	74,1	AGTTttagactattCTG	37
75	gtcaggacataaactcac	75,1	GTCaggacataaacTCAC	18
76	ttgttggtgtcagggaaaag	76,1	TTGttggtgtcagggaaaAG	20
77	tcctgaaatattgatgc	77,1	TCCtgaaatattgaTGC	51
78	tgccaaaatgactacagt	78,1	TGCcaaaatgactacAGT	54
79	ctcaaagttggatcgtaac	79,1	CTCaaagttggat^{m}cgTAAC	37
80	ttgcattttagaagttat	80,1	TTGCattttagaagTTAT	49

81	tgtcaattagtgtgtttag	81,1	TGTCaattagtgtgtttAG	20
82	cataatatttagtctcct	82,1	CATaatatttagtctCCT	40
83	tatagttacaatcacca	83,1	TATAgttacaatcaCCA	30
84	ttttgtacatactcttcc	84,1	TTttgtacatactcTTCC	11
85	tagcagtacttaaatggg	85,1	TAGcagtacttaaatGGG	28
86	tatgttacatatttggatga	86,1	TATgttacatatttggaTGA	41
87	catggtatcttttggagag	87,1	CATggtatcttttggagAG	36
88	caacatatccagtccag	88,1	CAAcatatccagtcCAG	22
89	taattgtgaagtagggtg	89,1	TAattgtgaagtagGGTG	33
90	actttagaggtttagtcc	90,1	ACTttagaggtttagtCC	55
91	gagcttttaattctatcc	91,1	GAgcttttaattctATCC	56
92	ctccttaaatacatgttac	92,1	CTCcttaaatacatgTTAC	49
93	gagataaatgtttgagaga	93,1	GAGAtaaatgtttgagAGA	41
94	atgatggtgatttaggat	94,1	ATGAtggtgatttagGAT	22
95	agtcattcaatttgagaaa	95,1	AGTCattcaatttgaGAAA	35
96	cagtggtggtaaggcac	96,1	CAGtggtggtaaggcAC	53
97	tgaaatggtttagttctg	97,1	TGAAatggtttagttCTG	41
98	tgccatagtgaaatggttt	98,1	TGCcatagtgaaatggtTT	57
99	caggaggacatactatt	99,1	CAGgaggacatacTATT	77
100	atatatacaggcacatgg	100,1	ATAtatacaggcacaTGG	71
101	gacaggagtctttaaaatg	101,1	GACAggagtctttaaAATG	80
102	tatttatatagtaatgtgtc	102,1	TATTtatatagtaatgTGTC	57
103	ggataaaacagtaccat	103,1	GGAtaaaacagtaCCAT	77
104	ggagtttagaagacacat	104,1	GGAgtttagaagacaCAT	33
105	gtacaactacagaggtt	105,1	GTACaactacagagGTT	65
106	aggaaatggtgatggaatg	106,1	AGGaaatggtgatggAATG	58
107	tcggagtaaaagtgtaaaca	107,1	TCGGagtaaaagtgtaaACA	81

For Compounds: Capital letters represent LNA nucleosides (beta-D-oxy LNA nucleosides were used), all LNA cytosines are 5-methyl cytosine, lower case letters represent DNA nucleosides, DNA cytosines preceded with a superscript ^{m} represents a 5-methyl C-DNA nucleoside. All internucleoside linkages are phosphorothioate internucleoside linkages.

Example 2. Testing *in vitro* potency and efficacy of selected oligonucleotides targeting rat Htra1 in C6 cell line in a dose response curve.

Rat C6 cell line was described in Example 1. The assay was performed as described in Example 1. Concentration of oligonucleotides: from 50 µM, half-log dilution, 8 points. 4 days after addition of oligonucleotides, the cells were harvested. RNA extraction, cDNA synthesis and qPCR were performed as described in Example 1. n=2 biological replicates. EC_{50} determinations were performed in GraphPad Prism6. The relative Htra1 mRNA level at treatment with 50 µM oligonucleotide is shown in the table as % of control (PBS). Additional primer sets (Htra1, Rn00668987_m1 [FAM-MGB] vs. Ppia, Rn006900933_m1 [VIC-MGB] and Hprt, Rn01527840_m1 [VIC-MGB]) were also tested and the same trends were observed using those primers (data not shown).

SEQ ID NO	CMP ID NO	EC_{50}	mRNA level at Max KD
12	12,1	3,3	14
16	16,1	3,2	11
32	32,1	4,3	27
35	35,1	2,6	8
50	50,1	1,9	9
55	55,1	2,0	6
58	58,1	4,4	25
65	65,1	3,1	14
68	68,1	4,1	8
70	70,1	1,5	2
75	75,1	3,7	16
76	76,1	4,9	21
81	81,1	3,0	18
84	84,1	2,2	9
88	88,1	6,8	20
94	94,1	2,9	15

Example 3 Testing *in vitro* efficacy of oligonucleotides targeting human HTRA1, in U251 cell line at single dose concentration.

Human glioblastoma U251 cell line was purchased from ECACC and maintained as recommended by the supplier in a humidified incubator at 37°C with 5% CO_2. For assays, 15000 U251 cells/well were seeded in a 96 multi well plate in starvation media (media recommended by the supplier with the exception of 1% FBS instead of 10%). Cells were incubated for 24 hours before addition of oligonucleotides dissolved in PBS. Concentration of oligonucleotides: 5 µM. 3-4 days after addition of compounds, media was removed and new media (without oligonucleotide) was added. 6 days after addition of oligonucleotides, the cells were harvested. RNA was extracted using the PureLink Pro 96 RNA Purification kit (Ambion, according to the manufacturer's instructions). cDNA was then synthesized using M-MLT Reverse Transcriptase, random decamers RETROscript, RNase inhibitor (Ambion, according the manufacturer's instruction) with 100mM dNTP set PCR Grade (Invitrogen) and DNase/RNase free Water (Gibco). For gene expressions analysis, qPCR was performed using TagMan Fast Advanced Master Mix (2X) (Ambion) in a doublex set up. Following TaqMan primer assays were used for qPCR: HTRA1, Hs01016151_ m1 (FAM-MGB) and house keeping gene, TBP, Hs4326322E (VIC-MGB) from Life Technologies. The relative HTRA1 mRNA expression level in the table is shown as % of control (PBS-treated cells).

SEQ ID NO	Motif	CMP ID NO	Compound	mRNA level
108	agatgggtgtgaaagg	108,1	AGAtgggtgtgaaAGG	35
109	atgttgtctatgttta	109,1	ATGttgtctatgtTTA	5
110	tatgttgtctatgttt	110,1	TATgttgtctatgTTT	5
111	gatgtttgcagtattt	111,1	GATgtttgcagtaTTT	17
112	tatatagtcgaatagg	112,1	TATatagtcgaatAGG	18
113	tttggcttcgtaagtg	113,1	TTTggcttcgtaaGTG	1
114	tgaggcagtggagttg	114,1	TGaggcagtggagtTG	32
115	tggacaggagggcagc	115,1	TGgacaggagggcaGC	92
116	tagagaaggtagaatg	116,1	TAGagaaggtagaATG	78
117	atttagattagagaag	117,1	ATTTagattagaGAAG	50
118	gttcttaaatgtcgtt	118,1	GTTcttaaatgtcGTT	10
119	aagggcttaccatctt	119,1	AAGggcttaccatCTT	62
120	tacttcaattatatac	120,1	TACttcaattataTAC	25
121	gcaatgtgtaagaagt	121,1	GCAatgtgtaagaAGT	15
122	aaactgttgggatctt	122,1	AAACtgttgggaTCTT	11
123	caaactgttgggatct	123,1	CAAActgttgggATCT	50
124	gcaaactgttgggatc	124,1	GCAaactgttgggATC	11
125	gatgtttgcagtattt	125,1	GAtgtttgcagtaTTT	22
126	attgggtttgatcggt	126,1	ATTgggtttgat^{m}cgGT	15
127	ctattgggtttgatcg	127,1	CTAttgggtttgatCG	16
128	tattgggtttgatcgg	128,1	TATtgggtttgatCGG	10
129	cgaatatgtgctttaa	129,1	CGAatatgtgcttTAA	8
130	gctgattatgacgtcg	130,1	GCTgattatga^{m}cgTCG	13
131	tgctgattatgacgtc	131,1	TGCtgattatga^{m}cGTC	10
132	attgggtttgatcggt	132,1	ATTgggtttgatCGGT	18
133	ctattgggtttgatcg	133,1	CTAttgggtttgATCG	49
134	tgctgattatgacgtc	134,1	TGCtgattatgaCGTC	46
135	tattgggtttgatcgg	135,1	TATTgggtttgaTCGG	58
136	cgaatatgtgctttaa	136,1	CGAAtatgtgctTTAA	13
137	gctgattatgacgtcg	137,1	GCTGattatga^{m}cGTCG	39

For Compounds: Capital letters represent LNA nucleosides (beta-D-oxy LNA nucleosides were used), all LNA cytosines are 5-methyl cytosine, lower case letters represent DNA nucleosides, DNA cytosines preceded with a superscript ^{m} represents a 5-methyl C-DNA nucleoside. All internucleoside linkages are phosphorothioate internucleoside linkages.

Example 4 Testing *in vitro* efficacy of a library of oligonucleotides targeting human HTRA1 mRNA in ARPE19 and U251 cell lines at 2 concentrations.

Identification of promising "hot spot" region for HTRA1. A library of n=129 human/cyno/rat HTRA1 LNA oligonucleotides were screened in U251 and ARPE19 cell lines. From this library we identified a series of active oligonucleotides targeting human HTRA1 pre-mRNA (SEQ ID NO 2) between position 33042 - 33064 as shown in figure 1.

Human retinal pigmented epithelium ARPE19 cell line was purchased by from ATCC and maintained in DMEM-F12 (Sigma, D8437), 10% FBS, 1% pen/strep in a humidified incubator at 37°C with 5% CO_2. The U251 cell line was described in example 3. For assays, 5000 ARPE19 cells/well were seeded in a 96 multi well plate in culture media (with the exception of 5% FBS instead of 10%). Cells were incubated for 1 hour before addition of oligonucleotides dissolved in PBS. 4 days after addition of oligonucleotides, the cells were harvested. The assay with the U251 cell line was performed as described in example 3. Concentration of oligonucleotides: 25 and 2.5 µM. RNA was extracted using the RNeasy 96 Biorobot 8000 kit (Qiagen, according to the manufacturer's instructions). cDNA was then synthesized using Retroscript cDNA synthesis kit (ThermoFisher, according the manufacturer's instruction). For gene expressions analysis, qPCR was performed using the Fluidigm Biomark system. Following TaqMan primer assays were used for qPCR: HTRA1, Hs01016151_m1 and house-keeping genes, TBP, Hs99999910_m1 and PPIA, Hs99999904_m1, from Life Technologies. n=2 biologial replicates. The relative HTRA1 mRNA expression level is shown in the table as % of control (PBS). Additional HTRA1 primer set (Hs00170197_m1) was also tested and the same trends were observed (data not shown).

SEQ ID NO	Comp #	Compound	ARPE19 mRNA level		U251 mRNA level	
			25µM	2.5 µM	25µM	2.5 µM
138	138,1	^{m}CAAAtatttacctgGTTG	79	97	11	60
139	139,1	TTtacctggttgtTGG	39	73	5	37
140	140,1	^{m}C^{m}CAAatatttacctgGTT	68	100	16	70
141	141,1	^{m}C^{m}CAaatatttacctggttGT	78	87	16	78
142	142,1	ATAtttacctggttgTTG	56	78	4	23
143	143,1	TATttacctggtTGTT	22	77	3	23

For Compounds: Capital letters represent LNA nucleosides (beta-D-oxy LNA nucleosides were used), all LNA cytosines are 5-methyl cytosine, lower case letters represent DNA nucleosides. All internucleoside linkages are phosphorothioate internucleoside linkages.

Example 5, Testing *in vitro* efficacy of selected human/rat HTRA1 targeting LNA oligonucleotidesin rat C6 cell lines at single dose concentration.

Rat C6 cell line was described in Example 1. The assay was performed as described in Example 1. Concentration of oligonucleotides: 25µM. n=2 biologial replicates. The relative Htra1 mRNA expression level in the table is shown as % of control (PBS-treated cells).

SEQ ID NO	CMP ID NO	mRNA level
139	139,1	24
140	140,1	6
142	142,1	26
143	143,1	16

Example 6, Testing *in vitro* potency and efficacy of of selected human/cyno/rat LNA oligonucleotides in ARPE19, U251 and C6 cell lines in a dose response.

ARPE19, U251 and C6 cell lines were described in example 4, 3 and 1, respectively. For assays, 2000 U251 or ARPE19 cells/well were seeded in a 96 multi well plate in culture media recommended by the supplier. Cells were incubated for 2 hours before addition of oligonucleotides dissolved in PBS. The C6 cell line assay was performed as described in example 1-2. Concentration of oligonucleotides: from 50 µM, half-log dilution, 8 points. 4 days after addition of oligonucleotides, the cells were harvested. RNA extraction, cDNA synthesis and qPCR were performed for all cell lines as described in Example 1. Following TaqMan primer assays were used for U251 and ARPE19 cells: HTRA1, Hs01016151_m1 (FAM-MGB) and house-keeping gene, TBP, Hs4326322E (VIC-MGB). All primer sets were purchased from Life Technologies. n=2 biologial replicates. EC50 determinations were performed in Graph Pad Prism6. The relative HTRA1 mRNA level at treatment with 50 µM oligonucleotide is shown in the table as % of control (PBS).

SEQ ID NO	CMP ID NO	ARPE19		U251		C6	
		EC50 (µM)	mRNA level at max KD	EC50 (µM)	mRNA level at max KD	EC50 (µM)	mRNA level at max KD
138	138,1	10	63	6,2	36	ND	ND
139	139,1	10	38	3,2	18	ND	ND
140	140,1	7,9	57	4,5	29	1,3	2
141	141,1	9,3	64	4,5	44	ND	ND
142	142,1	5,8	40	3,9	25	ND	ND

143	143,1	3,3	25	1,7	6,0	3,5	5

Example 7, Testing *in vitro* efficacy of selected human HTRA1 targeting oligonucleotides in ARPE19 and U251 cell lines at single dose concentration.

ARPE19 and U251 cell lines and assays were described in example 6. RNA extraction was performed as described in example 1, cDNA synthesis and qPCR were performed using qScript XLT one-step RT-qPCR ToughMix Low ROX, 95134-100 (Quanta Biosciences). Following TaqMan primer assays were used for U251 and ARPE19 cells in a douplex set up: HTRA1, Hs01016151_m1 (FAM-MGB) and house-keeping gene, GAPDH, Hs4310884E (VIC-MGB). All primer sets were purchased from Life Technologies. n=1 biological replicate. The relative HTRA1 mRNA expression level in the table is shown as % of control (PBS-treated cells). Additional primer sets (HTRA1, Hs00170197_m1 [FAM-MGB] vs. TBP Hs4326322E [VIC-MGB]) were also tested for U251 and the same trends were observed using those primers (data not shown). See figure 2.

SEQ ID NO	CMP ID NO	ARPE19 mRNA level	U251 mRNA level
143	143,1	46	7
143	143,2	49	10
143	143,3	50	11
144	144,1	44	19
144	144,2	16	9
145	145,1	51	24
145	145,2	40	9
145	145,3	42	4

Example 8, Testing in vitro efficacy and potency in human primary RPE cells.

Human primary Retinal Pigmented Epithelium (hpRPE) cells are purchased from Sciencell (Cat# 6540). For assays, 5000 hpRPE cells/well are seeded in a Laminin (Laminin 521, BioLamina Cat# LN521-03) coated 96 multi well plate in culture media (EpiCM, Sciencell Cat# 4101). They are expanded with this media for one week and differentiated using the following media for 2 weeks : MEM Alpha media (Sigma Cat# M-4526) supplemented with N1 supplement (Sigma Cat# N-6530), Glutamine-Penicillin-Streptomycin (Sigma Cat# G-1146), Non-Essential Amino Acid (NEAA, Sigma Cat# M-7145), Taurine (Sigma Cat# T-0625), Hydrocortisone (Sigma Cat# H-03966), Triiodo-thyronin (Sigma Cat# T-5516) and Bovine

Serum Albumin (BSA, Sigma Cat# A-9647). Cells are cultured in a humidified incubator at 37°C with 5% CO_2.

On the day of the experiment, cells are incubated for 1 hour with fresh differentiation media before addition of oligonucleotides. These are dissolved in PBS and applied on cells at day 0 and day 4. On day 7, cells are harvested with 50µl of RLT buffer with β-mercapto-ethanol (Qiagen Cat# 79216). The extraction of the RNA is performed according to the user's manual of the Qiagen RNeasy Mini Kit (Cat# 74104; Lot 151048073) including DNase I treatment (Cat# 79254; Lot 151042674). RNA quality control is performed with the Agilent Bioanalyzer Nano Kit (Agilent; Cat# 5067-1511; Lot 1446). Reverse transcription of total RNA into cDNA (cDNA synthesis) is performed using the High Capacity cDNA Reverse Transcription Kit which is based on random hexamer oligonucleotides, according to the manufacturer's instructions (Thermo Fisher Scientific, Cat# 4368814; Lot 00314158). The measurement of the cDNA samples is carried out in triplicates, in a 384-well plate format on the 7900HT real-time PCR instrument (Thermo Fisher Scientific). The following TaqMan primer assays are used for qPCR: HTRA1, Hs01016151_m1 and Hs00170197_m1, housekeeping genes, GAPDH, Hs99999905_m1 and PPIA, Hs99999904_m1, from Life Technologies. n=3 biological replicates. The relative HTRA1 mRNA expression level is shown in the table as % of control (PBS). See figure 3.

Example 9. Rat *in vivo* efficacy study, 7 days of treatment, intravitreal (IVT) injection, 30µg/eye.

Animals

Experiment was performed on pigmented male Brown Norway rats. Five animals were included in each group of the study, 15 in total.

Compounds and dosing procedures

To start the experiment, the animals were anesthetized with isoflurane, eyes were desinfected and dilated before an intravitreal injection of 30µg (in 3µl) per eye.

Euthanasia

At the end of the in-life phase (Day 7) all rats were euthanized with CO_2 before eyes were harvested for dissection. Retina, sclera and vitreous fluid were taken for further analysis.

Quantification of HTRA1 RNA expression

Retina samples were dissected. Rat retina snap frozen tissue was kept frozen and was lysed in the testing facility in RLT lysis buffer (Qiagen RNeasy Mini Kit) and RNA extraction was continued according to the user's manual of the Qiagen RNeasy Mini Kit (Cat# 74104; Lot 151039852) including DNase I treatment (Cat#79254; Lot 151048613). RNA quality control was performed with the Agilent Bioanalyzer Nano Kit (Agilent; Cat# 5067-1511; Lot 1446). Reverse transcription of total RNA into cDNA (cDNA synthesis) was performed using the High Capacity cDNA Reverse Transcription Kit which is based on random hexamer oligonucleotides,

according to the manufacturer's instructions (Thermo Fisher Scientific, Cat# 4368814, Lot 00314158). The measurement of the cDNA samples was carried out in triplicates, in a 384-well plate format on the 7900HT real-time PCR instrument (Thermo Fisher Scientific). Following TaqMan primer assays were used for qPCR: Htra1, Rn00581870_m1 and housekeeping genes, Gapdh, Rn01775763_g1 and Tbp, Rn01455646_m1, from Life Technologies. Rats/group: 5, n=10 eyes. Each eye was treated as an individual sample. The relative Htra1 mRNA expression level is shown as % of control (PBS). See figure 4.

Example 10 Rat *in vivo* efficacy study, 7 days of treatment, intravitreal (IVT) injection, dose response.

Animals

All experiments were performed on pigmented Brown Norway rats. 17 animals were included in each group of the study, 34 in total.

Compounds and dosing procedures

The animals were anesthetized with an intramuscular injection of a mix of xylazine and ketamine. The test item and negative control (PBS) were administered intravitreally in both eyes of anesthetized animals (3 µL per administration) on study day 1.

Euthanasia

At the end of the in-life phase (Day 8) were euthanized by intraperitoneal an overdose injection of pentobarbital.

Oligo content measurement and quantification of Htra1 RNA expression

Both eyeballs of all animals in low-dose and mid-dose group as well as from 5 first animals from high-dose and PBS groups were used for bioanalysis. Immediately after euthanasia, Vitreous (V), Retina (R) and Choroid (CH) were quickly and carefully dissected out on ice and stored at -80°C until shipment. Retina sample was lysed in 700 µL MagNa Pure 96 LC RNA Isolation Tissue buffer and homogenized by adding 1 stainless steel bead per 2 ml tube 2 x 1,5 min using a precellys evolution homogenizer followed by 30 min incubation at RT. The samples were centrifuges, 13000 rpm, 5 min. half was set aside for bioanalysis and for the other half, RNA extraction was continued directly

For bioanalysis, the samples were diluted 10-50 fold for oligo content measurements with a hybridization ELISA method. A biotinylated LNA-capture probe and a digoxigenin-conjugated LNA-detection probe (both 35nM in 5xSSCT, each complementary to one end of the LNA oligonucleotide to be detected) was mixed with the diluted homogenates or relevant standards, incubated for 30 minutes at RT and then added to a streptavidine-coated ELISA plates (Nunc cat. no. 436014).

The plates were incubated for 1 hour at RT, washed in 2xSSCT (300mM sodium chloride, 30mM sodium citrate and 0,05% v/v Tween-20, pH 7.0) The captured LNA duplexes were detected using an anti-DIG antibodies conjugated with alkaline phosphatase (Roche Applied Science cat. No. 11093274910) and an alkaline phosphatase substrate system (Blue Phos substrate, KPL product code 50-88-00). The amount of oligo complexes was measured as absorbance at 615 nm on a Biotek reader.

For RNA extraction, cellular RNA large volume kit (05467535001, Roche) was used in the MagNA Pure 96 system with the program: Tissue FF standard LV3.1 according to the instructions of the manufacturer, including DNAse treatment. RNA quality control and concentration were measured with an Eon reader (Biotek). The RNA concentration was normalized across samples, and subsequent cDNA synthesis and qPCR was performed in a one-step reaction using qScript XLT one-step RT-qPCR ToughMix Low ROX, 95134-100 (Quanta Biosciences). The following TaqMan primer assays were used in a duplex reaction: Htra1, Rn00581870_m1 and Rn00668987_m1 and housekeeping genes, HPRT, Rn01527840_m1 and Tbp, Rn01455646_m1, from Life Technologies. The qPCR analyses were run on a ViiA7 machine (Life Technologies). Rats/group: 5, n=10 eyes. Each eye was treated as an individual sample. The relative Htra1 mRNA expression level is shown as % of control (PBS).

Histology

Both eyeballs of the 2 remaining animals of high dose and PBS animals were removed and fixed in 10% neutral buffered formalin for 24 hours, trimmed and embedded in paraffin.

For ISH analysis, sections of formalin-fixed, paraffin-embedded rat retina tissue 4um thick were processed using the fully automated Ventana Dicovery ULTRA Staining Module (Procedure: mRNA Discovery Ultra Red 4.0 – v0.00.0152) using the RNAscope 2.5 VS Probe-Rn-HTRA1 (Cat No. 440959, Advanced Cell Diagnostic). Chromogen used is Fastred, Hematoxylin II counterstain.

Example 11

PoC study, Blue Light-induced retinal degeneration in albino rats

Animals

All experiments were performed on albino Sprague-Dawley rats. Sixteen animals were included in each group of the study, 42 in total.

Compounds and dosing procedures

The animals were anesthetized with an intramuscular injection of a mix of xylazine and ketamine. The test item and negative control (PBS) were administered intravitreally in both eyes of anesthetized animals (3 µL per administration) on study day -3.

The positive control item (PBN) was injected intraperitoneally on Day 0, 4 times (0.5 h before

starting light exposure, 2 h and 4 h after starting light exposure and just after the end of light exposure), at a dose volume of 2.5 mL/kg, using a 25-gauge needle mounted on a 1 mL- plastic syringe, protected from light.

Light exposure

The rats were dark adapted for 36 hours and then exposed to a continuous blue fluorescent light (400 - 540 nm) in clear plastic cages for 6 hours. After exposure, the rats were placed in dark room for 24 hours before returning to standard cyclic light conditions.

Electroretinogram (ERG)

Electroretinograms (ERGs) were be recorded at baseline and on Day 14 on both eyes after overnight darkadaption. A-wave and b-wave amplitudes were measured for each ERG recording

Euthanasia

At the end of the in-life phase (Day 14), the animals were anesthetized and euthanized by intraperitoneal an overdose injection of pentobarbital.

Outer Nuclear layer (ONL) thickness measurements

From the 10 main animals of each group, both eyeballs were enucleated, fixed in Bouin Hollande solution and embedded in paraffin. Thin sections (5 to 7 µm thick) were cut along the vertical meridian and stained with Trichrome-Masson. ONL thickness was measured at seven points (every 250 µm) from the optic nerve to the peripheral retina in each part (superior and inferior) of the retina. The thickness of the outer nuclear layer was measured at each point and the area under the curve (AUC) calculated.

Oligo content measurement and quantification of Htra1 RNA expression

Both eyeballs of 4 satellite animals from test article and PBS groups were used for bioanalysis.. Immediately after euthanasia, Vitreous (V), Retina (R) and Choroid (CH) were quickly and carefully dissected out on ice and stored at -80°C until shipment. Retina sample was lysed in 700 µL MagNa Pure 96 LC RNA Isolation Tissue buffer and homogenized by adding 1 stainless steel bead per 2 ml tube 2 x 1,5 min using a precellys evolution homogenizer followed by 30 min incubation at RT. The samples were centrifuges, 13000 rpm, 5 min. half was set aside for bioanalysis and for the other half, RNA extraction was continued directly.

For bioanalysis, the samples were diluted 10-50 fold for oligo content measurements with a hybridization ELISA method. A biotinylated LNA-capture probe and a digoxigenin-conjugated LNA-detection probe (both 35nM in 5xSSCT, each complementary to one end of the LNA oligonucleotide to be detected) was mixed with the diluted homogenates or relevant standards, incubated for 30 minutes at RT and then added to a streptavidine-coated ELISA plates (Nunc cat. no. 436014).

The plates were incubated for 1 hour at RT, washed in 2xSSCT (300mM sodium chloride, 30mM sodium citrate and 0,05% v/v Tween-20, pH 7.0) The captured LNA duplexes were

detected using an anti-DIG antibodies conjugated with alkaline phosphatase (Roche Applied Science cat. No. 11093274910) and an alkaline phosphatase substrate system (Blue Phos substrate, KPL product code 50-88-00). The amount of oligo complexes was measured as absorbance at 615 nm on a Biotek reader.

For RNA extraction, cellular RNA large volume kit (05467535001, Roche) was used in the MagNA Pure 96 system with the program: Tissue FF standard LV3.1 according to the instructions of the manufacturer, including DNAse treatment. RNA quality control and concentration were measured with an Eon reader (Biotek). The RNA concentration was normalized across samples, and subsequent cDNA synthesis and qPCR was performed in a one-step reaction using qScript XLT one-step RT-qPCR ToughMix Low ROX, 95134-100 (Quanta Biosciences). The following TaqMan primer assays were used in a duplex reaction: Htra1, Rn00581870_m1 and Rn00668987_m1 and housekeeping genes, HPRT, Rn01527840_m1 and Tbp, Rn01455646_m1, from Life Technologies. The qPCR analyses were run on a ViiA7 machine (Life Technologies). Rats/group: 5, n=10 eyes. Each eye was treated as an individual sample. The relative Htra1 mRNA expression level is shown as % of control (PBS).

Histology

Both eyeballs of the remaining 2 satellite animals from test article and PBS groups were removed and fixed in 10% neutral buffered formalin for 24 hours, trimmed and embedded in paraffin. ISH RNAscope was performed as described in example 10.

Example 12, Rat *in vivo* efficacy kinetic study, 3, 7 and 14 days of treatment, intravitreal (IVT) injection, single dose.

Knockdown (KD) at mRNA level was observed in the retina for 2 selected HTRA1 LNA oligonucleotides targeting the “hotspot” in human HTRA1 pre-mRNA between position 33042 – 33064 (SEQ ID NO 147). This was observed both with qPCR and ISH readouts (see figure 7A and /B and the following table).

Compound ID	Days of treatment	qPCR			ISH		
		Residual mRNA level	Stdev	n	Residual mRNA level	Stdev	N
143.1	3	59	31	12	11	14	4
	7	34	28	12	12	8	4
	14	39	35	12	3	5	4

145.3	3	30	29	12	7	5	4
	7	35	32	12	4	3	4
	14	30	21	12	10	9	4

The variation of the knockdown is relatively large, see the standard deviations listed in the table. The variation seems to be at the administration level which can be seen when plotting a dose response curve for oligo content vs. residual HTRA1 mRNA level (see figure 7C).

Animals

All experiments were performed on albino Sprague-Dawley rats.

Compounds and dosing procedures

The animals were anesthetized in isofluran.. The test item and negative control (PBS) were administered intravitreally in both eyes of anesthetized animals (3 µL per administration) on study day 1.

Euthanasia

At the end of the in-life phase (study day 4, 8 or 15) the rats were anesthetized and euthanized by decapitation.

Oligo content measurement and quantification of Htra1 RNA expression

Oligo content measurement and quantification of Htra1 mRNA expression was performed as described in Example 10.

The relative residual Htra1 mRNA expression level is shown as % of control (PBS).

Histology

Histology was performed as described in Example 10.

Example 13. Cynomolgus monkey (non-human primate, NHP) *in vivo* pharmacokinetics and pharmacodynamics (PK/PD) study, 21 days of treatment, intravitreal (IVT) injection, single dose.

Knockdown was observed for 1 selected HTRA1 LNA oligonucleotide, 145.3, targeting the "hotspot" in human HTRA1 pre-mRNA between position 33042 - 33064 both at mRNA in the retina and at protein level in the retina and in the vitreous (see figure 8).

Animals

All experiments were performed on Cynomolgus monkeys (*Macaca fascicularis*).

Compounds and dosing procedures

Buprenorphine analgesia was administered prior to, and two days after test compound injection. The animals were anesthetized with an intramuscular injection of ketamine and xylazine. The test item and negative control (PBS) were administered intravitreally in both eyes of anesthetized animals (50 µL per administration) on study day 1 after local application of tetracaine anesthetic.

Euthanasia

At the end of the in-life phase (Day 22) all monkeys were euthanized by intraperitoneal an overdose injection of pentobarbital.

Oligo content measurement and quantification of Htra1 RNA expression by qPCR

Immediately after euthanasia, eye tissues were quickly and carefully dissected out on ice and stored at -80°C until shipment. Retina sample was lysed in 700 µL MagNa Pure 96 LC RNA Isolation Tissue buffer and homogenized by adding 1 stainless steel bead per 2 ml tube 2 x 1,5 min using a precellys evolution homogenizer followed by 30 min incubation at RT. The samples were centrifuged, 13000 rpm, 5 min. Half was set aside for bioanalysis and for the other half, RNA extraction was continued directly.

For bioanalysis, the samples were diluted 10-50 fold for oligo content measurements with a hybridization ELISA method. A biotinylated LNA-capture probe and a digoxigenin-conjugated LNA-detection probe (both 35nM in 5xSSCT, each complementary to one end of the LNA oligonucleotide to be detected) was mixed with the diluted homogenates or relevant standards, incubated for 30 minutes at RT and then added to a streptavidine-coated ELISA plates (Nunc cat. no. 436014).

The plates were incubated for 1 hour at RT, washed in 2xSSCT (300mM sodium chloride, 30mM sodium citrate and 0,05% v/v Tween-20, pH 7.0) The captured LNA duplexes were detected using an anti-DIG antibodies conjugated with alkaline phosphatase (Roche Applied Science cat. No. 11093274910) and an alkaline phosphatase substrate system (Blue Phos substrate, KPL product code 50-88-00). The amount of oligo complexes was measured as absorbance at 615 nm on a Biotek reader.

For RNA extraction, cellular RNA large volume kit (05467535001, Roche) was used in the MagNA Pure 96 system with the program: Tissue FF standard LV3.1 according to the instructions of the manufacturer, including DNAse treatment. RNA quality control and concentration were measured with an Eon reader (Biotek). The RNA concentration was normalized across samples, and subsequent cDNA synthesis and qPCR was performed in a one-step reaction using qScript XLT one-step RT-qPCR ToughMix Low ROX, 95134-100 (Quanta Biosciences). The following TaqMan primer assays were used in singplex reactions: Htra1, Mf01016150_, Mf01016152_m1 and Rh02799527_m1 and housekeeping genes, ARFGAP2, Mf01058488_g1 and Rh01058485_m1, and ARL1, Mf02795431_m1, from Life Technologies. The qPCR analyses were run on a ViiA7 machine (Life Technologies). Eyes/group: n=3 eyes. Each eye was treated as an individual sample. The relative Htra1 mRNA expression level is shown as % of control (PBS).

Histology

Eyeballs were removed and fixed in 10% neutral buffered formalin for 24 hours, trimmed and embedded in paraffin.

For ISH analysis, sections of formalin-fixed, paraffin-embedded retina tissue 4µm thick were processed using the fully automated Ventana Dicovery ULTRA Staining Module (Procedure: mRNA Discovery Ultra Red 4.0 – v0.00.0152) using the RNAscope 2.5 VS Probe- Mmu-HTRA1, REF 486979, Advanced Cell Diagnostics, Inc.. Chromogen used is Fastred, Hematoxylin II counterstain.

HTRA1 protein quantification using a plate-based immunoprecipitation mass spectrometry (IP-MS) approach

Sample preparation, Retina

Retinas were homogenized in 4 volumes (w/v) of RIPA buffer (50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 0.25% deoxycholic acid, 1% NP-40, 1mM EDTA, Millipore) with protease inhibitors (Complete EDTA-free, Roche) using a Precellys 24 (5500, 15 s, 2 cycles). Homogenates were centrifuged (13,000 rpm, 3 min) and the protein contents of the supernatants determined (Pierce BCA protein assay)

Sample preparation, Vitreous

Vitreous humors (300 µl) were diluted with 5x RIPA buffer (final concentration: 50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 0.25% deoxycholic acid, 1% NP-40, 1mM EDTA) with protease inhibitors (Complete EDTA-free, Roche) and homogenized using a Precellys 24 (5500, 15 s, 2 cycles). Homogenates were centrifuged (13,000 rpm, 3 min) and the protein contents of the supernatants determined (Pierce BCA protein assay)

Plate-based HTRA1 immunoprecipitation and tryptic digest

A 96 well plate (Nunc MaxiSorp) was coated with anti-HTRA1 mouse monoclonal antibody (R&D MAB2916, 500 ng/well in 50 µl PBS) and incubated overnight at 4ºC. The plate was washed twice with PBS (200 µl) and blocked with 3% (w/v) BSA in PBS for 30 min at 20 ºC followed by two PBS washes. Samples (75 µg retina, 100 µg vitreous in 50 µl PBS) were randomized and added to the plate followed by overnight incubation at 4 ºC on a shaker (150 rpm). The plate was then washed twice with PBS and once with water. 10 mM DTT in 50 mM TEAB (30 µl) were then added to each well followed by incubation for 1 h at 20 ºC to reduce cysteine sulfhydryls. 150 mM iodoacetamide in 50 mM TEAB (5 µl) were then added to each well followed by incubation for 30 min at 20 ºC in the dark in order to block cysteine sulfhydryls. 10 µl Digestion solution were added to each well (final concentrations: 1.24 ng/µl trypsin, 20 fmol/µl BSA peptides, 26 fmol/µl isotope-labeled HTRA1 peptides, 1 fmol/µl iRT peptides, Biognosys) followed by incubation overnight at 20 ºC.

HTRA1 peptide quantification by targeted mass spectrometry (selected reaction monitoring, SRM)

Mass spectrometry analysis was performed on an Ultimate RSLCnano LC coupled to a TSQ Quantiva triple quadrupole mass spectrometer (Thermo Scientific). Samples (20 µL) were injected directly from the 96 well plate used for IP and loaded at 5 µL/min for 6 min onto a Acclaim Pepmap 100 trap column (100 µm x 2 cm, C18, 5 µm, 100 Å, Thermo Scientific) in loading buffer (0.5% v/v formic acid, 2% v/v ACN). Peptides were then resolved on a PepMap Easy-SPRAY analytical column (75 µm x 15 cm, 3 µm, 100 Å, Thermo Scientific) with integrated electrospray emitter heated to 40ºC using the following gradient at a flow rate of 250 nL/min: 6 min, 98% buffer A (2% ACN, 0.1% formic acid), 2% buffer B (ACN + 0.1% formic acid); 36 min, 30% buffer B; 41 min, 60% buffer B; 43 min, 80% buffer B; 49 min, 80% buffer B; 50 min, 2% buffer B. The TSQ Quantiva was operated in SRM mode with the following parameters: cycle time, 1.5 s; spray voltage, 1800 V; collision gas pressure, 2 mTorr; Q1 and Q3 resolution, 0.7 FWHM; ion transfer tube temperature 300 ºC. SRM transitions were acquired for the HTRA1 peptide “LHRPPVIVLQR” and an isotope labelled (L-[U-13C, U-15N]R) synthetic version, which was used an internal standard. Data analysis was performed using Skyline version 3.6.

CLAIMS

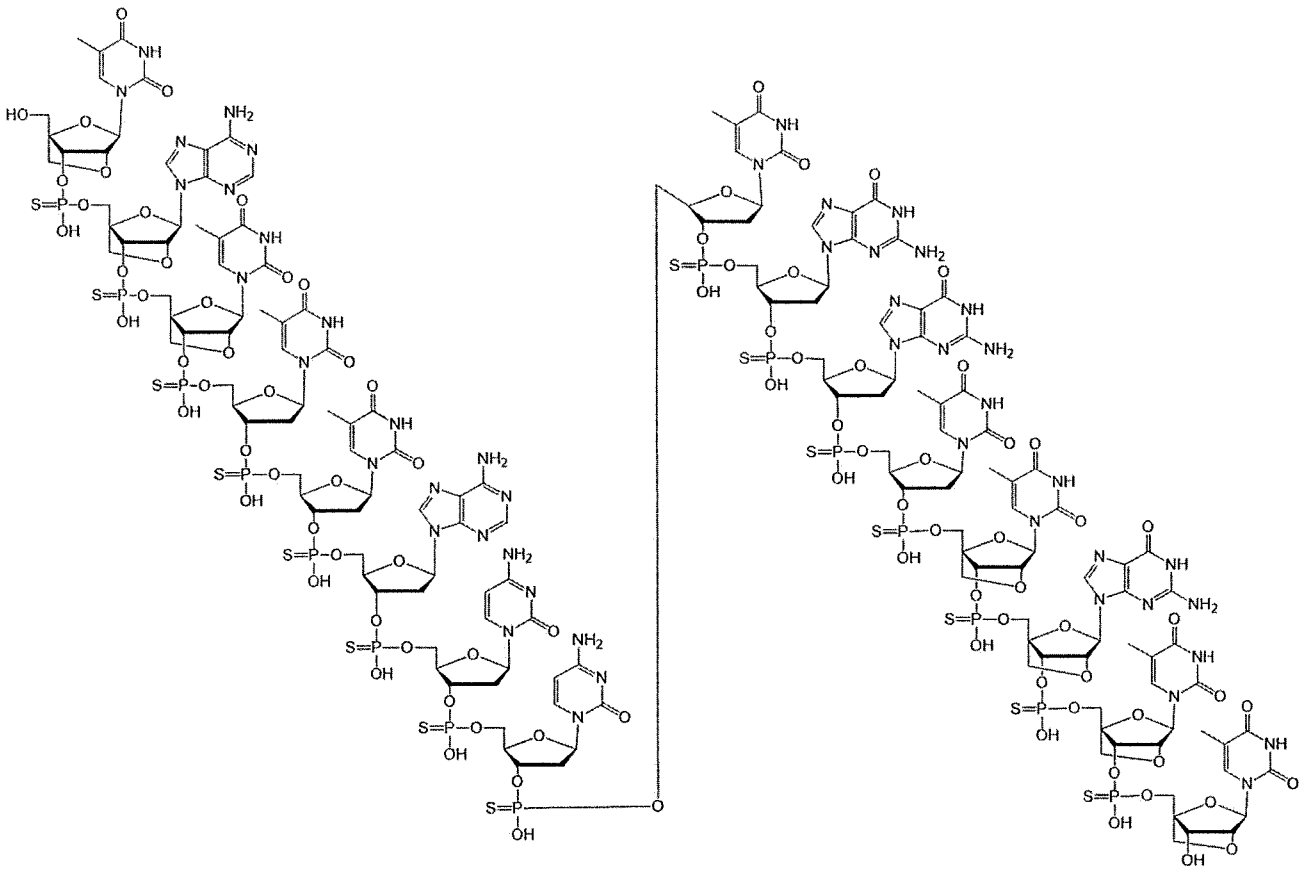
1. An antisense oligonucleotide of formula

$T_sA_sT_st_st_sa_sc_sc_st_sg_sg_st_sT_sG_sT_sT$ (SEQ ID NO 143),

wherein a capital letter represents an LNA nucleoside unit, a lower case letter represents a DNA nucleoside unit, subscript s represents a phosphorothioate internucleoside linkage.

2. The antisense oligonucleotide according to claim 1, wherein the LNA nucleosides are all beta-D-oxy LNA nucleosides.

3. The antisense oligonucleotide of claim 1, wherein the antisense oligonucleotide is of formula



4. The pharmaceutically acceptable salt of the antisense oligonucleotide according to any one of claims 1 - 3.

5. The pharmaceutically acceptable salt according to claim 4, wherein the salt is a sodium salt.

6. The pharmaceutically acceptable salt according to claim 4, wherein the salt is a potassium salt.

7. A pharmaceutical composition comprising the antisense oligonucleotide according to any one of claims 1 – 3; and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant.

8. The pharmaceutical composition according to claim 7, wherein the pharmaceutical composition comprises a pharmaceutically acceptable diluent.

9. The pharmaceutical composition according to claim 8, wherein the pharmaceutically acceptable diluent is phosphate buffered saline.

10. The pharmaceutical composition according to any one of claims 7 – 9, wherein the antisense oligonucleotide is in the form of a pharmaceutically acceptable salt.

11. A pharmaceutical composition comprising the pharmaceutically acceptable salt according to any one of claims 4 – 6; and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant.

12. The pharmaceutical composition according to any one of claims 7 - 11, wherein the pharmaceutically acceptable salt is a sodium salt or a potassium salt.

13. The antisense oligonucleotide according to any one of claims 1 – 3, or the pharmaceutically acceptable salt of any one of claims 4 – 6, or the pharmaceutical composition according to any one of claims 7 – 12, for use in medicine.

14. The antisense oligonucleotide according to any one of claims 1 – 3, or the pharmaceutically acceptable salt of any one of claims 4 – 6, or the pharmaceutical composition according to any one of claims 7 – 12, for use in the treatment or prevention of macular degeneration.

15. The use of the antisense oligonucleotide according to any one of claims 1 – 3, or the pharmaceutically acceptable salt of any one of claims 4 – 6, or the pharmaceutical composition according to any one of claims 7 - 12, for the preparation of a medicament for treatment or prevention of macular degeneration.

16. The antisense oligonucleotide, pharmaceutically acceptable salt, pharmaceutical composition, or use according to any one of claims 13 – 15, wherein the disease is selected from wetAMD, dryAMD, geographic atrophy, and intermediate dAMD.

17. An in vitro method for modulating HTRA1 expression in a target cell which is expressing HTRA1, said method comprising administering the antisense oligonucleotide, pharmaceutically acceptable salt, or pharmaceutical composition according to any one of claims 1 – 12 in an effective amount to said cell.