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(54) Title: ANTAGONISTS OF COMPLEMENT COMPONENT 8-BETA (C8-BETA) AND USES THEREOF

(57) Abstract: Disclosed are antagonists designed to inhibit or block expression of a mammalian complement component 8-beta (C8-beta). The invention has a wide range of uses including use in the preparation of a medicament for the enhancement of nerve regeneration following acute or chronic nerve damage in a mammal.

ANTAGONISTS OF COMPLEMENT COMPONENT 8-BETA (C8-BETA) AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATION

The present application is a continuation of U.S. Provisional Application No. 61/307,171 as filed on February 23, 2010. The present application claims priority to the U.S Provisional Application No. 61/307,171; the disclosure of which is hereby incorporated by reference.

FIELD OF THE INVENTION

The present invention features compositions and methods for modulating the expression of complement component 8-beta (C8-beta). In one embodiment, the invention relates to antagonists that reduce or block expression of that protein. The invention has a wide variety of applications including use to promote nerve regeneration in a mammal following acute or chronic injury to the nervous system.

BACKGROUND

The complement system includes a group of some thirty (30) proteins that are recognized to be an important part of the immunce response. The system can be activated by a classical (usually antibody-dependent) or alternative (usually antibody-dependent) pathway. Activation via either pathway leads to the generation of an enzyme called C5 convertase. The convertase helps form a protein called C5b that, amoung other functions, initiates what is often referred to as the terminal complement pathway. A goal of this pathway is to form a membrane attack complex (MAC) within the membrane of an invading pathogen, thereby causing lysis. The MAC is generally formed by the sequential assembly of complement proteins C6, C7, C8 and $(C9)_n$ along with C5b. See generally Walport, M.J. 2001. *N. Engl. J. Med.* 344: 1058-1066; and 1140–1144.

There are reports of natural and synthetic inhibitors of the complement system. These include certain small molecules, proteins, antibodies, flavanoids, and polysaccharides, for example. See S. Bureeva et al. (2005) *Drug Discovery Today* 10: 1535.

Neuronal degeneration is a hallmark of many acute and chronic neuropathies. One mode of axonal degeneration, termed Wallerian Degeneration (WD) is a highly destructive process in which the part of an axon distal to an injury dies. Initial abnormities can be seen as early as

several hours after injury with more visible WB apparent a day or two later (Ballin RH and Thomas PK (1969) *Acta Neuropathol* (Berl) 14: 237. For instance, myelin sheaths collapse and become engulfed by scavenging cells (Leonhard et al. (2002) *Eur. J. Neurosci.* 16: 1654). These processes are associated with eventual nerve repair and regeneration. There are reports that certain complement components mediate the myelin phagocytosis (Dailey et al. (2002) *J. Neurosci* 18: 6713; and Liu (1999) *J. Peripher. Nerv. Syst.* 4: 123). Although there is some uncertainty about which complement components are needed to mediate these processes, MAC formation has been reported to essential for rapid WD (Ramaglia, V. et al. (2007) *J. Neurosci.* 27: 7663).

A variety of nucleic acid antagonists are known. For example, various antisense oligomers have been shown to be useful for several therapeutic, diagnostic, and research applications (see e.g, Cheson, BD (2007) *Ther Clin Risk Manag.* 3(5):855 (discussing, for instance, favorable clinical trial data for oblimersen). Short interfering RNA (siRNA), a type of RNA antagonist, has been proposed to be a useful therapeutic and research tool (McManus and Sharp, (2002) *Nature Reviews Genetics* 3: 737. Other RNA antagonists such as RNAi-induced silencing complexes with a discontinuous passenger strand have also been reported (Leuschner, et al. (2006) *EMBO Reports* 7:314).

It would be desirable to have antagonists that block or inhibit activity of a mammalian complement component 8-beta (C8-beta) protein. It would be further desirable to have antagonists that can be used to prevent, treat, or reduce the severity of neuropathies that are known or suspected of being associated with formation of the MAC.

SUMMARY OF THE INVENTION

The present invention features antagonists that reduce or block activity of a mammlian complement component 8-beta (C8-beta) protein. Illustrative antagonists can be used to prevent, treat or reduce the severity of neuropathies that are known or suspected of being associated with formation of a membrane attack complex (MAC). Particular antagonists feature single- and multi-stranded nucleic acids (typically about one, two or about three strands) that block or reduce expression of the mammalian complement 8-beta (C8-beta) protein. The invention has a wide

variety of applications including use to promote nerve regeneration in a mammal following acute or chronic nerve damage.

In one aspect, the present invention provides an oligomer of between about 10 to 50 nucleotides in length having a contiguous nucleobase sequence with at least 80% sequence identity to a corresponding region of a nucleic acid which encodes the COMPLEMENT component 8-beta (C8-beta) sequence represented by SEQ ID NO: 1 (human), SEQ ID NO: 333 (rat) or SEQ ID NO: 334 (mouse) or a naturally occuring allelic variant thereof. Preferred oligomers include at least one nucleotide analogue and are capable of reducing the level of C8-beta mRNA expression in a mammal by at least about 20% as determined by, for instance, a PCR assay.

For the sake of simplicity, the phrase «mammalian complement component 8-beta (C8-beta)» will be abbreviated as «C8-beta», « mammalian C8-beta protein» and the like unless specified otherwise.

In another aspect, the invention features a double-stranded nucleic acid compound that preferably includes a first oligomer (passenger strand) and a second oligomer (antisense strand) preferably targeted to a nucleic acid molecule encoding a mammalian C8-beta protein, particularly human, rat of mouse C8-beta. In one embodiment, each strand of the compound includes from between about 12 to about 35 nucleobases and the antisense strand consists of a contiguous nucleobase sequence with at least 80% sequence identity to a corresponding region of a nucleic acid which encodes the COMPLEMENT COMPONENT 8-BETA (C8-BETA) sequence represented by SEQ ID NO: 1 (human), SEQ ID NO: 333 (rat) or SEQ ID NO: 334 (mouse) or a naturally occuring allelic variant thereof. A preferred oligomer includes at least one oligonucleotide analogue.

In another aspect, the invention features a composition that includes an RNA complex with a core double-stranded region that includes an antisense strand consisting of a contiguous nucleobase sequence with at least 80% sequence identity to a corresponding region of a nucleic acid which encodes the COMPLEMENT COMPONENT 8-BETA (C8-BETA) sequence represented by SEQ ID NO: 1 (human), SEQ ID NO: 333 (rat) or SEQ ID NO: 334 (mouse) or a

naturally occuring allelic variant thereof. Preferably, the oligomer includes at least one oligonucleotide analogue, the RNA complex further comprising a discontinuous passenger strand that is hybridised to the antisense strand.

Further provided by the present invention is a method of reducing or inhibiting the expression of a mammalian C8-beta such as human C8-beta, in a cell or a tissue. In one embodiment, the method includes the step of contacting the cell or tissue with at least one oligomer, double-stranded compound or other composition of the invention in an amount that sufficient to reduce or inhibit expression of the C8-beta protein in the cell or tissue.

The invention also provides for a method for treating, preventing or reducing symptoms of a disorder mediated by undesired activity of the complement system and particularly undesired formation of the MAC. In one embodiment, the method includes the step of administring a composition of the invention (therapeutically or prophylactically) to a mammal in need thereof and in an amount sufficient to reduce or block MAC formation in the mammal. A preferred disorder within the scope of the present invention is one in which nerve regeneration is deficient or otherwise abnormal.

Further provided by the present invention is a method of enhancing nerve regeneration in a mammal that includes the step of administering to the mammal (therapeutically or prophylactically) an amount of at least one composition of the invention sufficient to reduce or inhibit expression of C8-beta in the mammal and enhance nerve regeneration therein. Preferably, formation of the MAC is also reduced or inhibited in the mammal.

Practice of the invention provides important advantages.

For instance, there are reports that the liver can sometimes sequester nucleic acids and reduce activity of nucleic acid based therapeutics with targets outside the liver. However, the liver is a major site of complement protein synthesis. Accordingly, it is believed that the sequesteration of the invention compounds will advantageously reduce or block C8-beta protein expression.

Additionally, compounds of the invention can be used alone or in combination with other agents (including at least one other invention composition) to reduce or inhibit MAC formation in a mammal that has or is suspected of having an acute or chronic neuropathy. It is believed that use of the invention before, during or after the injury will help promote nerve regeneration in the mammal.

Further uses and advantages of the invention are discussed, *infra.*

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleic acid sequence encoding human complement component 8-beta (C8-beta) (SEQ ID NO:1). The ATG start site is indicated.

Figures 2A-2E shows certain selected oligomers (SEQ ID Nos:2-236).

Figures 3A-D show sequences of human (SEQ ID NO:1), rat (SEQ ID NO: 333) and mouse (SEQ ID NO: 334) complement component 8-beta (C8-beta). Also shown (boxes) are selected oligomer sequences from the human, rat and mouse (SEQ ID Nos: 237-332).

Figure 4 is a graph showing C8-beta complement mRNA levels after three days of treatment in mice with complement antisense LNA. Batch Nos (Y-axis) are explained in Example 2.

Figure 5 shows graphs showing results of a footlick assay in which oligo 1018 and 1119 improved nerve function in a nerve crush assay.

Figure 6 shows graphs in which oligos 1018 and 1119 showed strong knockdown of intended targets (C8b and C6, respectively). The figure also shows results of an ALT enzyme assay.

DETAILED DESCRIPTION

As discussed, the invention features antagonists that preferably block or inhibit activity of a mammalian C8-beta. Reference herein to a «nucleic acid antagonist» means a compound that

includes or consists of nucleic acid and, preferably, one or more nucleic acid analogues as disclosed herein. An «RNA antagonist» is a nucleic acid antagonist whose intended function is to reduce or block expression of a particular RNA(s).

In one aspect, the invention provides oligomeric compounds (oligomers) for use in decreasing the function of nucleic acid molecules that encode the mammalian C8-beta, preferably to reduce the amount of the C8-beta produced. An example is an antisense compound. This goal is accomplished, for example, by providing antisense compounds which specifically hybridize with one or more nucleic acids encoding the mammalian C8-beta. As used herein, the terms "target nucleic acid" and "nucleic acid encoding C8-beta» encompass DNA encoding the mammalian C8-beta, RNA encoding the mammalian C8-beta (including pre-mRNA and mRNA) transcribed from such DNA, and also cDNA derived from such RNA. A particular mammalian C8-beta of interest is the human complement component 8-beta (C8-beta) encoded by the cDNA sequence represented by Figure 1 (SEQ ID NO: 1). Another mammalian C8-beta of interest is the rat and mouse C8-beta sequences represented by SEQ ID Nos. 333 and 334, respectively.

As used herein, "oligonucleotide" refers to a component of an invention compound such as an oligomer or polymer of ribonucleic acid (RNA) or deoxyribonucleic acid (DNA) or analogues thereof. This term includes oligonucleotides composed of naturally-occurring nucleobases, sugars and covalent internucleoside (backbone) linkages as well as oligonucleotides having non-naturally-occurring portions. Such modified or substituted oligonucleotides are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target and increased stability in the presence of nucleases, for instance. Accordingly, an «oligomer» in accord with the invention, including plural forms, is an oligonucleotide that includes naturally-occuring nucleobases, sugars and covalent backbone linkages as well as constructs that include one or more analogues thereof.

In the present context, the term "nucleotide" means a 2-deoxyribose (DNA) unit or a ribose (RNA) unit which is bonded through its number one carbon to a nitrogenous base, such as adenine (A), cytosine (C), thymine (T), guanine (G) or uracil (U), and which is bonded through its number five carbon atom to an internucleoside linkage group (as defined below) or to a terminal groups (as defined herein). Accordingly, when used herein the term "nucleotide"

encompasses RNA units (or monomers) comprising a ribose unit which is bonded through its number one carbon to a nitrogenous base, such as A, C, T, G or U, and which is bonded through its number five carbon atom to a phosphate group or to a terminal group. Analogously, the term "nucleotide" also encompasses DNA units (or monomers) comprising a 2-deoxyribose unit which is bonded through its number one carbon to a nitrogenous base, such as A, C, T, G or U, and which is bonded through its number five carbon atom to a phosphate group or to a terminal group. The term "nucleotide" also covers variants or analogues of such RNA and DNA monomers as described herein.

By "nucleoside" is meant a 2-deoxyribose (DNA) unit or a ribose (RNA) unit which is bonded through its number one carbon to a nitrogenous base, such as adenine (A), cytosine (C), thymine (T), guanine (G) or uracil (U). Accordingly, when used herein the term "nucleoside" encompasses RNA units (or monomers) comprising a ribose unit which is bonded through its number one carbon to a nitrogenous base, such as A, C, T, G or U. Analogously, the term "nucleoside" also encompasses DNA units (or monomers) comprising a 2-deoxyribose unit which is bonded through its number one carbon to a nitrogenous base, such as A, C, T, G or U. The term "nucleoside" also covers variants or analogues of such RNA and DNA monomers as provided herein. It will be understood that the individual nucleosides are linked together by an internucleoside linkage group such as those naturally-occuring and synthetic linkages as provided herein.

Antisense Oligomers

Without wishing to be bound to theory, it is believed that the specific hybridization of an oligomeric compound with its target nucleic acid interferes with the normal function of the nucleic acid. This modulation of function of a target nucleic acid by compounds which specifically hybridize to it is generally referred to as "antisense". The functions of DNA to be interfered with include, for instance, replication and transcription. The functions of RNA to be interfered with include at least some vital functions such as, for example, translocation of the RNA to the site of protein translation, translation of protein from the RNA, splicing of the RNA to yield one or more mRNA species, and catalytic activity which may be engaged in or facilitated by the RNA. The overall effect of such interference with target nucleic acid function is modulation of the expression of the mammalian C8-beta protein. In the context of the present

invention, "modulation" means either an increase (stimulation) or a decrease (inhibition) in the expression of a gene relative to a suitable control such as expression in the absence of the oligomer. In the context of the present invention, inhibition is the preferred form of modulation of gene expression and mRNA is one target.

As used herein, "hybridization" generally refers to hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleoside or nucleotide bases. For example, adenine and thymine are complementary nucleobases which pair through the formation of hydrogen bonds. "Complementary," as used herein, refers to the capacity for precise pairing between two nucleotides. For example, if a nucleotide at a certain position of an oligonucleotide is capable of hydrogen bonding with a nucleotide at the same position of a DNA or RNA molecule, then the oligonucleotide and the DNA or RNA are considered to be complementary to each other at that position. The oligonucleotide and the DNA or RNA are complementary to each other when a sufficient number of corresponding positions in each molecule are occupied by nucleotides which can hydrogen bond with each other. Thus, "specifically hybridizable" and "complementary" are terms which are used to indicate a sufficient degree of complementarity or precise pairing such that stable and specific binding occurs between the oligonucleotide and the DNA or RNA target.

It is understood that the sequence of an invention compound need not be 100% complementary to that of its target nucleic acid to be specifically hybridizable. An antisense compound, for instance, is specifically hybridizable when binding of the compound to the target DNA or RNA molecule interferes with the normal function of the target DNA or RNA to cause a loss of utility, and there is a sufficient degree of complementarity to avoid non-specific binding of the antisense compound to non-target sequences under conditions in which specific binding is desired, i.e., under physiological conditions in the case of *in vivo* assays or therapeutic treatment, and in the case of in vitro assays, under conditions in which the assays are performed.

Preferred oligomers of the invention are typically identified through *in silico* design and, in some cases, *in vitro* and/or *in vivo* testing. The target sites to which preferred invention sequences are complementary are hereinbelow referred to as "active sites" and are therefore

preferred sites for targeting. Therefore another embodiment of the invention encompasses compounds which hybridize to these active sites.

It is an object of the invention to use particular oligomers as antisense compounds, for instance. "Targeting" an antisense or other invention compound to a particular nucleic acid is a multistep process. The targeting process usually begins with the identification of a nucleic acid sequence whose function is to be modulated. This may be, for example, a cellular gene (or mRNA transcribed from the gene) whose expression is associated with a particular disorder or disease state, or a nucleic acid molecule from an infectious agent. In the present invention, the target is a nucleic acid molecule encoding a mammalian C8-beta protein, particularly the human, rat and mouse C8-beta sequences represented in Fig. 1 (SEQ ID NOs.1, 333 and 334). The targeting process also includes determination of a site or sites within this gene for the antisense interaction to occur including, but not limited to, detection or modulation of expression of the protein.

Additional considerations include selecting oligomers with reduced capacity to cross-hybridize with undesired targets and to assume difficult secondary structures in solution. More preferred oligomers of the invention are selected for reduced toxic and miRNA-like seed region motifs and passenger-strand mediated off-targeting. Still further preferred oligomers in accord with the invention are shown in Figs. 2A-2E and Figs. 3A-3D, for instance. These oligomers were selected for reduced cross-hybridization capacity, reduced toxic and miRNA-like seed region motifs and passenger-strand mediated off-targeting, and a reduced tendency to assume difficult secondary structures in solution as discussed above.

Referring now to Figs. 2A-2E, SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 are preferred targets of the human C8-beta sequence represented by Fig. 1 (SEQ ID NO:1) with sequences immediately below each showing oligomers in order of decreasing preference. Thus, SEQ ID NO: 2 is one preferred target of human C8-beta with oligomers represented by SEQ ID Nos: 3-23, being preferred, in decreasing order of preference, for targeting that site. One embodiment therefore provides an oligomer of between about 8 to 50 nucleotides (e.g., 8 to 20 or 10 to 20 or 25 to 50 nucleotides) in length comprising a contiguous nucleobase sequence with at least 80% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2,

24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos. In an embodiment said oligomer comprises a contiguous nucleobase sequence with at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos. Another embodiment provides an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos.

Referring again to Figs. 2A-2E, additionally preferred targets include those sequences represented by SEQ ID Nos: 222, 225, 228, 231 and 234 and RNA and reverse complement versions thereof shown immediately below each target. Rat and mouse C8-beta is expected to have identical or very similar target sites. One embodiment therefore provides an oligomer of between about 8 to 50 nucleotides in length (e.g, 8 to 20 or 10 to 20 or 19 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos. In an embodiment said oligomer comprises a contiguous nucleobase sequence with at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos. Another embodiment provides an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos.

Referring now to Table 1, SEQ ID Nos. 335, 337, 339, 341 and 343 are illustrative targets of the human C8-beta sequence represented by Fig. 1 (SEQ ID NO:1). One embodiment therefore provides an oligomer of between about 8 to 50 nucleotides in length (e.g, 8 to 20 or 10 to 20 or 16 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80%

sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos. In an embodiment said oligomer comprises a contiguous nucleobase sequence with at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos. Another embodiment provides an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos.

As shown in Table 1, SEQ ID Nos. 336, 338, 340, 342 and 344 represent sequences that are suitable for targeting the above mentioned C8-beta sequences. One embodiment therefore provides an oligomer of between about 8 to 50 nucleotides in length (e.g., 8 to 20 or 10 to 20 or 16 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos. Said oligomer can be targeted to SEQ ID No. 335 or 337 or 303 or 341 or 343. In an embodiment said oligomer comprises a contiguous nucleobase sequence with at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos. Another embodiment provides an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos.

Table 1 shows illustrative LNA modified oligomers of the invention comprising SEQ ID Nos. 336, 338, 340, 342 and 344. It is to be understood, however, that although the presence of at least one nucleotide analogue is preferred, this is not necessary for some applications. Moreover, besides LNA modifications, many other kinds of modifications are allowed, as explained in more

detail herein. Hence, any nucleotide sequence, either natural or artificial, is embraced by the term "sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos".

Additionally preferred oligomers for certain embodiments show 100% sequence identity between the human, rat and mouse sequences (e.g., Fig. 3A-3D; SEQ ID NO: 243). As will be appreciated, such oligomers can be used in the human, rat and mouse without substantial missmatch problems or the need to have multiple oligomer designs for each mammal.

More particular oligomers according to the invention are sufficiently complementary to the target, i.e., hybridize sufficiently well and with sufficient specificity, to give intended results. Preferably, the desired effect is a reduction or total inhibition of expression of mammalian C8-beta such as the human, rat or mouse C8-beta protein, manifested as a reduction or total inhibition of the amount of the corresponding C8-beta mRNA as determined, for instance, by the polymerase chain reaction (PCR) and/or immunological approaches using an anti-C8-beta antibody to monitor protein.

In one PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any organism of interest. An example of a suitable cDNA is the human C8-beta sequence represented by Fig. 1 (SEQ ID NO: 1). Methods for designing PCR primers and PCR cloning are generally known in the art and are disclosed in Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y.) hereinafter "Sambrook". See also Innis et al., eds. (1990) *PCR Protocols: A Guide to Methods and Applications* (Academic Press, New York); Innis and Gelfand, eds. (1995) PCR Strategies (Academic Press, New York); and Innis and Gelfand, eds. (1999) *PCR Methods Manual* (Academic Press, New York). Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially-mismatched primers, and the like. A method for performing qPCR is described in the Examples section.

If desired, additional functionality of a particular oligomer can be tested and optionally quantified by using what is known as a total hemolytic ((CH50) assay). In this approach, plasma, blood or other suitable biological sample is isolated from a mammal to which has been administered one or more of the oligomers. The assay measures the ability of the test sample to lyse 50% of a standardized suspension of sheep erythrocytes coated with anti-erythrocyte antibody. Total complement activity is said to be abnormal if any component is defective. See, for example, Kabat, E. A and Mayer, M. M. (1961) Complement and Complement Fixations. In: *Experimental Immunochemistry,* 2nd Edition, Charles C. Thomas, Springfield, IL. p.133-240.

In another approach, MAC formation can be detected and quantified if desired using immunological approaches described by Ramaglia, V. et al. (2007) *J. Neurosci.* 27:7663.

Additionally preferred oligomers of the invention will exhibit good capacity to block or reduce mRNA encoding for human, rat or mouse C8-beta. More specifically, such oligomers will be capable of reducing the level of a particular C8-beta mRNA in a mammal such as human, rat or mouse, by at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, up to about about 100% as determined by a suitable PCR assay, preferably qPCR. Additionally preferred oligomers are substantially non-toxic in a mammalian host such as a rodent. That is, they do not kill the mammal over the course of an assay in which a therapeutic amount of the oligomer is administered to the mammal for a suitable period (eg., about 1 to about 10mg/kg IP daily for up to a few days or weeks), the liver excised from that mammal and used as a source of nucleic acid, typically RNA. The nucleic acid prepared from the liver using standard procedures and is subjected to qPCR to measure C8-beta mRNA levels using the Roche Lightcycler 480 and universal probes recommended by the manufacturer. An illustrative assay is provided in Example 1 in which several invention oligomers were found to be relatively non-toxic and able to reduce mouse C8-beta mRNA by at least about 20%, 30%, 40%, at least about 50%, 60%, 70%, at least about 80% or more up to about 90%, 95%, to about 99% or 100%. Reference herein to an «oligomer validation test» will refer to the foregoing specific assay to confirm non-toxicity and ability to inhibit C8-beta mRNA expression in vivo.

Preferred use of the oligomers features preventing, treating, or reducing the severity of neuropathies that are known or suspected of being associated with formation of the MAC.

Although the invention provides for one or a combination of suitable oligomers, a generally preferred oligomer is one that is between about 10 to about 50 nucleobases in length, for instance, between about 12 to about 45 nucleobases in length, between about 15 to about 40 nucleobases in length, between about 16 to about 35 nucleobases in length with about 18 to about 30 nucleobases in length being useful for many applications. Preferably, the oligomer includes a contiguous nucleobase sequence of a total of between 10-50 nucleobases, for instance, between about 12 to about 45 nucleobases in length, between about 15 to about 40 nucleobases in length, between about 16 to about 35 nucleobases in length with about 18 to about 30 nucleobases in length being useful for many applications in which the contiguous nucleobase sequence is at least 80% sequence identify, for instance, such as about 85%, about 90%, about 95% or about 98% sequence identity to a corresponding region of a nucleic acid which encodes the mammalian C8-beta of interest. A particular sequence of interest is the human C8-beta represented by SEQ ID NO: 1, rat C8-beta represented by SEQ ID NO: 333 and mouse C8-beta represented by SEQ ID NO: 334 (as well as naturally-occuring allelic variants of SEQ ID Nos: 1, 333 and 334). «Naturally occurring allelic variants» can be identified with the use of well-known molecular biology techniques, such as, for example, polymerase chain reaction (PCR) and hybridization techniques as outlined herein.

The exent of homology between a pair of nucleic acids can be determined by one or a combination of strategies. In one approach, the percent sequence identity is determined by inspection. Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller (1988) *CABIOS* 4:11-17; the local homology algorithm of Smith et al. (1981) *Adv. Appl. Math.* 2:482; the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453; the search-for-similarity-method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.* 85:2444-2448; the algorithm of Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are

not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, Calif.); the ALIGN program (Version 2.0); the ALIGN PLUS program (Version 3.0, copyright 1997); and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package of Genetics Computer Group, Version 10 (available from Accelrys, 9685 Scranton Road, San Diego, Calif., 92121, USA). The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915). Alignments using these programs can be performed using the default parameters. Other alignment considerations are within the skill of those working in the field. See also U.S. Pat No. 7,378,499 and references cited therein.

Unless otherwise stated, nucleotide and amino acid sequence identity/similarity values provided herein refer to the value obtained using GAP with default parameters, or any equivalent program. By "equivalent program," any sequence comparison program is intended that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program. See Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443-453 for more information.

For purposes of the present invention, comparison of nucleotide or protein sequences for determination of percent sequence identity to the human, rat and mouse C8-beta sequences described herein is preferably made using the GAP program in the Wisconsin Genetics Software Package (Version 10 or later) or any equivalent program. For GAP analyses of nucleotide sequences, a GAP Weight of 50 and a Length of 3 was used.

As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may

be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif.).

As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1° C. to about 20°C., depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

In one embodiment of the foregoing oligomers, the contiguous nucleobase sequence includes no more than about 3, such as no more than about 1 or about 2 mismatches with respect to the corresponding region of a nucleic acid which encodes the mammalian C8-beta of interest, particularly SEQ ID NO:1. For example, the contiguous nucleobase sequence can include no more than a single mismatch to the corresponding region of a nucleic acid which encodes the mammalian C8-beta of interest. Alternatively, the contiguous nucleobase sequence includes no mismatches, (e.g. is fully complementary to) with the corresponding region of a nucleic acid which encodes the mammalian C8-beta of interest. In another embodiment, the nucleobase sequence of the oligomer consists of the contiguous nucleobase sequence.

Practice of the invention is compatible with a wide range of mammalian C8-beta sequences including those human, rat and mouse sequences specified herein. The nucleic acid and protein sequences of such proteins are available from the U.S. National Center for Biotechnology Information ((NCBI)-Genetic Sequence Data Bank (Genbank). In particular, sequence listings can be obtained from Genbank at the National Library of Medicine, 38A, 8N05, Rockville Pike, Bethesda, Md. 20894. Genbank is also available on the internet. See generally Benson, D. A. et al. (1997) *Nucl. Acids. Res.* 25: 1 for a description of Genbank. Protein and nucleic sequences not specifically referenced can be found in Genbank or other sources disclosed herein. See (BC_090023) disclosing a rat C8-beta sequence, (NM_133882) disclosing a mouse C8-beta sequence, for instance.

Other oligomer embodiments are within the scope of the present invention. For example, and in one embodiment, the contiguous nucleobase sequence of the oligomer includes a contiguous subsequence of at least 6, for example, about 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or about 30-32 nucleobase residues which, when formed in a duplex with the complementary human, rat or mouse C8-beta target RNA, for instance, is capable of recruiting RNaseH. By «recruiting RNase H» is meant that the enzyme contacts the complex as determined by one or a combination of assays that can detect and quantify activity of the enzyme. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Cleavage of the RNA target can be routinely detected by gel electrophoresis.

Thus in one embodiment, the contiguous nucleobase sequence of the oligomer can include a contiguous subsequence of at least 7, such as at least 8, at least 9 or at least 10 nucleobase residues which, when formed in a duplex with the complementary mammalian C8-beta target is capable of recruiting RNaseH. In another embodiment, the contiguous subsequence is at least 9 or at least 10 nucleobases in length, such as at least 12 nucleobases or at least 14 nucleobases in length, such as 14, 15 or 16 nucleobases residues which, when formed in a duplex with the complementary mammalian C8-beta target RNA is capable of recruiting RNaseH.

Additionally preferred oligomers for use with the invention will be of a length suitable for intended use. Thus in one embodiment, the oligomer has a length of between about 8 to about 50 nucleobases, about 9 to about 50 nucleotides, about 10 to about 50 nucleotides, about 9 to about 40 nucleobases, about 10 to about 35 nucleobases, about 10 to about 22 nucleobases, for instance, about 12 to about 18 nucleobases, about 14, about 15 or about 16 nucleobases, about 10, 11, 12, 13 or about 14 nucleobases.

As will be appreciated, a nucleoside is a base-sugar combination. The base portion of the nucleoside is normally a heterocyclic base. The two most common classes of such heterocyclic bases are the purines and the pyrimidines. Nucleotides are nucleosides that further include a phosphate group covalently linked to the sugar portion of the nucleoside. For those nucleosides that include a pentofuranosyl sugar, the phosphate group can be linked to the 2', 3' or 5' hydroxyl moiety of the sugar. In forming oligonucleotides, the phosphate groups covalently link adjacent nucleosides to one another to form a linear polymeric compound. In turn the respective ends of this linear polymeric structure can be further joined to form a circular structure, however, open linear structures are generally preferred. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside backbone of the oligonucleotide. The normal linkage or backbone of RNA and DNA is a 3' to 5' phosphodiester linkage.

While the foregoing oligomers will be preferred for certain applications, use of oligomers with one or more oligonucleotide analogues will often be preferred (sometimes referred to herein as oligonucleotide «mimetics or derivatives»). Thus in one invention embodiment, oligomers of the invention will include one or more non-nucleobase compounds alone or in combination with

modified backbones or non-natural internucleoside linkages therein. As defined in this specification, oligonucleotides having modified backbones include those that retain a phosphorus atom in the backbone and those that do not have a phosphorus atom in the backbone. For the purposes of this specification, and as sometimes referenced in the field, modified oligonucleotides that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides.

Illustrative modified oligonucleotide backbones include, for example, phosphorothioates, chiral phosphorothioates, phosphoro-dithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates including 3'-alkylene phosphonates, 5'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates including 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkyl-phosphonates, thionoalkylphosphotriesters, selenophosphates and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein one or more internucleotide linkages is a 3' to 3', 5' to 5' or 2' to 2' linkage. Preferred oligonucleotides having inverted polarity comprise a single 3' to 3' linkage at the 3'-most internucleotide linkage i.e., a single inverted nucleoside residue which may be abasic (the nucleobase is missing or has a hydroxyl group in place thereof). Various salts, mixed salts and free acid forms are also included. See, for example, U.S. Pat. Nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; 5,194,599; 5,565,555; 5,527,899; 5,721,218; 5,672,697, 7,335,764, and 5,625,050, for disclosure relating to making and using such compositions.

Thus in one invention embodiment, an oligomer of the invention has a backbone that is fully phosphorothiolyated.

Additional modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These include those having

morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; riboacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S and CH_2 component parts. See, for example, U.S. Pat. Nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312; 5,633,360; 5,677,437; 5,792,608; 5,646,269, 7,335,764, and 5,677,439, for disclosure relating to making and using such compositions.

In other oligonucleotide analogues, both the sugar and the internucleoside linkage, i.e., the backbone, of the nucleotide units are replaced with other groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, in particular an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. See, for instance, U.S. Pat. Nos. 5,539,082; 5,714,331; 5,719,262, and Nielsen et al., *Science*, 1991, 254, 1497-1500.

Additional embodiments of the invention are oligomers with phosphorothioate backbones and oligonucleosides with heteroatom backbones, and in particular --CH_2--NH--O--CH_2--, --CH_2--$N(CH_3)$--O--CH_2-- [known as a methylene (methylimino) or MMI backbone], --CH_2--O--$N(CH_3)$--CH_2--, --CH_2--$N(CH_3)$--$N(CH_3)$--CH_2-- and --O--$N(CH_3)$--CH_2--CH_2-- [wherein the native phosphodiester backbone is represented as --O--P--O--CH_2--] of the above referenced U.S. Pat. No. 5,489,677, and the amide backbones of the above referenced U.S. Pat. No. 5,602,240. Further oligonucleotides having morpholino backbone structures of the above-referenced U.S. Pat. No. 5,034,506, for example.

Modified oligomers in accord with the invention may also contain one or more substituted sugar moieties. Illustrative oligonucleotides comprise one of the following at the 2' position: OH; F; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; O-, S- or N-alkynyl; or O-alkyl-O-alkyl, wherein the

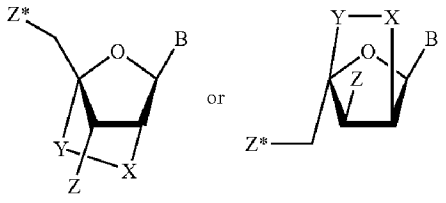
alkyl, alkenyl and alkynyl may be substituted or unsubstituted C_1 to C_{10} alkyl or C_2 to C_{10} alkenyl and alkynyl. Particularly preferred are $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nOCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nONH_2$, and $O(CH_2)_nON[(CH_2)_nCH_3)]_2$, where n and m are from 1 to about 10. Other preferred oligonucleotides comprise one of the following at the 2' position: C_1 to C_{10} lower alkyl, substituted lower alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving the pharmacokinetic properties of an oligonucleotide, or a group for improving the pharmacodynamic properties of an oligonucleotide, and other substituents having similar properties. A preferred modification includes 2'-methoxyethoxy (2'-O--$CH_2CH_2OCH_3$, also known as 2'-O--(2-methoxyethyl) or 2'-MOE) (Martin et al., *Helv. Chim. Acta*, 1995, 78, 486-504) i.e., an alkoxyalkoxy group. A further preferred modification includes 2'-dimethylaminooxyethoxy, i.e., a $O(CH_2)_2ON(CH_3)_2$ group, also known as 2'-DMAOE, as described in examples hereinbelow, and 2'-dimethylaminoethoxyethoxy (also known in the art as 2'-O-dimethylaminoethoxyethyl or 2'-DMAEOE), i.e., 2'-O--CH_2--O--CH_2--$N(CH_2)_2$, also described in examples hereinbelow.

A preferred modification includes Locked Nucleic Acids (LNAs) in which the 2'-hydroxyl group is linked to the 3' or 4' carbon atom of the sugar ring thereby forming a bicyclic sugar moiety. The linkage is, for instance, a methelyne (--CH_2--)$_n$ group bridging the 2' oxygen atom and the 4' carbon atom wherein n is 1 or 2. LNAs and preparation thereof are described in WO 98/39352 and WO 99/14226.

Other modifications for use with the invention include so called “bridged nucleic acids” and related compounds such as those discussed by U.S. Pat. No. 6,743,902 and references disclosed therein.

Additionally suitable LNA monomers (sometimes called "locked nucleic acid monomer", "locked nucleic acid residue", "LNA monomer" or "LNA residue") refer to a bicyclic nucleotide analogue as disclosed, for example, WO 00/56746, WO 00/56748, WO 01/25248, WO 02/28875, WO 03/006475, U.S. Patent Publication No. 2007/0191294, WO 03/095467, U.S. Pat. Nos. 6,670,461, 6,794,499, 7,034,133, 7,053,207 (L-Ribo-LNA), 7,060,809, and 7,084,125 (Xylo-

LNA). The LNA monomer may also be defined with respect to its chemical formula. Thus, an example of an "LNA monomer" as used herein has the following structure:



wherein, X is selected from the group consisting of O, S and NR^H--, where R^H is H or alkyl, such as C_{1-6}-alkyl; Y is (--CH_2)$_r$, where r is an integer of 1-6; with the proviso that when X=O then r is not 2. Z and Z* are independently absent or selected from the group consisting of an internucleoside linkage group, a terminal group and a protection group; and B is a nucleobase. In one embodiment, r=1 and X is O and each of Z, Z* is independently absent or selected from the group consisting of an internucleoside linkage group, terminal group and a protection group and B is a nucleobase. The foreoing LNA monomers can be in the beta-D form, the alpha-L-form as described, for example, in the U.S. Patent Publication 2007/0191294.

Also included within the phrase "LNA monomer" are oligomers in which one or more nucleotides are substituted by amino-LNA, thio-LNA or both. By «amino-LNA» and «thio-LNA» is meant the LNA monomer shown in the above formula in which the oxygen atom of the pentose ring is replaced with a nitrogen or sulfur atom, respectively. Methods for making and using such LNA monomers are disclosed, for instance, in US Pat. Nos. 7,060,809; 7,034,133; 6,794,499; 6,670,461; and references cited therein. A particular subsitution is C- or T- amino-LNA; or C- or T-thio LNA. Certain amino-LNA and thio-LNA analogues are available from Ribotask A/S.

By the phrase "C_{1-6}-alkyl" is meant a linear or branched saturated hydrocarbon chain wherein the longest chains has from one to six carbon atoms, such as methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, sec-butyl, tert-butyl, pentyl, isopentyl, neopentyl and hexyl. A branched hydrocarbon chain is intended to mean a C_{1-6}-alkyl substituted at any carbon with a hydrocarbon chain. «

Specific examples of terminal groups include terminal groups selected from the group consisting of hydrogen, azido, halogen, cyano, nitro, hydroxy, Prot-O--, Act-O--, mercapto, Prot-S--, Act-S--, C_{1-6}-alkylthio, amino, Prot-N(R^H)--, Act-N(R^H)--, mono- or di(C_{1-6}-alkyl)amino, optionally substituted C_{1-6}-alkoxy, optionally substituted C_{1-6}-alkyl, optionally substituted C_{2-6}-alkenyl, optionally substituted C_{2-6}-alkenyloxy, optionally substituted C_{2-6}-alkynyl, optionally substituted C_{2-6}-alkynyloxy, monophosphate including protected monophosphate, monothiophosphate including protected monothiophosphate, diphosphate including protected diphosphate, dithiophosphate including protected dithiophosphate, triphosphate including protected triphosphate, trithiophosphate including protected trithiophosphate, where Prot is a protection group for --OH, --SH and --NH(R^H), and Act is an activation group for --OH, --SH, and --NH(R^H), and R^H is hydrogen or C_{1-6}-alkyl.

In the present context, the term "C_{1-4}-alkyl" is intended to mean a linear or branched saturated hydrocarbon chain wherein the longest chains has from one to four carbon atoms, such as methyl, ethyl, n-propyl, isopropyl, n-butyl, isobutyl, sec-butyl and tert-butyl. A branched hydrocarbon chain is intended to mean a C_{1-4}-alkyl substituted at any carbon with a hydrocarbon chain.

When used herein the term "C_{1-6}-alkoxy" is intended to mean C_{1-6}-alkyl-oxy, such as methoxy, ethoxy, n-propoxy, isopropoxy, n-butoxy, isobutoxy, sec-butoxy, tert-butoxy, pentoxy, isopentoxy, neopentoxy and hexoxy.

In the present context, the term "C_{2-6}-alkenyl" is intended to mean a linear or branched hydrocarbon group having from two to six carbon atoms and containing one or more double bonds. Illustrative examples of C_{2-6}-alkenyl groups include allyl, homo-allyl, vinyl, crotyl, butenyl, butadienyl, pentenyl, pentadienyl, hexenyl and hexadienyl. The position of the unsaturation (the double bond) may be at any position along the carbon chain.

In the present context the term "C_{2-6}-alkynyl" is intended to mean linear or branched hydrocarbon groups containing from two to six carbon atoms and containing one or more triple bonds. Illustrative examples of C_{2-6}-alkynyl groups include acetylene, propynyl, butynyl, pentynyl and hexynyl. The position of unsaturation (the triple bond) may be at any position along

the carbon chain. More than one bond may be unsaturated such that the "C_{2-6}-alkynyl" is a di-yne or enedi-yne as is known to the person skilled in the art.

Examples of protection groups for --OH and --SH groups include substituted trityl, such as 4,4'-dimethoxytrityloxy (DMT), 4-monomethoxytrityloxy (MMT); trityloxy, optionally substituted 9-(9-phenyl)xanthenyloxy (pixyl), optionally substituted methoxytetrahydropyranyloxy (mthp); silyloxy, such as trimethylsilyloxy (TMS), triisopropylsilyloxy (TIPS), tert-butyidimethylsilyloxy (TBDMS), triethylsilyloxy, phenyldimethylsilyloxy; tert-butylethers; acetals (including two hydroxy groups); acyloxy, such as acetyl or halogen-substituted acetyls, e.g. chloroacetyloxy or fluoroacetyloxy, isobutyryloxy, pivaloyloxy, benzoyloxy and substituted benzoyls, methoxymethyloxy (MOM), benzyl ethers or substituted benzyl ethers such as 2,6-dichlorobenzyloxy (2,6-Cl_2Bzl). Moreover, when Z or Z* is hydroxyl they may be protected by attachment to a solid support, optionally through a linker.

As indicated above, Z and Z*, which serve for an internucleoside linkage, are independently absent or selected from the group consisting of an internucleoside linkage group, a terminal group and a protection group depending on the actual position of the LNA monomer within the compound. It will be understood that in embodiments where the LNA monomer is located at the 3' end, Z is a terminal group and Z* is an internucleoside linkage. In embodiments where the LNA monomer is located at the 5' end, Z is absent and Z* is a terminal group. In embodiments where the LNA monomer is located within the nucleotide sequence, Z is absent and Z* is an internucleoside linkage group.

Examples of other suitable terminal groups, protecting groups, and particular LNA monomers suitable for use with the present invention can be found, for instance, in U.S. Pat. Publ. 2007/0191294 and references cited therein.

Other nucleotide analogues for use with the present invention, include 2'-methoxy (2'-O--CH_3), 2'-aminopropoxy (2'-O$CH_2CH_2CH_2NH_2$), 2'-allyl (2'--CH_2—CH=CH_2), 2'--O-allyl (2'-O--CH_2—CH=CH_2) and 2'-fluoro (2'-F). The 2'-modification may be in the arabino (up) position or ribo (down) position. A preferred 2'-arabino modification is 2'-F. Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the

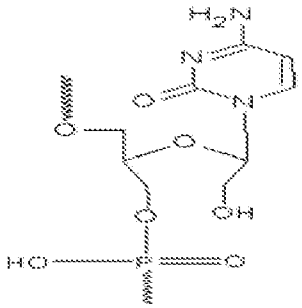
3' terminal nucleotide or in 2'-5' linked oligonucleotides and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics (sugar derivatives) such as cyclobutyl moieties in place of the pentofuranosyl sugar. See, for example, U.S. Pat. Nos. 4,981,957; 5,118,800; 5,319,080; 5,359,044; 5,393,878; 5,446,137; 5,466,786; 5,514,785; 5,519,134; 5,567,811; 5,576,427; 5,591,722; 5,597,909; 5,610,300; 5,627,053; 5,639,873; 5,646,265; 5,658,873; 5,670,633; 7,335,764, 5,792,747; and 5,700,920 for disclosure relating to making and using such analogues.

Oligomers within the scope of the present invention include those having one or more nucleobase modifications, substitutions, and/or additions. As used herein, "unmodified" or "natural" nucleobases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Modified nucleobases include other synthetic and natural nucleobases such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl (--C≡C--CH_3) uracil and cytosine and other alkynyl derivatives of pyrimidine bases, 6-azo uracil, cytosine and thymine, 5-uracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5-bromo, 5-trifluoromethyl and other 5-substituted uracils and cyto-sines, 7-methylguanine and 7-methyladenine, 2-F-adenine, 2-amino-adenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine and 3-deazaguanine and 3-deazaadenine. Further modified nucleobases include tricyclic pyrimidines such as phenoxazine cytidine (1H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), phenothiazine cytidine (1H-pyrimido[5,4-b][1,4]benzothiazin-2(3H)-one), G-clamps such as a substituted phenoxazine cytidine (e.g. 9-(2-aminoethoxy)-H-pyrimido[5,4-b][1,4]benzoxazin-2(3H)-one), carbazole cytidine (2H-pyrimido[4,5-b]indol-2-one), pyridoindole cytidine (H-pyrido[3',2':4,5]pyrrolo[2,3-d]pyrimidin-2-one). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example, 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in U.S. Pat. No. 3,687,808, those disclosed in *The Concise Encyclopedia of Polymer Science And Engineering*, pages 858-859, Kroschwitz, J. I., ed. John Wiley & Sons, 1990, those disclosed by Englisch et al., *Angewandte Chemie,* International Edition, 1991, 30, 613, and those

disclosed by Sanghvi, Y. S., Chapter 15, *Antisense Research and Applications*, pages 289-302, Crooke, S. T. and Lebleu, B., ed., CRC Press, 1993.

For many invention applications, it will be preferred to have oligomers in which the nucleoside analogue includes at least methylated cytosine to reduce or block unwanted stimulation of the immune system. See the Examples section.

Additional oligomers within the scope of the present invention include those with at least one acyclic nucleotide therein (e.g., 1, 2, 3, or 4), preferably a 3',4''-seco nucleotide analogues such as those disclosed by Neilson, P. Et al. (1994) *NAR* 22:703; And Neilson, P. Et al. (1995) *Bioorganic & Med. Chem.* (1995) 19-28. More specific examples of such acylic nucleotides include 3',4'-secothymidine (seco-RNA-thymidine), 3'4'-secocytosine (seco-RNA-cytosine), 3',4'-secoadenine (seco-RNA-adenine), and 3'-4'-secoguanine (seco-RNA-guanine). The structure of a 3'4'-secocytosine (seco-RNA-cytosine) group is provided below:



Additional materials for making and using 3',4'-seco nucleic acids can be obtained from Ribotask A/S (Odense, DK). Without wishing to be bound to theory, it is believed that the use of seco-RNA can help increase the utility of certain compositions of the invention including those which rely, at least on part, on enzymatic degradation of nucleic acids, such as siRNA.

Certain of the foregoing nucleobases may be useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and O-6 substituted purines, including 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2 °C. (Sanghvi, Y. S., Crooke, S. T. and Lebleu, B., eds., *Antisense Research and Applications*, CRC Press, Boca Raton, 1993, pp. 276-278) and

are presently preferred base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar and certain other modifications as disclosed herein such as LNA. See, for instance, U.S. Pat. Nos. 3,687,808, 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,594,121, 5,596,091; 5,614,617; 5,645,985; 5,830,653; 5,763,588; 6,005,096; 7,335,764, 5,750,692 and 5,681,941.

While it will often be preferred to use one or a combination of the foregoing invention oligomers in a given application, such compositions can be further modified as desired to suit an intended use. Thus in one embodiment, a particular oligomer of the invention can be chemically linked with one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the oligonucleotide. The compounds of the invention thus may include conjugate groups covalently bound to functional groups such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugates groups include cholesterols, lipids, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve oligomer uptake, enhance oligomer resistance to degradation, and/or strengthen sequence-specific hybridization with RNA. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve oligomer uptake, distribution, metabolism or excretion. Representative conjugate groups are disclosed in International Patent Application PCT/US92/09196, for example. Conjugate moieties include but are not limited to lipid moieties such as a cholesterol moiety (Letsinger et al., *Proc. Natl. Acad. Sci. USA*, 1989, 86, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Let.,* 1994, 4, 1053-1060), a thioether, e.g., hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.,* 1992, 660, 306-309; Manoharan et al., *Bioorg. Med. Chem. Let.,* 1993, 3, 2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.,* 1992, 20, 533-538), an aliphatic chain, e.g., dodecandiol or undecyl residues (Saison-Behmoaras et al., *EMBO J.,* 1991, 10, 1111-1118; Kabanov et al., *FEBS Lett.,* 1990, 259, 327-330; Svinarchuk et al., *Biochimie*, 1993, 75, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et

al., *Tetrahedron Lett.,* 1995, 36, 3651-3654; Shea et al., *Nucl. Acids Res.*, 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantane acetic acid (Manoharan et al., *Tetrahedron Lett.,* 1995, 36, 3651-3654), a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta,* 1995, 1264, 229-237), or an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, 277, 923-937. Compounds of the invention, including antisense compounds disclosed herein, may also be conjugated to active drug substances, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fenbufen, ketoprofen, (S)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indomethicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Oligonucleotide-drug conjugates and their preparation are described in U.S. patent application Ser. No. 09/334,130 (filed Jun. 15, 1999), for example. See also, U.S. Pat. Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928, 7,335,764 and 5,688,941, for disclosure relating to making and using such compounds.

As will be appreciated, it will not always be necessary or desirable for all positions in a given compound to be uniformly modified. More than one of the aforementioned modifications may be incorporated in a single compound or even at a single nucleoside within an oligonucleotide. The present invention also includes oligomers which are chimeric compounds. "Chimeric" oligomer compounds, for example, or oligomeric "chimeras," in the context of this invention, are oligonucleotides such as antisense compounds, which contain two or more chemically distinct regions, each made up of at least one monomer unit, i.e., a nucleotide or analogue thereof in the case of an oligonucleotide compound. These oligonucleotides typically contain at least one region wherein the oligonucleotide is modified so as to confer upon the oligonucleotide increased resistance to nuclease degradation, increased cellular uptake, and/or

increased binding affinity for the target nucleic acid. An additional region of the oligonucleotide may serve as a substrate for enzymes capable of cleaving RNA:DNA or RNA:RNA hybrids. By way of example, RNase H is a cellular endonuclease which cleaves the RNA strand of an RNA:DNA duplex. Activation of RNase H, therefore, results in cleavage of the RNA target, thereby greatly enhancing the efficiency of oligonucleotide inhibition of gene expression. Consequently, comparable results can often be obtained with shorter oligonucleotides when chimeric oligonucleotides are used, compared to phosphorothioate deoxyoligonucleotides hybridizing to the same target region. Cleavage of the RNA target can be routinely detected by gel electrophoresis and, if necessary, associated nucleic acid hybridization techniques known in the art.

The term "at least one", as used herein encompasses an integer larger than or equal to 1, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and so forth.

Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics as described above. Such compounds have also been referred to in the art as hybrids, wingmers or gapmers. See, for instance, U.S. Pat. Nos. 5,013,830; 5,149,797; 5,220,007; 5,256,775; 5,366,878; 5,403,711; 5,491,133; 5,565,350; 5,623,065; 5,652,355; 5,652,356; 5,700,922, 7,335,764, and U.S. Pat. Publ. 2007/0191294.

The oligomers used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives. Preferably, the oligomers according to the invention are synthesized *in vitro* and do not include compositions of biological origin, or genetic vector constructs designed to direct the *in vivo* synthesis of such compositions. Single-stranded oligomers will be preferred for many invention applications.

As discussed, in some invention embodiments it will be useful to enhance the affinity of an oligomer for its target. This can be achieved by one or a combination of methods as disclosed herein. In one approach, the contiguous nucleobase sequence comprises at least one affinity enhancing nucleotide analogue such as those disclosed herein including 2'-MOE and LNA monomers. In one embodiment of an oligomer that includes at least one affinity enhancing nucleotide analogue, the contiguous nucleobase sequence comprises a total of abaout 2, 3, 4, 5, 6, 7, 8, 9 or about 10 affinity enhancing nucleotide analogues, such as between 5 and 8 affinity enhancing nucleotide analogues. In another embodiment, an oligomer of the invention includes at least one affinity enhancing nucleotide analogue, wherein the remaining nucleobases are selected from the group consisting of DNA nucleotides or RNA nucleotides or acyclic nucleotides as described herein.

In a more specific embodiment of the foregoing oligomers, the oligomer includes a sequence of nucleobases of formula, in 5' to 3' direction, A-B-C, and optionally of formula A-B-C-D in which:

«A» consists or includes at least one nucleotide analogue, such as 1, 2, 3, 4, 5 or 6 nucleotide analogues, for example, between 2-5 nucleotide analogues, such as 2, 3 or 4 nucleotide analogues, or 2, 3 or 4 consecutive nucleotide analogues and;

«B» consists or comprises at least five consecutive nucleobases which are capable of recruiting RNAseH (when formed in a duplex with a complementary RNA molecule, such as a mammalian C8-beta target, for instance, the human C8-beta nucleic acid represented by SEQ ID NO. 1. In one embodiment, the DNA nucleobases of the oligomer such as 5, 6, 7, 8, 9, 10, 11 or 12 consecutive nucleobases which are capable of recruiting RNAseH, or between 6-10, or between 7-9, such as 8 consecutive nucleobases which are capable of recruiting RNAseH, and;

«C» consists or comprises of at least one nucleotide analogue, such as 1, 2, 3, 4, 5, or 6 nucleotide analogues, preferably between 2-5 nucleotide analogues, such as 2, 3 or 4 nucleotide analogues, most preferably 2, 3 or 4 consecutive nucleotide analogues, and;

«D» when present, consists or comprises, preferably consists, of one or more DNA nucleotides, such as between 1-3 or 1-2 DNA nucleotides.

In one embodiment of the foregoing composition, the oligomer further includes at least one acyclic nucleotide in at least one of A, B, C or D, preferably 1, 2, 3 or 4 of same in region B such as about 1 or about 2 acylic nucleotides. Preferably, the acyclic nucleotide is selected from the group consisting of 3',4'-secothymidine (seco-RNA-thymidine), 3'4'-secocytosine (seco-RNA-cytosine), 3',4'-secoadenine (seco-RNA-adenine), and 3'-4'-secoguanine (seco-RNA-guanine) as described above.

In one embodiment, region A consists or comprises of 2, 3 or 4 consecutive nucleotide analogues. Additionally, B can consist of or include about 7, 8, 9 or about 10 consecutive DNA nucleotides or equivalent nucleobases which are capable of recruiting RNAseH when formed in a duplex with a complementary RNA, such as the mammalian C8-beta nucleic acid target. Also, C in the above oligomer can consist or include about 2, 3 or about 4 consecutive nucleotide analogues. Region D, as provided above, can consist of, where present, one or two DNA nucleotides. Accordingly, and in one embodiment, region A, as defined above, consists or includes 3 contiguous nucleotide analogues; B, as defined above, consists or includes about 7, 8, 9 or about 10 contiguous DNA nucleotides or equivalent nucleobases which are capable of recruiting RNAseH when formed in a duplex with a complementary RNA, such as the mammalian C8-beta target; and C, as defined above, consists or includes about 3 contiguous nucleotide analogues; and region D, when present, consists of one or two DNA nucleotides.

In a particular embodiment of the foregoing oligomer, the contiguous nucleobase sequence consists of about 10, 11, 12, 13 or about 14 nucleobases, and wherein; region A consists of about 1 ,2 or about 3 contiguous nucleotide analogues; region B consists of about 7, 8, or about 9 consecutive DNA nucleotides or equivalent nucleobases which are capable of recruiting RNAseH when formed in a duplex with a complementary RNA, such as the mammalian C8-beta nucleic acid target; region C consists of about 1 ,2 or about 3 contiguous nucleotide analogues; and region D consists, where present, of one DNA nucleotide.

For many invention applications, it will be generally preferred to have an oligomer in which region B includes at least one LNA monomer (nucleobase). As an example, such an LNA can be in the alpha-L configuration, such as alpha-L-oxy LNA. Additionally suitable nucleotide analogues (whether in one of or all of regions A, B, C and D as defined above) are independently

or collectively selected from the group consisting of: Locked Nucleic Acid (LNA) units; 2'-O-alkyl-RNA units, 2'-OMe-RNA units, 2'-amino-DNA units, 2'-fluoro- DNA units, PNA units, HNA units, and INA units. In a preferred invention embodiment, the nucleotide analogue will include and more preferably consist of LNA monomers.

In invention embodiments in which a particular oligomer includes at least one LNA monomer (sometimes called a unit), generally about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 LNA units such as between 2 and 8 nucleotide LNA units will be useful. Other LNA monomers will be useful for certain invention applications including those selected from oxy-LNA, thio-LNA, [beta]-D-oxy-LNA, and amino-LNA, in either of the beta-D and alpha-L configurations or combinations thereof. In one embodiment, all the LNA monomers of the oligomer are [beta]-D-oxy-LNA. Thus in a particular invention embodiment, the nucleotide analogues or nucleobases of regions A and C are [beta]-D-oxy-LNA.

As mentioned, and for certain applications, it will be useful to have oligomers that include at least one modified nucleobase. In one embodiment, the modified nucleobase is selected from the group consisting of 5-methylcytosine, isocytosine, pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-aminopurine, inosine, diaminopurine, and 2-chloro-6-aminopurine.

Practice of the invention is compatible with use of one or a combination of different oligomers as disclosed herein. For example, and in one embodiment, an invention hybridises with a corresponding mammalian C8-beta nucleic acid (e.g., mRNA) with a T_m of at least 40°C, such as of at least 50°C. In a particular embodiment, the oligomer hybridises with a corresponding mammalian C8-beta nucleic acid (e.g., mRNA) with a T_m of no greater than 90°C, such as no greater than 80°C.

In most invention embodiments, oligomers with modified backbones as described previously will be generally preferred, especially for *in vivo* use. In one embodiment, the internucleoside linkages are independently selected from the group consisting of: phosphodiester, phosphorothioate and boranophosphate. In a particular example, the oligomer includes at least one phosphorothioate internucleoside linkage. The internucleoside linkages can be adjacent to or

between DNA or RNA units, or within region B (as described above) are phosphorothioate linkages. In one example of an invention oligomer, at least one pair of consecutive nucleotide analogues is a phosphodiester linkage. In some embodiments, all the linkages between consecutive nucleotide analogues will preferably be phosphodiester linkages, for instance, all the internucleoside linkages can be phosphorothioate linkages.

More specific oligomers according to the invention include those targeted to the preferred target sites shown in Fig. 2A-2E and Fig. 3A-3D and referred to above. Such oligomers will generally consist of between from about 10 to about 20 nucleotides such as about 12 to about 18 nucleotides, in which the backbone is fully or partially phosphorothiolated. Additionally preferred oligomers will further include between from about one to about six (6) LNA monomers preferably positioned at the 3'and 5'ends of the oligomers. More specific oligomers will include about 2 or 3 of such LNA monomers positioned at each of the ends (ie., wingmers or gapmers).

Also envisioned is any of the forgoing oligomers in which at least one non-nucleotide or non-polynucleotide moiety covalently attached to said compound. Examples include those groups mentioned above.

Additional oligomers of the invention are provided below in the Examples and Drawings.

Double-stranded Compounds

As mentioned, the invention also provides for a double-stranded compound comprising a passenger strand and an antisense strand targeted to a nucleic acid molecule encoding a mammalian complement component 8-beta (C8-beta) protein such as the human, rat and mouse sequences provided herein. In one embodiment, each strand comprises from between about 12 to about 35 nucleobases, preferably about 12 to about 30 nucleotides, more preferably about 14 to about 25 nucleotides with about 15 to about 20 nucleotides (e.g., 18 or 19 nucleotides) being preferred for many applications. Preferably, the antisense strand consists of a contiguous nucleobase sequence with at least about 80%, 85%, 90%, 95%, 98%, 99% up to about 100% sequence identity to a corresponding region of a nucleic acid which encodes the complement component 8-beta (C8-beta) sequence represented by SEQ ID NOs: 1 (human), 333 (rat) or 334

(mouse) or a naturally occuring allelic variant thereof. Also preferably, the oligomer includes at least one oligonucleotide analogue such as an LNA monomer.

Preferred double-stranded compounds according to the invention can be made using one or a combination of those oligomers disclosed herein. More preferred oligomers are designed to target those preferred target sites already discussed in relation to Figs. 2A-2E and Fig. 3A-3D, for example. Additionally preferred oligomers for use with the double-stranded compound will be essentially non-toxic as determined by the animal tests described herein and particularly the Examples section. Such oligomers may additionally show good ability to decrease C8-beta mRNA expression according to the assay.

In one embodiment of the double-stranded compound, one or both of the passenger strand and the antisense strand comprises at least one modified internucleoside linkage as described previously (oligonucleotide backbones) such as a phosphorothioate linkage. In a particular embodiment, all of the internucleoside linkages of the passenger strand and the antisense strand are phosphorothioate linkages. Typically, the passenger strand will additionally include at least one LNA monomer, for instance, between from about 1 to about 10 LNA monomers (e.g. 2, 3, 4, 5, 6, 7, 8, or 9 LNA monomers). In one embodiment, the at least one LNA monomer is located at the 5' end of the passenger strand, for instance, at least two LNA monomers are located at the 5' end of the passenger strand. Alternatively, or in addition, the at least one LNA monomer is located at the 3' end of the passenger strand, for instance, at least two LNA monomers are located at the 3' end of the passenger strand. Additional embodiments of the double-stranded compound include constructs in which the antisense strand comprises at least one LNA monomer, for instance, between from about 1 to about 10 LNA monomers (e.g. 2, 3, 4, 5, 6, 7, 8, or 9 LNA monomers). In one invention example, the at least one LNA monomer of the compound is located at the 3' end of the antisense strand such as embodiments in which at least two LNA monomers are located at the 3' end of the antisense strand, for instance, at least three LNA monomers are located at the 3' end of the antisense strand. However, in other embodiments it may be useful to have 1 or no (0) LNA monomer located at the 5' end of the antisense strand. Double-stranded compounds of the invention include those constructs in which the passenger strand comprises at least one LNA and the antisense strand comprises at least one LNA monomer, for instance, about 1 to about 10 LNA monomers (e.g. 2, 3, 4, 5, 6, 7, 8, or 9 LNA

monomers) and the antisense strand comprises about 1 to about 10 LNA monomers (e.g. 2, 3, 4, 5, 6, 7, 8, or 9 LNA monomers).

In one embodiment of the foregoing double-stranded compound comprising the first oligomer (passenger strand) and the second oligomer (antisense strand), the passenger strand comprises at least one LNA monomer at the 5' end (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 LNA monomers) and at least one LNA monomer at the 3' end (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 LNA monomers) such as the embodiment in which the antisense strand comprises at least one LNA monomer at the 3' end. As an example, the passenger strand comprises at least one LNA monomer at the 5' end (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 LNA monomers) and at least one LNA monomer at the 3' end (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 LNA monomers). In a particular embodiment, the antisense strand comprises at least two LNA monomers at the 3' end. In certain embodiments, the passenger strand comprises at least two LNA monomers at the 5' end and at least two LNA monomers at the 3' end, for example, the the antisense strand can include at least two LNA monomers at the 3' end. Thus in a particular invention embodiment, the passenger strand comprises at least two LNA monomers at the 5' end and at least two LNA monomers at the 3' end, and, for example, the antisense strand comprises at least three LNA monomers at the 3' end. However in certain invention embodiments it will be useful to have 1 or no (0) LNA monomer is located at the 5' end of the antisense strand.

In a preferred embodiment, T in the composition is replaced by U (T=>U). However, for some or preferably all of the LNA monomers, T will not be replaced by U, i.e., T=T.

More specific double-stranded compositions are within the scope of the present invention including those in which the passenger strand comprises at least one LNA monomer in at least one of the positions 9-13 counted, sequentially, from the 5' end. For example, the passsenger strand can include an LNA monomer in position 10 counted, sequentially, from the 5' end. Alternatively, or in addition the passenger strand can include an LNA monomer in position 11 and/or position 12 therein.

In certain embodiments of the double-stranded compound, the first and the second oligomers therein (passenger and antisense strands) each include between from about 17 to about

25 nucleotides such as 18 to about 24 nucleotides, about 19 to about 23 nucleotides, and about 20 to about 22 nucleotides.

If desired to achieve an invention objective, each of the passenger and antisense strands may independently include a 3' overhang. Alternatively, or in addition, the compound may include at least one (e.g, 1, 2, 3, 4, or 5) acyclic nucleoside located therein e.g., seco-RNA-thymidine, seco-RNA-cytosine, seco-RNA-adenine, and seco-RNA-guanine). In one embodiment, the acylic nucleotide is located on the passenger strand. In another embodiment, the acylic nucleotide is located on the antisense strand of the compound.

In one invention embodiment, the nucleobases of the first oligomer, the second oligomer, or both will be designed to hybridize to target exemplified by SEQ ID Nos: 222, 225, 228, 231 and 234 (see Figs. 2A-2E) and RNA and reverse complement versions thereof shown immediately below each target. Rat and mouse C8-beta is expected to have identical or very similar target sites. Included within the group of such specific oligomers for use as constituents of the double-stranded compounds are derivatives of these sequences in which one or more of the sugar group, nucleobase, or internucleoside linkage, for example, has been modified as disclosed herein. Preferred modifications will include modifying the sequence to conisist essentially of phosphorothioate linkages and at least one LNA monomer.

Accordingly, and in one embodiment, the double-stranded compound features all phosphorothioate linkages and about one, two or three LNA monomers at the 3'end of the antisense strand, for instance, two of same. In one embodiment, the passenger or passenger strand includes one, two, or three LNA monomers at the 5'end of the passenger strand, for instance, two of same.

In some invention embodiments, it may be useful to have more substitution with LNA monomer such as when stronger hybridization bewteen the strands is desirable. Thus in one embodiment, the double-stranded compound features all phosphorothioate linkages and about one, two or three LNA monomers at the 3'end of the antisense strand, for instance, two of same. The passenger strand includes one, two, or three LNA monomers at the 5'end of the passenger strand, for instance, two of same. However in one embodiment, the passenger strand includes an

additional one, two, three, four or five LNA monomers between the 3'and 5'end of the passenger strand such as at position 3, 9, 13, and 15 relative to the 5'end (position 1) 3'overhang positions.

Other embodiments of the double-stranded compound as already disclosed herein are possible provided intended results are achieved. For example, both the passenger strand and the antisense strand of the double-stranded compound may include or consist essentially of phosphodiester internucleotide linkages. However, in other embodiments it may be useful to have at least one phosporothioate internucleotide linkage either in the passenger strand or in the antisense strand or in both strands, for instance, between from about 1 to about 19 phosphorothioate internucleotide linkages (e.g. 2, 3, 4, 5, 6, 7,8 , 9, 10 , 11, 12, 13 , 14 , 15, 16, 17 ,18, or 19 phosphorothioate internucleotide linkages). In this example of the invention, position 9-10-11 of the passenger strand, counting from the 5' end is not modified. Additional embodiments of the double-stranded compound include constructs in which the passenger strand includes at least two and up to seven LNA monomers, for instance, at least two LNA monomers are located at the 3' end of the passenger strand. Alternatively, or in addition, at least one LNA monomer is located at the 5' end of the passenger strand. Alternatively, or in addition, at least one or up to four LNA monomers are located at position 3, 9, 13, or 15 counting from the 5' end of the passenger strand. Additional embodiments of the double-stranded compound include constructs in which the antisense strand includes at least one LNA monomer, for instance, between from about 1 to about 3 LNA monomers (e.g. 2, 3, LNA monomers). In one invention example, at least one LNA monomer of the compound is located at the 3' end of the antisense strand such as embodiments in which at least two LNA monomers are located at the 3' end of the antisense strand, for instance, at least three LNA monomers are located at the 3' end of the antisense strand. However, in other embodiments it may be useful to have 1 or no (0) LNA monomer located at the 5' end of the antisense strand.

For example, the following structures are possible (L bold, underlined =LNA, r=RNA):

5′ rrrrrrrrrrrrrrrrrrr**LL** 3′passenger
3′ **LL**rrrrrrrrrrrrrrrrrrr 5′antisense

5′ **L**rrrrrrrrrrrrrrrrrrr**LL** 3′passenger
3′ **LL**rrrrrrrrrrrrrrrrrrr 5′antisense

5′ rr**L**rrrrr**L**rrr**L**r**L**rrrr**LL** 3′ passenger
3′ **LL**rrrrrrrrrrrrrrrrrrr 5′ antisense

For example, the following structures are possible (L bold, underlined =LNA, r=RNA):

in which with respect to both structures, the compounds can include at least one optional phosphorothioate, for example, they can be fully or partially phosphorothiolayted. Additional compounds, when a C residue is present, may include an optional methyl C to reduce or eliminate an immune response when used for in vivo applications. Other modifications, as discussed herein are possible.

In a more specific invention embodiment, the following structures are possible in which LNA is represented by bold and underlined text:

5′ CUGCAUUGCCAGAAAGUUA**GA** 3′ passenger

3′ **GC**GACGUAACGGUCUUUCAAU 5′ antisense

5′ CU**G**C**A**UTG**C**CAG**A**A**A**GTUA**GA** 3′ passenger

3′ **GC**GACGUAACGGUCUUUCAAU 5′ antisense

Other embodiments are possible depending on parameters such as intended use.

Without wishing to be bound to theory, it is believed that in some instances, particular double-stranded compounds of the invention can benefit by having at least one acyclic nucleotide analogue therein, preferably one, two, three or four of same positioned on one or both of the antisense and passenger strands. A preferred acyclic nucleotide is a 3', 4'-seco nucleotide as disclosed herein, more preferably 3',4'-secothymidine (seco-RNA-thymidine), 3'4'-secocytosine (seco-RNA-cytosine), 3',4'-secoadenine (seco-RNA-adenine), and 3'-4'-secoguanine (seco-RNA-guanine). In one embodiment, the antisense strand includes 1 acyclic nucleotide, preferably positioned between the 3'and 5'ends, for instance, between from about 3 to about 20 nucleotides from the 3'end, preferably between from about 5 to about 19 nucleotides from the 3'end. In one embodiment, the antisense stand further includes one, two, or three LNA monomers, for instance, two of same positioned at the 3''end. The passenger strand, in one embodiment, includes one, two or three acyclic nucleotides at the 3'end, preferably one of same.

In one embodiment, the following compound is possible (L bold, underlined =LNA, r=RNA, S underlined *italic* = seco):

5' rrrrrrrrrrrrrrrrrr*S* 3'passenger

3' **LL**rrrrrrrrrrrr*S*rrrrr 5'antisense

in which the compound can include at least one optional phosphorothioate, for example, it can be fully or partially phosphorothiolayted. Additional compounds, when a C residue is present, may include an optional methyl C to reduce or eliminate an immune response when used for in vivo applications. Other modifications, as discussed herein are possible.

Thus in one embodiment, the following compound is within the scope of the invention in which underlined/italicized text is a seco derivative and bold and underlined text is LNA:

5' CUGCAUUGCCAGAAAGUUAG*A* 3' passenger

3' **GC**GACGUAACGGUCU*U*UCAAU 5' antisense

Particular invention compounds will sometimes be referred to herein as "siLNA" to denote broadly a compound with at least one LNA monomer. As used herein, the term "siRNA" refers to a double stranded stretch of RNA or modified RNA monomers. In a typical siRNA compound, the two strands usually have about 19 nucleotides complementary to each other thereby creating a double strand that is about 19 nucleotides long and each strand having a 3'-end of two overhanging nucleotides. It will be appreciated that an siRNA of the invention may be slightly longer or shorter, and with or without overhangs. Choice of a particular siRNA construct will depend on recognized parameters such as intended use. In siRNA, one oligomer strand is guiding and complementary to the target RNA (antisense strand), and the other oligomer strand (passenger strand) has the same sequence as the target RNA and hence is complementary to the guiding/antisense strand. Herein, regulatory RNAs such as "micro RNA" ("miRNA") and "short RNA" ("shRNA") and a variety of structural RNAs such as tRNA, snRNA, scRNA, rRNA are used interchangeably with the term "siRNA". The term "mRNA" means the presently known mRNA transcript(s) of a targeted gene, and any further transcripts, which may be identified.

Such double-stranded compounds according to the invention can be conjugated (ie. covalently bound) to at least one non-nucleotide or non-polynucleotide moiety. Examples include those described previously.

As will be appreciated, to be stable *in vitro* or *in vivo* the sequence of an siLNA or siRNA compound need not be 100% complementary to its target nucleic acid. The terms "complementary" and "specifically hybridisable" thus imply that the siLNA or siRNA compound binds sufficiently strong and specific to the target molecule to provide the desired interference with the normal function of the target whilst leaving the function of non-target mRNAs unaffected

Discontinuous Strand RNA Complexes

In another aspect, the present invention provides for a composition comprising a nucleic acid complex, typically comprising or consisting of RNA or one or more oligonucleotide analogues thereof, and preferably a pharmaceutically acceptable diluent, carrier, or adjuvant. In one embodiment, the complex includes a core double-stranded region that includes an antisense

strand consisting of a contiguous nucleobase sequence with at least about 80% sequence identity, at least about 85%, 90%, 95%, 98%, 99%, up to about 100% sequence identity to a corresponding region of a nucleic acid which encodes the COMPLEMENT COMPONENT 8-BETA (C8-BETA) sequence represented by SEQ ID NOs: 1 (human), 333 (rat) or 334 (mouse) or a naturally occuring allelic variant thereof. Preferred complexes include at least one oligonucleotide analogue, the RNA complex further comprising a discontinuous passenger strand that is typically hybridised to the antisense strand. For most applications, the discontinuous passenger strand includes a discontinuity such as a nick or a gap or a linker or other such interruption as described herein.

In one embodiment of the foregoing, the RNA complex is generally capable of mediating nucleic acid modifications of a corresponding target nucleic acid. Preferably, the nucleic acid modification is selected from one or more of the group consisting of RNA interference, gene-silencing, gene-suppression, translation arrest, translation inhibition, RNA degradation, RNA cleavage and DNA methylation. Typical RNA complexes mediate degradation of a target RNA or mediate translational inhibition of a target RNA or a combination of both.

In a particular RNA complex of the invention, the core double-stranded region includes between about 15 to about 40 base pairs such as 18 base pairs, 19 base pairs, 20 base pairs, 21 base pairs, 22 base pairs and 23 base pairs. In one embodiment, the RNA complex includes one or more overhangs, for instance, one or two overhangs. An example of an overhang is a 3'-overhang. In one embodiment, the passenger of the RNA complex comprises the 3'-overhang.

Although a variety of overhang lengths are compatible with the invention, generally the length of the overhang is between about 1 and about 8 nucleotides such as 1 nucleotide, 2 nucleotides and 3 nucleotides. RNA complexes in accord can include at least one blunt end including having both ends blunt ended. The length of the RNA complex can be nearly any length sufficient to achieve intended results including between about 18 to about 22 base pairs. In this embodiment, it is preferred that the antisense strand and the passenger strand each include a 3'-overhang of between about 1 to about 3 nucleotides.

As mentioned, particular RNA complexes of the invention include a discontinuous passenger strand. In one embodiment, the complex includes at least a first and a second RNA-molecule, which together, optionally with one or more further RNA molecules, form the discontinuous passenger strand. Preferably, the first RNA molecule is hybridised to the downstream part of the antisense strand and the second RNA molecule is hybridised to the upstream part of the antisense strand. In one embodiment, the passenger strand comprises between about 1 to about 4 further RNA molecules, which together with the first and second RNA-molecules preferably form the discontinuous passenger strand. In another embodiment, the passenger strand includes only the first and second-RNA molecules, and, for example, no further RNA molecules.

A discontinuity on the passenger strand can be formed, for instance, by a nick or nicks in which the at least first and second RNA molecules, and optionally the further RNA molecules of the passenger strand are separated thereby. If desired however, the at least first and second RNA molecules and optionally said further RNA molecules of the passenger strand are separated by a gap, or optionally gaps, such as those selected from the group consisting of: a 1 nucleotide gap, a 2 nucleotide gap, a 3 nucleotide gap, a 4 nucleotide gap, a 5-nucleotide gap, a 6-nucleotide gap, a 7-nucleotide gap, an 8- nucleotide gap, a 9-nucleotide gap, a 10-nucleotide gap, an 11-nucleotide gap and a 12-nucleotide gap. In embodiments in which the discontinuity is related to a linker, the first RNA molecule of the passenger strand can be connected to the antisense strand by the linker. In one embodiment, the linker connects the 5' end of the first RNA molecule of the passenger strand to the 3' end of the antisense strand. In another embodiment, the second RNA molecule of the passenger strand can be connected to the antisense strand by the linker. If desired, the linker can connect the 3' end of the second RNA molecule of the passenger strand to the 5' end of the antisense strand. The at least first and the second RNA molecules of the passenger strand, and optionally said further RNA molecules of the passenger strand can be connected by the linker, or optionally a plurality of linkers. A variety of linkers are compatible with the invention such as those which are not a single stranded RNA linker.

In some invention embodiments of the RNA complex, the antisense strand is not covalently linked to the passenger strand. If desired, the RNA molecules which form the

discontinuous passenger strands are not covalently linked to any other of the RNA molecules which form the discontinuous passenger strands.

Certain RNA complexes according to the invention feature three non-linked RNA molecules, namely the antisense strand, and the first and the second RNA molecules which together form the discontinued passenger strand. In one embodiment, the discontinued passenger strand has a discontinuity at a position selected from the group of: position 3, position 4, position 5, position 6, position, position 7, position 8, position 9, position 10, position 11, position 12, position 13, position 14, position 15 position 16, position 17, position 18, position 19, position 20, position 21, position 22, position 23, position 24, position 25. Preferably, the position is calculated in the 5' to 3' direction from the first nucleotide of the passenger strand base paired to the antisense strand in the of the passenger strand.

For some invention embodiments, it will be useful to have an RNA complex in which the 5-ends of the RNA complex are either phosphorylated or available for phoshorylation. In one embodiment, the first RNA molecule comprises a 5'-end phosphate group and a 3'-end hydroxy group. In another embodiment, the second RNA molecule comprises a 5'-end phosphate group and a 3'-end hydroxy group. In certain embodiments, all the RNA molecules which form the discontinuous passenger strand each comprise a 5'-end phosphate group and a 3'-end hydroxy group.

It will often be useful to have RNA complexes that include or in some cases consist of at least one nucleotide analogue such as those disclosed herein. In one embodiment, the passenger strand of the RNA complex comprises at least one nucleotide analogue such as between 2 and 10 nucleotide analogues. Alternatively, or in addition, the first RNA molecule of the passenger strand comprises one or more nucleotide analogues such as at least 2 nucleotide analogues. Alternatively, or in addition, the second RNA molecule of the passenger strand comprises one or more nucleotide analogue such as at least 2 nucleotide analogues.

In embodiments in which an RNA complex includes a nucleotide analogue, the location of the analogue is preferably within the three terminal (5' or 3' respectfully) nucleobase units of the first and/or second RNA molecule. Alternatively, or in addition, at least one of the further

RNA molecules of the passenger strand comprise at least one nucleotide analogue. For instance, each further RNA molecule which forms part of the discontinuous passenger strand comprises at least one nucleotide analogue such as at positions 10 and 12 from the 5' end of the passenger strand. In one embodiment, each RNA molecule which forms part of the discontinuous passenger strand and comprises at least one nucleotide analogue, such as at least two nucleotide analogues.

In one embodiment, the passenger strand includes an additional one, two, three, four or five LNA monomers between the 3'and 5'end of the passenger strand such as at position 3, 9, 13, and 15 relative to the 5'end (position 1) and the 3'overhang positions. However in this example of the invention, the passenger strand is broken in two parts, for instance, between positions 10 and 11. Thus in one embodiment, each portion of the passenger strand includes at least one LNA monomer, for instance, one, two, three, four, five, six or seven of same, more preferably five or six of same in which one, two, or three, or four LNA monomers are position on one of the passenger strands and the remaining monomers positioned on the other strand.

It will often be useful to make and use an RNA complex that has desirable melting temperature properties. Thus in one embodiment, the melting temperature (T_m) for each of the first, second and optionally further RNA molecules which form the discontinuous passenger strand, when formed in a duplex with a complementary RNA molecule with phosphodiester linkages is at least 40^0C.

Preferred lengths of the RNA complexes of the invention will be guided by intended use. Thus in one embodiment, the length of each of the first, second and optionally further RNA molecules which form the discontinuous passenger strand is at least three nucleobase units. In one embodiment, the antisense strand comprises at least 1 nucleotide analogue such as the example where the antisense strand comprises at least 1 nucleotide analogue within the duplex region formed with the discontinuous passenger strand. Alternatively, or in addition, the antisense strand comprises at least one nucleotide analogue at a position which is within 4 nucleobases as counted from the 3' end of the antisense strand. In one embodiment, at least one of the nucleobases present in about the 9 5' most nucleobase units of the antisense strand is a nucleotide analogue. In another embodiment, at least one of the nucleobases present in the region

within 4 - 10 nucleobases from the 3' end 10 of the antisense strand is a nucleotide analogue. In yet another embodiment, the antisense strand has a nucleotide analogue at position 11 from the 5' end of the antisense strand. In yet another embodiment, the antisense strand has RNA nucleotides at position 10 and 12 from the 5' end of the antisense strand. In other embodiment, the 5' most nucleobase units of the antisense strand is an RNA nucleotide unit. Alternatively, or in addition, the antisense strand comprises at least 2 nucleotide analogues.

A wide variety of nucleotide analogues are compatible with the invention. Typically suitable analogues are those that are or are suspected of being compatible with the formation of an A-form or A/B for conformation of the RNA complex. Illustrative analogues include the group consisting of: 2'-O- alkyl-RNA monomers, 2'-amino-DNA monomers, 2'-fluoro-DNA monomers, LNA monomers, arabino nucleic acid (ANA) mononmers, 2'-fluoro-ANA monomers, HNA monomers, INA monomers. A preferred nucleotide analogue is present in discontinuous passenger and/or antisense strand and consists of at least one LNA monomer such as those already disclosed herein. Alternatively, or in addition, the nucleotide analogues present in the discontinuous passenger and/or antisense strand include at least one 2'-MOE-RNA (2'-O-methoxyethyl-RNA) unit or 2'Fluoro DNA unit, such as between about 1 and about 25 units independently selected from either 2'-MOE-RNA (2'-O- methoxyethyl-RNA) units or 2'Fluoro DNA units.

As mentioned, it will often useful to have an RNA complex in which at least one nucleotide is substituted with at least one LNA unit. In one embodiment, the LNA unit or units are independently selected from the group consisting of oxy-LNA, thio-LNA, and amino-LNA, in either of the D-β and L-α configurations or combinations thereof. If desired, the nucleotide analogues present in the antisense strand include at least one LNA unit and/or the nucleotide analogues present in the passenger strand include at least one LNA unit. In one embodiment, the nucleotide analogues present in antisense strand are LNA units. Alternatively, or in addition, all the nucleotide analogues present in passenger strand are LNA units. Various preferred LNA monomers have been disclosed above.

In many embodiments of the RNA complex described herein, at least one of the nucleotide analogues present in the discontinuous passenger strand forms a base pair with a

complementary nucleotide analogue present in the antisense strand. In one embodiment, the passenger strand does not comprise any nucleotide analogues and/or in another embodiment the antisense strand does not comprise any nucleotide analogues. In another embodiment, the antisense strand and discontinuous strand form a complementary duplex of between about 18 to about 22 base pairs. In one embodiment, the duplex may comprise a mismatch.

In one embodiment the number of nucleotide analogues present in the antisense strand or passenger strand (or both, either as separate entities or as a combined total of nucleotide analogues within the RNA complex) is selected from the group consisting of: at least one nucleotide analogue, 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, at least 16, at least 17, at least 18, at least 19 or at least 20, at least 21, at least 22, at least 23, at least 24 and at least 25 nucleotide analogues. Suitably the number of nucleotide analogues may be less than 20, such as less than 18, such as less than 16, such as less than 14, such as less than 12, such as less than 10.

In one embodiment the nucleotide analogues present in discontinuous passenger strand (or antisense strand, or both, either as separate entities or as a combined total of nucleotide analogues within the RNA complex) include at least one 2'-O-alkyl-RNA monomer (such as 2'OME), such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 2'-O-alkyl-RNA monomers (such as 2'OME). Complexes comprising or consisting of 2'OME and LNA are also envisioned.

In one embodiment, which may be the same of different, the nucleotide analogues present in discontinuous passenger strand (or antisense strand, or both, either as separate entities or as a combined total of nucleotide analogues within the RNA complex) include at least one 2'- fluoro-DNA monomer, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 2'-fluoro-DNA monomers.

For many invention applications it will generally be preferred to have at least one LNA monomer present in discontinuous passenger strand. In one embodiment, which may be the same of different, the nucleotide analogues present in discontinuous passenger strand (or antisense

strand, or both, either as separate entities or as a combined total of nucleotide analogues within the RNA complex) include at least one LNA monomer, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 LNA monomers.

In one embodiment the LNA unit or units are independently selected from the group consisting of oxy-LNA, thio-LNA, and amino-LNA, in either of the D-β and L-α configurations or combinations thereof. In one embodiment the nucleotide analogues present in the antisense strand include at least one Locked Nucleic Acid (LNA) unit, 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, at least 16, at least 17, at least 18, at least 19 or at least 20 LNA units. Suitable the number of LNA units may be less than 20, such as less than 18, such as less than 16, such as less than 14, such as less than 12, such as less than 10. In one embodiment all the nucleotide analogues present in antisense strand are Locked Nucleic Acid (LNA) units.

In another embodiment, the antisense strand only comprises a few nucleotide analogue units, such as LNA units. Typically it is preferred the nucleotide units present in the antisense strand a positioned within the 3' half of the antisense strand such as between positions 1 and 9 of the antisense strand, such as position 1, 2, 3, 4, 5, 6, 7, 8, or 9 of the antisense strand, such as within the region of a 3 over-hang, or within the first 3, such first, second or third, nucleobase positions of the duplex as measured from the 3' end of the antisense strand.

In one embodiment the nucleotide analogues present in the passenger strand (or antisense strand, or both, either as separate entities or as a combined total of nucleotide analogues within the RNA complex) include at least one LNA unit 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, at least 16, at least 17, at least 18, at least 19 or at least 20 LNA units. Suitable the number of LNA units may be less than 20, such as less than 18, such as less than 16, such as less than 14, such as less than 12, such as less than 10. In one embodiment all the nucleotide analogues present in passenger strand are Locked Nucleic Acid (LNA) monomers (units).

In one embodiment at least one of the nucleotide analogues present in the discontinuous passenger strand forms a base pair with a complementary nucleotide analogue present in the antisense strand.

In one embodiment all the nucleotide analogues present in the discontinuous passenger strand forms a base pair with a complementary nucleotide analogue present in the antisense strand, other than those nucleotide analogue present in the 3' overhang (if present).

In one embodiment all the nucleotide analogues present in the antisense strand forms a base pair with a complementary nucleotide analogue present in the discontinuous passenger strand, other than those nucleotide analogue present in the 3' overhang (if present). In one embodiment the passenger strand consists or comprises of a 9 - 11 nucleotide (nucleobase) RNA molecule, such as a 10 nucleotide RNA molecule, with between 1 and five nucleotide analogues, such as LNA units, such as two LNA units and a 11 - 13 nucleotide RNA molecule, such as a 12 nucleotide RNA molecule, comprising between 1 and 5 nucleotide analogue units, such as LNA units, such as three LNA residues.

By way of example, and not limitation, the following particular invention complex has the following structure in which bold and underlined text is LNA:

5′ CU**G**CAUTG**C**C 3′ 5′AG**A**A**A**GTUA**GA** 3′ passenger

3′ **GC**GACGUAACGGUCUUUCAAU 5′ antisense

Further disclosure relating to making and using the RNA complexes of the invention (sometimes called sisiRNA) can be found in the following: WO2007/107162 (PCT/DK2007/000146), PA 2006 00433 (DK), and PA 2006 01254 (DK) for disclosure related to making and using such complexes.

Practice of the present invention can be achieved by using one or a combination of the RNA complexes disclosed herein. In one embodiment, the RNA complex has reduced off-target effects as compared to a native RNA complex comprising a non-modular passenger strand. In one embodiment, the RNA complex produces a reduced immune response as compared to a

native RNA complex comprising a non-modular passenger strand. In another embodiment, the RNA complex has a prolonged effect on target nucleic acids as compared to an RNA complex comprising a non-modular passenger strand. Thus in one embodiment, the RNA complex has an increased effect on its target nucleic acid as compared to an RNA complex comprising a non-modular passenger strand. A preferred target nucleic acid is the C8-beta sequence disclosed as SEQ ID NO: 1 (human), SEQ ID NO: 333 (rat), or SEQ ID NO: 334 (mouse).

The RNA complexes of the invention can be made by one or a combination of strategies. In one approach, the method includes incubating an antisense strand with the at least two RNA molecules which form a discontinuous passenger strand, and optionally further RNA molecules of the passenger strand under conditions wherein a RNA complex comprising a core double stranded region is formed. Preferably, the RNA complex is capable of mediating RNA interference of a corresponding cellular RNA, wherein either said incubation occurs within a pharmaceutically acceptable diluent, carrier, or adjuvant, or said RNA complex is subsequently admixed with a pharmaceutically acceptable diluent, carrier, or adjuvant.

The foregoing RNA complexes have a variety of uses. In one embodiment, the invention features use of an RNA complex as defined herein for the manufacture of a medicament for the treatment of a disease associated with undesired formation of a membrane attack complex (MAC) such as those mentioned below.

Also provided is a method for treating, preventing or reducing onset of the disease or reducing symptoms thereof in a patient, the method comprising administering one or more of the RNA complexes disclosed herein preferably in combination with a pharmaceutically acceptable, buffer, adjuvant, or vehicle as described herein.

The present invention also features a method of reducing the level of a target RNA (or gene expression) in a cell or an organism comprising contacting the cell or organism with at least one RNA complex as defined herein sufficient to modulate that gene expression. Preferably, the antisense strand of the RNA complex is essentially complementary to a region of the target RNA.

As discussed, an RNA complex suitable for use with the invention can include at least one nucleotide analogue. In one embodiment, the first RNA molecule of the passenger strand does not comprise a 2'-O-methyl ribose at position 9 from the 5' end. In another embodiment, the first RNA molecule of the passenger strand does not comprise a 2'-O-methyl ribose at position 9 from the 5' end.

Also provided by the present invention is a method of mediating nucleic acid modifications of a target nucleic acid in a cell or an organism preferably comprising at least one of and preferably all of the steps:

a. contacting said cell or organism with the RNA complex as defined herein and under conditions wherein target specific nucleic acid modifications can occur, and

b. mediating a target specific nucleic acid modification guided by the antisense strand of the RNA complex.

In one embodiment of the foregoing method, the step of mediating nucleic acid modifications is selected from the group consisting of RNA interference, gene-silencing, RNA degradation, RNA cleavage and DNA methylation.

The invention also provides a method of examining the function of a gene in a cell or organism comprising:

a. introducing an RNA complex as defined herein that targets the RNA encoded by the gene, such as an mRNA or other functional RNA, for degradation or silencing or suppression into the cell or organism, thereby producing a test cell or test organism,

b. maintaining the test cell or test organism under conditions under which degradation or silencing or suppression of the RNA encoded by the gene occurs, thereby producing a test cell or test organism in which mRNA levels of the gene is reduced, and

c. observing the phenotype of the test cell or organism produced in step b and optionally comparing the observed phenotype with the phenotype of an appropriate control cell or control organism, thereby providing information about the function of the gene.

Practice of the invention provides important advantages particularly in embodiments in which an invention compound (e.g., antisense, siRNA, sisiRNA) includes an LNA monomer.

For example, one advantage of embodiments in which a compound of the invention includes an LNA monomer (e.g., antisense compound, siLNA, sisiLNA) is their improved stability in biological fluids, such as serum. Thus, one embodiment of the invention includes the incorporation of LNA monomers into a standard DNA or RNA oligonucleotide to increase the stability of the resulting siLNA compound or antisense oligomer in biological fluids e.g. through the increase of resistance towards nucleases (endonucleases and exonucleases). Accordingly, the compounds of the invention will, due to incorporation of LNA monomers, exhibit an increased circulation half-life as a result of its increased melting temperature and/or its increased nuclease resistance. The extent of stability will depend on the number of LNA monomers used, their position in the oligonucleotides and the type of LNA monomer used. Compared to DNA and phosphorothioates the following order of ability to stabilise an oligonucleotide against nucleolytic degradation can be established: DNA<<phosphorothioates, LNA-phosphordiester<LNA-phosphorothioates.

For many applications, preferred compounds according to the invention include compounds which, when incubated in serum (e.g. human, bovine or mice serum), such as in 10% foetal bovine serum in a physiological salt solution at 37°C for 5 hours, are degraded to a lesser extent than the corresponding ssDNA, ssRNA or dsRNA compound. Preferably, less than 25% of the initial amount of the compound of the invention is degraded after 5 hours, more preferably less than 50% of the initial amount of the compound of the invention is degraded after 5 hours, even more preferably less than 75% of the initial amount of the compound of the invention is degraded after 5 hours. In another embodiment, it is preferred that less than 25% of the initial amount of the compound of the invention is degraded after 10 hours, and even more preferred that less than 50% of the initial amount of the compound of the invention is degraded after 10 hours.

As will be apparent from the foregoing, compounds of the invention may include one or more LNA monomers alone or in combination with nucleotides that are either naturally-occuring

or nucleotide analogues. Such other residues may be any of the residues discussed herein and include, for example, native RNA monomers, native DNA monomers as well as nucleotide variants and analogues such as those mentioned in connection with the definition of "nucleotide" above. Specific examples of such nucleotide variants and analogues include, 2'-F, 2'-O-Me, 2'-O-methoxyethyl (MOE), 2'-O-(3-aminopropyl) (AP), hexitol nucleic acid (HNA), 2'-F-arabino nucleic acid (2'-F-ANA) and D-cyclohexenyl nucleoside (CeNA). Furthermore, the internucleoside linkage may be a phosphorodiester, phosphorothioate or N3'-P5' phosphoroamidate internucleoside linkages as described above.

In general, the individual strands of the compounds of the invention that include one or more LNA monomers will contain at least about 5%, at least about 10%, at least about 15% or at least about 20% LNA monomer, based on total number of nucleotides in the strand. In certain embodiments, the compounds of the invention will contain at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80% or at least about 90% LNA monomer, based on total number of nucleotides in the strand.

Compounds of the invention can be manufactured using techniques disclosed herein including syntheses provided by U.S. Pat. Publication No. 2007/0191294 and WO2007/107162.

Pharmaceutical Compositions and Administration

A preferred use of the compounds of the invention will be as drugs for the treatment, prevention, and/or alleviation of symptoms associated with acute or chronic neuropathy. The design of a potent and safe drug often requires the fine-tuning of diverse parameters such as affinity/specificity, stability in biological fluids, cellular uptake, mode of action, pharmacokinetic properties and toxicity. These and other parameters will be known to the art-skilled.

Accordingly, in a further aspect the present invention relates to a pharmaceutical composition comprising a compound according to the invention and a pharmaceutically acceptable diluent, carrier or adjuvant.

In a still further aspect the present invention relates to a compound according to the invention for use as a medicament.

As will be understood, dosing is dependent on severity and responsiveness of the neuropathy to be treated and the course of treatment lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved. Optimal dosing schedules can be calculated from measurements of drug accumulation in the body of the patient. Optimum dosages may vary depending on the relative potency of individual invention compounds and/or the indication to be treated (see below). Generally it can be estimated based on EC_{50}s found to be effective in *in vitro* and *in vivo* animal models. In general, dosage is from 0.01 micrograms to 1 g per kg of body weight, and may be given once or more daily, weekly, monthly or yearly, or even once every 2 to 10 years or by continuous infusion for hours up to several months. The repetition rates for dosing can be estimated based on measured residence times and concentrations of the drug in bodily fluids or tissues. Following successful treatment, it may be desirable to have the patient undergo maintenance therapy to prevent the recurrence of the disease state.

As will be appreciated, the present invention also features a pharmaceutical composition, which comprises at least one compound of the invention (e.g., antisense compound, siLNA, siRNA, sisiLNA) as an active ingredient. It should be understood that the pharmaceutical composition according to the invention optionally comprises a pharmaceutical carrier, and that the pharmaceutical composition optionally comprises further compounds, such as anti-inflammatory compounds (e.g., non-steroid and steroid anti-inflammatory agents) and/or immuno-modulating compounds.

A compound of the invention can be employed in a variety of pharmaceutically acceptable salts. As used herein, the term refers to salts that retain the desired biological activity of the herein-identified compounds and exhibit minimal undesired toxicological effects. Non-limiting examples of such salts can be formed with organic amino acid and base addition salts formed with metal cations such as zinc, calcium, bismuth, barium, magnesium, aluminum, copper, cobalt, nickel, cadmium, sodium, potassium, and the like, or with a cation formed from ammonia, N,N-dibenzylethylene-diamine, D-glucosamine, tetraethylammonium, or

ethylenediamine.

In one embodiment of the invention the invention compound may be in the form of a pro-drug. Oligonucleotides are by virtue negatively charged ions. Due to the lipophilic nature of cell membranes the cellular uptake of oligonucleotides are reduced compared to neutral or lipophilic equivalents. This polarity "hindrance" can be avoided by using the pro-drug approach (see e.g. Crooke, R. M. (1998) in Crooke, S. T. *Antisense research and Application*. Springer-Verlag, Berlin, Germany, vol. 131, pp. 103-140). In this approach the oligonucleotides are prepared in a protected manner so that the oligo is neutral when it is administered. These protection groups are designed in such a way that they can be removed when the oligo is taken up by the cells. Examples of such protection groups are S-acetylthioethyl (SATE) or S-pivaloylthioethyl (t-butyl-SATE). These protection groups are nuclease resistant and are selectively removed intracellularly.

Pharmaceutically acceptable binding agents and adjuvants may comprise part of the formulated drug. Capsules, tablets and pills etc. may contain for example the following compounds: microcrystalline cellulose, gum or gelatin as binders; starch or lactose as excipients; stearates as lubricants; various sweetening or flavouring agents. For capsules the dosage unit may contain a liquid carrier like fatty oils. Likewise coatings of sugar or enteric agents may be part of the dosage unit. The invention compounds may also be emulsions of the active pharmaceutical ingredients and a lipid forming a micellular emulsion. A compound of the invention may be mixed with any material that do not impair the desired action, or with material that supplement the desired action. These could include other drugs including other nucleotide compounds. For parenteral, subcutaneous, intradermal or topical administration the formulation may include a sterile diluent, buffers, regulators of tonicity and antibacterials. The active compound may be prepared with carriers that protect against degradation or immediate elimination from the body, including implants or microcapsules with controlled release properties. For intravenous administration the preferred carriers are physiological saline or phosphate buffered saline.

Preferably, an invention compound is included in a unit formulation such as in a pharmaceutically acceptable carrier or diluent in an amount sufficient to deliver to a patient a therapeutically effective amount without causing serious side effects in the treated patient.

The pharmaceutical compositions of the present invention may be administered in a number of ways depending upon whether local or systemic treatment is desired and upon the area to be treated. Administration may be (a) oral (b) pulmonary, e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, (c) topical including epidermal, transdermal, ophthalmic and to mucous membranes including vaginal and rectal delivery; or (d) parenteral including intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial, e.g., intrathecal or intraventricular, administration. In one embodiment the pharmaceutical composition is administered IV, IP, orally, topically or as a bolus injection or administered directly in to the target organ. Pharmaceutical compositions and formulations for topical administration may include transdermal patches, ointments, lotions, creams, gels, drops, sprays, suppositories, liquids and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, gloves and the like may also be useful. Preferred topical formulations include those in which the compounds of the invention are in admixture with a topical delivery agent such as lipids, liposomes, fatty acids, fatty acid esters, steroids, chelating agents and surfactants. Compositions and formulations for oral administration include but is not restricted to powders or granules, microparticulates, nanoparticulates, suspensions or solutions in water or non-aqueous media, capsules, gel capsules, sachets, tablets or minitablets. Compositions and formulations for parenteral, intrathecal or intraventricular administration may include sterile aqueous solutions which may also contain buffers, diluents and other suitable additives such as, but not limited to, penetration enhancers, carrier compounds and other pharmaceutically acceptable carriers or excipients.

Pharmaceutical compositions of the present invention include, but are not limited to, solutions, emulsions, and liposome-containing formulations. These compositions may be generated from a variety of components that include, but are not limited to, preformed liquids, self-emulsifying solids and self-emulsifying semisolids. Delivery of drug to tumour tissue may be enhanced by carrier-mediated delivery including, but not limited to, cationic liposomes, cyclodextrins, porphyrin derivatives, branched chain dendrimers, polyethylenimine polymers, nanoparticles and microspheres (Dass C R. *J Pharm Pharmacol* 2002; 54(1):3-27). The pharmaceutical formulations of the present invention, which may conveniently be presented in

unit dosage form, may be prepared according to conventional techniques well known in the pharmaceutical industry. Such techniques include the step of bringing into association the active ingredients with the pharmaceutical carrier(s) or excipient(s). In general the formulations are prepared by uniformly and intimately bringing into association the active ingredients with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product. The compositions of the present invention may be formulated into any of many possible dosage forms such as, but not limited to, tablets, capsules, gel capsules, liquid syrups, soft gels and suppositories. The compositions of the present invention may also be formulated as suspensions in aqueous, non-aqueous or mixed media. Aqueous suspensions may further contain substances which increase the viscosity of the suspension including, for example, sodium carboxymethyl-cellulose, sorbitol and/or dextran. The suspension may also contain stabilizers. The compounds of the invention may also be conjugated to active drug substances, for example, aspirin, ibuprofen, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic. Other useful conjugates have been disclosed above.

Diluents, carriers, and buffers that render an oligonucleotide orally available to a mammal such as a rodent or human patient are within the scope of the present invention. A particular example of such a carrier is a caprate salt, for example, sodium caprate. See Tillman, LG et al. (2008) *J. of Pharmaceutical Sciences*, Jan. 97(1) 225; Gonzalez, FM et al. (2003) *Eur. J. Pharm. Biopharm*, Jan: 55(1): 19-26; Aouadi, M et al. (2009) *Nature* 458: 1180; and references disclosed therein for information relating to making formulations suitable for orally administering an oligonucleotide.

It will be appreciated that a particular formulation or administration route of the invention may include a single invention compound as the sole active agent. However, in other invention embodiments, the formulation or administration route includes two or more invention compounds such as 2, 3, 4, 5, 6 7, 8, 9, or 10 of such compounds. Generally, the number of invention compounds empolyed will be less than 5, such as one, two or three. For example, such a formulation or administration may contain one or more siLNA or sisiLNA compounds, targeted to a first nucleic acid and one or more additional siLNA or sisiLNA compounds targeted to a second nucleic acid target. Two or more combined compounds may be used together or sequentially.

The compounds of the invention are useful for a number of therapeutic applications as indicated above. In general, therapeutic methods of the invention include administration of a therapeutically effective amount of a desired compound (or one or more compounds such as 1, 2, 3, or 4 of same) to a mammal, particularly a human. In a certain embodiment, the present invention provides pharmaceutical compositions containing (a) one or more compounds of the invention, and (b) one or more other agents such as anti-inflammatory agents or complement antagonists such as those disclosed herein. When used with the compounds of the invention, such compositions and agents may be used individually, sequentially, or in combination with one or more other such compositions and agents including other therapies including those accepted for the prevention or treatment of acute or chronic neuropathies.

The compounds of the present invention can be utilized for as research reagents for diagnostics, therapeutics and prophylaxis. In research, the compound may be used to specifically inhibit the synthesis of target genes in cells and experimental animals thereby facilitating functional analysis of the target or an appraisal of its usefulness as a target for therapeutic intervention. In one embodiment, the oligomers, siRNA and sisiRNA compositions of the invention may be used to detect and quantitate target 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 target is treated by administering the compounds in accordance with this invention. Further provided are methods of treating an animal particular mouse and rat and treating a human, suspected of having or being prone to a disease or condition, associated with expression of target by administering a therapeutically or prophylactically effective amount of one or more of the compounds or compositions of the invention.

Nerve Regeneration

As discussed, the present invention further provides for a method for treating, preventing or reducing symptoms of a disorder mediated by undesired activity of the complement system. In one embodiment, the method includes administering at least one compound of the invention, particularly at least one pharmaceutical composition as described herein to a mammal (e.g, a

primate or non-primate mammal, especially a human patient) in need thereof. By the phrase «disorder mediated by undesired activity of the complement system» is meant a neuronal disorder manifested in whole or in part by an inability or insufficiency in nerve regeneration. Examples of such disorders include those manifesting an inability or insufficiency in nerve regeneration following acute or chronic injury to nerves in the peripheral nervous system (PNS) or central nervous system (CNS). An inability or insufficiency to regenerate nerves (or to improve the function of damaged nerves can be detected and in some cases quantified by tests known in the field. See e.g., Ramaglia, V. et al. (2007) *J. Neurosci.* 27:7663 (describing, among other things, assays to detect and optionally quantify nerve degeneration and regeneration in rats); Wolf, SL (2001) *Stroke* 32:1635 (motor function test); S. Van Tuijl, et al. (2002) *Spinal Cord* 40:51 (motor function test); Sheikh, K et al. (1980) *Rheumatology* 19:83 (motor function test); Chan A.We et al. (2001) J. *Neurol. Neurosurg. Psychology* 55:56 (sensory function test) ; and Mayuko. W et al. (2005) *J. Jap. Soc. For Surgery of the* Hand (2005) 22:842 (multiple sensory function tests); and references cited therein.

Methods for monitoring an improvement in axonal regeneration have been described and generally include various functional tests that can be conducted in human patients. Such tests generally monitor recovery of sensory and/or motor function such as the Weinstein Enhanced Sensory Test (WEST), Semmes-Weinstein Monofilament Test (SWMT) and others. See WO2008/044928 (PCT/NL2007/050490), Ristic S, et al. (2000) *Clin Orthop Relat Res.* 370:138; and references cited therein for methods for detecting and monitoring neuronal regeneration and for methods of classifying various neuronal insults. The appropriate dose of a compound of the invention is one that can be shown to promote axonal regeneration according to these or other acceptable tests as described herein. By «effective dose», «therapeutic amount» or related phrase is meant that amount sufficient to achieve a desired therapeutic outcome as determined by these or other acceptable tests.

Compositions and methods of the invention can be used to prevent, treat, or reduce symptoms associated with an acute or chronic nerve injury. Conditions requiring axonal regeneration, whether acute or chronic, have been disclosed, for instance, in WO2007/044928 and references cited therein. Acute trauma to peripheral nerves is relatively common including blunt trauma or from penetrating missiles, such as bullets or other objects. Injuries from stab

wounds or foreign bodies (eg, glass, sheet metal) resulting in clean lacerations of nerves are known as are nerve injuries stemming from bone fractures and fracture-dislocations including ulnar nerve neurapraxia and radial nerve lesions and palsies. In general, acute nerve injury often produces a long-lasting neuropathic pain, manifested as allodynia, a decrease in pain threshold and hyperplasia, and an increase in response to noxious stimuli. See Colohan AR, et al. (1996) *Injury to the peripheral nerves.* In: Feliciano DV, Moore EE, Mattox KL. *Trauma.* 3rd ed. Stamford, Conn: Appleton & Lange; 1996:853.

Further acute nerve injuries within the scope of the present invention include traumatic brain injury (TBI) and acute injuries to the spinal cord and peripheral/sensory nerves, various sports injuries involving nerve insult. See also WO2007/044928 and references cited therein.

In embodiments in which it is desired to promote axonal regeneration in response to an acute nerve injury, it will be generally preferable to administer at least one invention compound (e.g., one, two, or three of same) as soon as possible after the insult such as within about 24, 12, 6, 3, 2, 1, or less hours, preferably within 5, 10, 20, 30 or 40 minutes after the insult. Additionally, at least one of the invention compounds can be administered propholactically (as a precautionary measure) before a medical intervention (e.g., surgery) associated with some risk of nerve damage. In this invention embodiment, nerve regeneration will be favorably enhanced and recovery times shortened.

As mentioned, the invention is useful for treating, preventing, or reducing symptoms associated with chronic injury to the nervous system. Non-limiting examples include those already described in WO2007/044928 including many chronic demyelinating neuropathies (CMT1 type), HMSN (CMT) disease type 1A and 1B, HNPP and other pressure palsies, Bethlem's myopathy, Limb-Geridle muscular dystrophy, Miyoshi myhopathy, rhizomelic chondrodysplasia punctata, HMSN-Lom, PXE (pseudoxanthomatosis elastica), CCFDN (congential cataract facial dysmorphism and neuoropathy), Alzheimer's disease, Huntington's disease, Charcot-Marie-Tooth disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), Guillain-Barré syndrome (GBS, also known as acute inflammatory demyelinating polyneuropathy or AIDP), leukodystrophy, Parkinson's disease, motor neuron disease, diabetic neuropathies, distal axonopathies such as those resulting from a metabolic or toxic neuronal

derangement (e.g., relating to diabetes, renal failure, exposure to a drug or toxin (e.g., an anti-cancer drug), malnutrition or alcoholism), mononeuropathies, radiculopathies (*e.g.*, of cranial nerve VII; Facial nerve), Hansen's disease (leprosy) and plexopathies such as brachial neuritis; and focal entrapment neuropathies (e.g., carpal tunnel syndrome).

Further non-limiting examples include myasthenia gravis, chronic inflammatory demyelinating polyradiculoneuropathy (CIPD) and age-related macular degeneration (wet and dry forms), organ transplantation (ischemic reperfusion, allograft rejection), rheumatoid arthritis and cardiovascular disease (e.g., atherosclerosis)..

In embodiments in which the therapeutic goal is to treat a chronic nerve insult, more long term administration protocols will be generally preferred. Thus in one embodiment, at least one invention compound (e.g., one, two, or three of same) will be administered by any acceptable route mentioned herein for at least 24 hours, preferably for a few days, weeks or months up to a few years as needed to treat or reduce symptoms associated with the particular indication.

As mentioned, compounds of the invention can be used alone or in combination with other agents to treat, prevent or reduce symptoms of a disorder mediated by undesired activity of the complement system. In one embodiment in which inflammation accompanies or is suspected of accompanying the disorder, the method will include the step of administering at least one anti-inflammatory agent (e.g., 1, 2 or 3 of same) and/or a complement inhibitor. A non-limiting example of an anti-inflammatory agent is a steroid (e.g., a corticosteroid) or a non-steroidal anti-inflammatory drug (NSAID). Examples of other suitable steroids include cortisone, hydrocortisone, triamcinolone (kenacort), methylprednisolone (medrol), prednisolone (prelone), prednisone and dexamethasone (decadron). Illustrative NSAIDs include acetylsalicylic acid (aspirin, ecotrin), choline magnesium salicylate (trilisate), Cox-2 inhibitors, diclofenac (voltaren, cataflam, coltaren-XR), diflunisal (dolobid), etodolac, (lodine), fenoprofen (nalfon), flurbiprofen (ansaid), ibuprofen, indomethacin, (indocin, indocin-SR), ketoprofen, meclofenamate, (meclomen), nabumetone, (relafen), naproxen, (naprosyn, naprelan, anaprox, aleve), oxaprozin, (daypro), phenylbutazone, (butazolidine), piroxicam, (feldene), salsalate, (disalcid, salflex), tolmetin, (tolectin) and valdecoxib, (bextra).). Administration of an invention compound may be

before, during or after administration of any other therapeutically effective drug disclosed herein provided intended results are acheived.

In embodiments in which a composition of the invention is used to prevent, treat or reduce symptoms associated with multiple sclerosis, the composition may be used alone or in combination with one or more approved drugs such as Rebif ®(interferon beta-1a, Serono, Pfizer), Avonex® (interferon beta-1a, Biogen-Idec), Betaseron® (interferon beta-1b, Bayer Schering), Copaxone® (glatiramer acetate,Teva), Novantrone® (mitozantrone, Serono), Gilenya® (FTY720, fingolimod; Novartis) and Tysabri® (natalizumab, Biogen-Idec). As discussed in more detail below, co-administration of an invention compound will allow a patient to be exposed to less of an approved drug over a particular time period, thereby decreasing chances for undesirable side effects.

Drug Holiday

As discussed, it is possible to prevent, treat or reduce the severity of disorders mentioned herein by administering at least one invention compound . However, it has been found that it is not necessary to expose subjects to the compound continuously to achieve a desired effect. That is, it is possible to reduce administration of the compound, sometimes substantially, over a time period referred to herein as a "drug holiday." During the drug holiday, complement mRNA remains low (less than about 10%, 20%, 30%, 40%, 50%, or more compared to control and using qPCR) over a several days, over a few weeks, up to about a month after administration of the invention compound. It is believed that the amount of complement mRNA produced under these conditions is insufficient to produce normal levels of the encoded protein. Administration of an invention compound, either alone or in combination with another drug is not needed over this time period. After the drug holiday, administration of one or more invention compounds alone or in combination with other drug(s) can be resumed.

Practice of this aspect of the invention provides important advantages.

For example, use of the invention can provide human patients with much sought after relief from invasive, sometimes painful, and often repetitive and expensive treatment protocols. Potentially serious side effects can be reduced, delayed, or in some instances eliminated. By way

of example, risk of developing nausea, flu-like symptoms, injection site reactions, alopecia, infections, pneumonia, menstruation problems, depression, cholelithiasis, and/or progressive multifocal leukoencephalopathy (PNL) has been reported in some patients receiving drugs to treat multiple sclerosis. These and other side effects can be reduced or avoided in some cases by practice of the invention.

Additionally, costs associated with repeated and frequent dosing of drugs can be reduced by use of the invention. As an example, each of Rebif ®, Avonex® , Betaseron®, Gilenya® and Copaxone® is said to be administered to multiple sclerosis patients once or more every week, usually by a painful injection. It is believed that co-administration of an invention compound will result in less drug being required per administration. Alternatively, or in addition, less frequent dosing of drug will be needed. In either case, patient treatment costs are lowered and patient comfort is enhanced. Other drugs used to treat multiple sclerosis are said to be administered to patients every few months (eg., Novantrone®, and Tysabri®). Even in these embodiments, practice of the invention can reduce the amount of drug required, or result in less frequent dosing, thereby providing less risk of side effects and lower costs.

It is a further object of the invention to provide a method to prevent, treat, or reduce symptoms of a disorder referred to herein in which administration of an invention compound alone or in combination with a known drug is reduced during the drug holiday period. In one embodiment, administration of the drug is eliminated entirely during the drug holiday period. After or sometimes during the drug holiday period, the invention compound, known drug (or both) are administered again to the mammal in an amount that is the substantially the same or different (e.g., lower) from the amount administered previously. That second drug administration can be followed by another drug holiday if desired. Thus it is a feature of the invention to provide for at least one drug holiday in which each drug holiday is preferably followed by administration of an amount of at least one of an invention compound, known drug (or both) to achieve a desired therapeutic outcome.

Thus in a particular embodiment, an invention compound is administered to a human patient suffering from (or suspected of suffering from) multiple sclerosis. The invention compound can be administered alone or in combination with a known multiple sclerosis drug

such as Rebif ®, Avonex®, Betaseron®, Copaxone®, Gilenya®, Novantrone® or Tysabri® in an amount that is therapeutically effective. During the drug holiday period, further administration of the invention compound and/or the multiple sclerosis drug can be substantially reduced or even avoided. The method can be repeated once, twice, thrice, or as often as needed to provide a therapeutic regimen that features one, two, three, or more drug holidays. The invention methods can be repeated as needed, e.g., every few days, every few weeks, every few months up to the lifetime of the patient to prevent, treat or reduce symptoms associated with multiple sclerosis.

Prior to induction of a drug holiday, the amount of the invention compound or known drug is preferably, but not exclusively, one that is therapeutically effective. In one embodiment, the amount of the invention compound is generally sufficient to reduce presence of complement mRNA compared to a control and as determined, for example, by pPCR. To begin the drug holiday, the amount of the invention compound or known drug is reduced or eliminated entirely. The drug holiday period is not tied to any particular level of complement mRNA in vivo so long as levels remain below a control as mentioned previously. Following the drug holiday period, the mammal can be subjected to additional therapy including further administration of at least one invention compound either alone or in combination with the known drug such as those used to treat multiple sclerosis as mentioned herein.

Use of a particular drug holiday protocol will be guided by recognized parameters such as the patient's general health, sex, severity of the disorder, type of known drug being administered, etc.

In embodiments in which a composition of the invention is used to prevent, treat or reduce symptoms associated with Parkinson's Disease, the composition may be used alone or in combination with one or more approved drugs such as Levodopa (L-dopa), Sinemet, levodopa, carbidopa (Atamet), Pramipexole (Mirapex), ropinirole (Requip), bromocriptine (Parlodel), Selegiline (Eldepryl, Deprenyl), rasagiline (Azilect), Amantadine or anticholinergic medications and Entacapone. As discussed above (for multiple sclerosis), co-administration of an invention compound will allow a patient to be exposed to less of an approved drug to treat Parkinson's Disease over a particular time period, thereby decreasing chances for undesirable side effects.

Thus in a particular embodiment, an invention compound is administered to a human patient suffering from (or suspected of suffering from) Parkinson's Disease. The invention compound can be administered alone or in combination with a known drug for treating Parkinson's Disease as mentioned above and in an amount that is therapeutically effective. During the drug holiday period, further administration of the invention compound and/or the Parkinson's Disease drug can be substantially reduced or even avoided. The method can be repeated once, twice, thrice, or as often as needed to provide a therapeutic regimen that features one, two, three, or more drug holidays. The invention methods can be repeated as needed, e.g., every few days, every few weeks, every few months up to the lifetime of the patient to prevent, treat or reduce symptoms associated with Parkinson's Disease.

As mentioned above, prior to induction of a drug holiday, the amount of the invention compound or known drug is preferably, but not exclusively, one that is therapeutically effective. In one embodiment, the amount of the invention compound is generally sufficient to reduce presence of complement mRNA compared to a control and as determined, for example, by pPCR. To begin the drug holiday, the amount of the invention compound or known drug is reduced or eliminated entirely. The drug holiday period is not tied to any particular level of complement mRNA in vivo so long as levels remain below a control as mentioned previously. Following the drug holiday period, the mammal can be subjected to additional therapy including further administration of at least one invention compound either alone or in combination with the known drug such as those used to treat Parkinson's Disease as mentioned herein.

In embodiments in which a composition of the invention is used to prevent, treat or reduce symptoms associated with myasthenia gravis, the composition may be used alone or in combination with one or more approved drugs such as Mestinon® (pyridostigmine hydroxide, Valeant), Prostigmin® (neostigmine bromide, Valeant) or Mytelase® (ambenonium hydroxide, Sanofi-Aventis). As discussed above (for multiple sclerosis and Parkinson's Disease), co-administration of an invention compound will allow a patient to be exposed to less of an approved drug to treat myasthenia gravis over a particular time period, thereby decreasing chances for undesirable side effects.

Thus in a particular embodiment, an invention compound is administered to a human patient suffering from (or suspected of suffering from) myasthenia gravis. The invention compound can be administered alone or in combination with a known drug for treating myasthenia gravis as mentioned above and in an amount that is therapeutically effective. During the drug holiday period, further administration of the invention compound and/or the myasthenia gravis drug can be substantially reduced or even avoided. The method can be repeated once, twice, thrice, or as often as needed to provide a therapeutic regimen that features one, two, three, or more drug holidays. The invention methods can be repeated as needed, e.g., every few days, every few weeks, every few months up to the lifetime of the patient to prevent, treat or reduce symptoms associated with myasthenia gravis.

As mentioned above, prior to induction of a drug holiday, the amount of the invention compound or known drug is preferably, but not exclusively, one that is therapeutically effective. In one embodiment, the amount of the invention compound is generally sufficient to reduce presence of complement mRNA compared to a control and as determined, for example, by pPCR. To begin the drug holiday, the amount of the invention compound or known drug is reduced or eliminated entirely. The drug holiday period is not tied to any particular level of complement mRNA in vivo so long as levels remain below a control as mentioned previously. Following the drug holiday period, the mammal can be subjected to additional therapy including further administration of at least one invention compound either alone or in combination with the known drug such as those used to treat myasthenia gravis as mentioned herein.

In embodiments in which a composition of the invention is used to prevent, treat or reduce symptoms associated with Guillian-Barre Syndrome (GBS) and/or chronic inflammatory demyelinating polyradiculoneuropathy (CIDP), the composition may be used alone or in combination with one or more approved drugs/treatments such as plasma exchange, intravenous immunoglobin administration and/or corticosteroid treatment. As discussed above (for multiple sclerosis, Parkinson's Disease and myasthenia gravis), co-administration of an invention compound will allow a patient to be exposed to less of an approved drug to treat the GBS/CIPD over a particular time period, thereby decreasing chances for undesirable side effects.

Thus in a particular embodiment, an invention compound is administered to a human patient suffering from (or suspected of suffering from) GBS and/or CIPD. The invention compound can be administered alone or in combination with a known drug for treating GBS and/or CIPD as mentioned above and in an amount that is therapeutically effective. During the drug holiday period, further administration of the invention compound and/or the GBS/CIPD drug can be substantially reduced or even avoided. The method can be repeated once, twice, thrice, or as often as needed to provide a therapeutic regimen that features one, two, three, or more drug holidays. The invention methods can be repeated as needed, e.g., every few days, every few weeks, every few months up to the lifetime of the patient to prevent, treat or reduce symptoms associated with myasthenia gravis.

As mentioned above, prior to induction of a drug holiday, the amount of the invention compound or known drug is preferably, but not exclusively, one that is therapeutically effective. In one embodiment, the amount of the invention compound is generally sufficient to reduce presence of complement mRNA compared to a control and as determined, for example, by pPCR. To begin the drug holiday, the amount of the invention compound or known drug is reduced or eliminated entirely. The drug holiday period is not tied to any particular level of complement mRNA in vivo so long as levels remain below a control as mentioned previously. Following the drug holiday period, the mammal can be subjected to additional therapy including further administration of at least one invention compound either alone or in combination with the known drug such as those used to treat GBS/CIPD as mentioned herein.

In embodiments in which a composition of the invention is used to prevent, treat or reduce symptoms associated with age-related macular degeneration (AMD, wet and dry forms), the composition may be used alone or in combination with one or more approved drugs/treatments such as VEGF therapy (e.g., with Avastin), laser photocoagulation therapy, photodynamic therapy, surgery, administration of vitamins and/or lifestyle changes (e.g., cessation of smoking). As discussed above (for multiple sclerosis, Parkinson's Disease and myasthenia gravis, for instance), co-administration of an invention compound will allow a patient to be exposed to less of an approved drug to treat the AMD over a particular time period, thereby decreasing chances for undesirable side effects.

Thus in a particular embodiment, an invention compound is administered to a human patient suffering from (or suspected of suffering from) AMD. The invention compound can be administered alone or in combination with a known drug for treating AMD as mentioned above and in an amount that is therapeutically effective. During the drug holiday period, further administration of the invention compound and/or the AMD drug/treatment can be substantially reduced or even avoided. The method can be repeated once, twice, thrice, or as often as needed to provide a therapeutic regimen that features one, two, three, or more drug holidays. The invention methods can be repeated as needed, e.g., every few days, every few weeks, every few months up to the lifetime of the patient to prevent, treat or reduce symptoms associated with AMD.

As mentioned above, prior to induction of a drug holiday, the amount of the invention compound or known drug is preferably, but not exclusively, one that is therapeutically effective. In one embodiment, the amount of the invention compound is generally sufficient to reduce presence of complement mRNA compared to a control and as determined, for example, by pPCR. To begin the drug holiday, the amount of the invention compound or known drug is reduced or eliminated entirely. The drug holiday period is not tied to any particular level of complement mRNA in vivo so long as levels remain below a control as mentioned previously. Following the drug holiday period, the mammal can be subjected to additional therapy including further administration of at least one invention compound either alone or in combination with the known drug such as those used to treat AMD as mentioned herein.

As mentioned, it is within the scope of the present invention to administer a therapeutically effective dose of an invention compound to prevent, treat or reduce symptoms associated with an organ transplantation, (ischemic reperfusion, allograft rejection), rheumatoid arthritis and cardiovascular disease (e.g., atherosclerosis). In these embodiments, the invention compound may be used alone or in combination with another drug for preventing, treating or reducing symptoms of the particular condition.

Thus in one embodiment, a therapeutically effective amount of one or more of the invention compounds is administered to a patient to which an organ transplant will be, is being or has been performed or which is suffering from or suspected of suffering from ischemic reperfusion or allograft rejection. In this embodiment, the therapeutically effective amount of the

invention compound may be administered with a recognized immunosuppresent or other drug for treating the condition such as azathioprine, cyclosporin (e.g, cyclosporine A), D-penicillamine, gold salts, hydroxychloroquine, leflunomide, methotrexate (MTX), minocycline, sulfasalazine (SSZ). Administration of the invention compound may be before, during or after administration of the known drug. If desired, use of the invention compound in this example of the invention may provide a beneficial "drug holiday" along lines discussed above.

In another embodiment, a therapeutically effective amount of one or more of the invention compounds is administered to a patient suffering from or suspected of suffering from arthritis and particularly rheumatoid arthritis. In this embodiment, the therapeutically effective amount of the invention compound may be administered with a recognized drug for treating this disorder such as cyclophosphamide, tumor necrosis factor alpha (TNFα) blockers (e.g., etanercept (Enbrel), infliximab (Remicade), adalimumab (Humira), certolizumab pegol (Cimzia), golimumab (Simponi)),Interleukin 1 (IL-1) blockers such as anakinra (Kineret), monoclonal antibodies against B cells such as rituximab (Rituxan), T cell costimulation blocker such as abatacept (Orencia), Interleukin 6 (IL-6) blockers such as tocilizumab (an anti-IL-6 receptor antibody) (RoActemra, Actemra). Use of anti-inflammatory drugs and analgesics are also within the scope of this invention embodiment, particularly use of glucocorticoids and NSAIDs, aspirin, paracetamol (acetaminophen in US and Canada), opiates, diproqualone, and lidocaine. Administration of the invention compound may be before, during or after administration of the known drug . If desired, use of the invention compound in this example of the invention may provide a beneficial "drug holiday" along lines discussed above.

In another embodiment, a therapeutically effective amount of one or more of the invention compounds is administered to a patient suffering from a cardiovascular ailment such as atherosclerosis. In this embodiment, the therapeutically effective amount of the invention compound may be administered with a recognized drug or treatment for treating this disorder such as one or more of the statins, particularly Atorvastatin, Cerivastatin, Fluvastatin, Lovastatin, Mevastatin, Pitavastatin, Rosuvastatin, Simvastatin, Simvastatin+Ezetimibe, Lovastatin+Niacin formulations, Atorvastatin+Amlodipine Besylate,Simvastatin+Niacin formulations, and ballon angioplasty. Administration of the invention compound may be before, during or after

administration of the known drug. If desired, use of the invention compound in this example of the invention may provide a beneficial "drug holiday" along lines discussed above.

The invention further provides a method of enhancing nerve regeneration in a mammal comprising administering to the mammal (therapeutically or prophylactically) an amount of at least one of the compounds of the invention sufficient to reduce or inhibit expression of C8-beta in the mammal and enhance nerve regeneration therein. Methods for evaluating nerve regeneration enhancement have been described herein including various tests to detect and optionally quantify motor and sensory nerve function.

If desired, one of more of the invention compounds disclosed herein can be combined with one or more of the compounds disclosed in WO 2010/005310 (PCT/NL2009/050418); the disclosure of which is incorporated herein by reference. In this embodiment, combining compounds that target different MAC complex components can reduce expression of the complex.

Other more specific embodiments are within the scope of the present invention. For instance, the invention provides an oligomer of between about 10 to 50 nucleotides in length having a contiguous nucleobase sequence with at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a corresponding region of a nucleic acid which encodes the COMPLEMENT COMPONENT 8-beta (C8-beta) sequence represented by SEQ ID NO: 1 or a naturally occurring allelic variant thereof in which the oligomer includes at least one nucleotide analogue. Preferably, the oligomer is capable of reducing the level of C8-beta mRNA expression in a mammal by at least 20% as determined by a qPCR assay. In one embodiment, the oligomer further includes at least one of a modified internucleoside linkage and a modified nucleobase. Examples are provided herein and include a modified sugar moiety selected from the group consisting of: 2'-O-methoxyethyl modified sugar moiety, a 2'-methoxy modified sugar moiety, a 2'-O-alkyl modified sugar moiety, and a bicyclic sugar moiety. A typically preferred bicyclic sugar moiety for use with this embodiment is an LNA monomer. In a more particular embodiment, the oligomer is a gapmer comprising 2 or 3 LNA momomers at each of the 3' and 5' ends of the oligomer. In one example, the oligomer further includes one or more 2'-

deoxynucleotides positioned between the 5' and 3' wing segments. Optionally, the gapmer may include an additional 2'-deoxynucleotide positioned at the 3' end, the 5' end or both the 3'- and 5' ends of the oligormer. A typically useful modified internucleotide linkage for use with the foregoing invention example is a phosphorothioate internucleoside linkage. The modified nucleobase can be a 5-methylcytosine. Smaller oligomers will often be useful such as between about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 to about 20 nucleotides, more specifically between about 10 to about 18 nucleotides in length, such as 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 nucleotides in length,

Typically useful oligomers for many invention embodiments are those that are targeted to about nucleotides 1-669,700-1098, 1181-1763 from the ATG start site of SEQ ID NO: 1 (starting at the "A"); particularly about nucleotides 55-582, 607-669, 700-830, 887-1098, 1181-1299, 1303-1710; more particularly about 116- 582, 607-669, 723-830, 887-1075, 1181-1228, 1303-1466, 1637-1699 even more particularly for instance, the specific target sites referred to in Tables 1 and 2, below. As will be appreciated, such oligomers may posess less than 100% sequence identify with the sequence represented by SEQ ID NO: 1 provided intended results are achieved. Thus in one embodiment, the oligomer comprises one, two, three, four or five mismatches with respect to the Complement Component C8-beta sequence represented by SEQ ID NO:1. A generally useful oligomer is an antisense oligonucleotide.

Also provided is a pharmaceutical composition that includes at least one oligomer as disclosed herein and a pharmaceutically acceptable diluent, carrier, salt or adjuvant. For many invention embodiments, an oligomer provided as an orally acceptable formulation will be useful.

Also provided is an oligomer according to the present invention for use as a medicament.

Additionally provided is a method of reducing or inhibiting the expression of COMPLEMENT COMPONENT 8-beta in a cell or a tissue in vitro or in vivo, the method comprising the step of contacting said cell or tissue with the oligomer of claim 1 so that expression of the COMPLEMENT COMPONENT 8-beta is reduced or inhibited. The method may include the further step of measuring at least one of the Complement Component 8-beta (C8-

beta) (e.g., by immunodetection methods) , mRNA encoding the protein (e.g., by pPCR) and a membrane attack complex (MAC, e.g., by CH50 assay) following administration of the oligomer.

Also within the scope of the present invention is a method of reducing or inhibiting the production of a membrane attack complex (MAC) in a cell or a tissue in vitro or in vivo, the method comprising the step of contacting said cell or tissue with the oligomer of claim 1 so that expression of the MAC is reduced or inhibited. The method may include the further step of measuring at least one of the Complement Component 8-beta (C8-beta) (e.g., by immunodetection methods) , mRNA encoding the protein (e.g., by pPCR) and a membrane attack complex (MAC, e.g., by CH50 assay) following administration of the oligomer.

The invention further provides an oligomer according to the present invention for use in the treatment of a disorder mediated by undesired activity of the complement system. Also provided is a use of at least one oligomer according to the present invention for the manufacture of a medicament for the treatment of a disorder mediated by undesired activity of the complement system.

The invention also provides a method for treating, preventing or reducing symptoms of a disorder mediated by undesired activity of the complement system. Preferably, the method includes administering at least one of the oligomers and/or pharmaceutical compositions disclosed herein to a mammal in need thereof. In one embodiment, the disorder is a chronic demyelinating neuropathy such as multiple sclerosis (e.g., RRMS type). The method is flexible and can be used so that the pharmaceutical composition includes one or more invention compounds. Alternatively, the pharmaceutical composition can further include a known drug or treatment such as at least one of Rebif® (interferon beta-1a), Avonex® (interferon beta-1a), Betaseron® (interferon beta-1b), Copaxone® (glatiramer acetate), Novantrone® (mitozantrone), and Tysabri® (natalizumab); Levodopa (L-dopa), Sinemet, levodopa, carbidopa (Atamet), Pramipexole (Mirapex), ropinirole (Requip), bromocriptine (Parlodel), Selegiline (Eldepryl, Deprenyl), rasagiline (Azilect), Amantadine or anticholinergic medications and Entacapone; Mestinon® (pyridostigmine hydroxide), Prostigmin® (neostigmine bromide) or Mytelase® (ambenonium hydroxide), plasma exchange, intravenous immunoglobin administration and/or corticosteroid treatment, VEGF therapy (e.g., with Avastin), laser photocoagulation therapy,

photodynamic therapy, surgery, administration of vitamins and/or lifestyle changes (e.g., cessation of smoking), for example.

Also provided is a method for treating, preventing or reducing symptoms of a disorder mediated by undesired activity of the complement system. Preferably, the method includes administering at least one of the pharmaceutical compositions disclosed herein to a mammal in need thereof and further including the administration of one or more of an anti-inflammatory agent and a complement inhibitor.

A particular disorder for which the invention methods are useful is neuronal trauma which may be acute or chronic. An example of acute neuronal trauma is traumatic brain injury (TBI).

The invention further provides an oligomer according to the present invention for use in the treatment of a condition requiring axonal regeneration. Also provided is a use of at least one oligomer according to the present invention for the manufacture of a medicament for the treatment of a condition requiring axonal regeneration. The invention also provides a method for treating, preventing or reducing symptoms of a condition requiring axonal regeneration. Preferably, the method includes administering at least one of the oligomers and/or pharmaceutical compositions disclosed herein to a mammal in need thereof.

Further provided is use of at least one of the compositions or oligomers of the invention (e.g., 1, 2 or 3) for the manufacture of a medicament for the treatment of a condition requiring axonal regeneration.

Further provided is an oligomer according to the present invention for use in the treatment of a chronic dyemylinating condition. A use of at least one oligomer according to the present invention for the manufacture of a medicament for the treatment of a chronic dyemylinating condition is also herewith provided. Non-limiting examples of said chronic dyemylinating conditions are multiple sclerosis and other conditions mentioned herein such as Parkinson's disease, GBS/CIPD, AMD, and myasthenia gravis, organ transplantation (including restenosis and allograft rejection, rheumatoid arthritis and a cardiovascular disorder such as atherosclerosis.

One embodiment provides an oligomer or a use according to the present invention wherein the chronic dyemylinating condition is multiple sclerosis. The invention also provides a method for treating, preventing or reducing symptoms of a chronic dyemylinating condition. Preferably, the method includes administering at least one of the oligomers and/or pharmaceutical compositions disclosed herein to a mammal in need thereof.

Further provided is use of at least one of the compositions or oligomers of the invention (e.g., 1, 2 or 3) for the manufacture of a medicament for the treatment of a chronic dyemylinating condition such as multiple sclerosis or other condition mentioned herein such as Parkinson's disease, GBS/CIPD, AMD, and/or myasthenia gravis, organ transplantation (including restenosis and allograft rejection), rheumatoid arthritis and a cardiovascular disorder such as atherosclerosis.

As described herein before, SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178, 200 are preferred targets of the human C8-beta sequence (Figs. 2A-2E). Further provided is therefore an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer of between about 8 to 50 nucleotides in length (such as 8 to 20 or 10 to 20 or 10 to 50 or 25 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos. Also provided is an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos.

Referring again to Figs. 2A-2E, additionally preferred targets include those sequences represented by SEQ ID Nos: 222, 225, 228, 231 and 234. The invention therefore further provides an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer of between about 8 to 50 nucleotides in length

(such as 8 to 20 or 10 to 20 or 19 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos. Also provided is an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos.

As described herein before, SEQ ID Nos. 335, 337, 339, 341 and 343 (Table 1) are illustrative targets of the human C8-beta sequence. Further provided is therefore an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer of between about 8 to 50 nucleotides in length (such as 8 to 20 or 10 to 20 or 16 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos. Also provided is an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos.

As shown in Table 1, SEQ ID Nos. 336, 338, 340, 342 and 344 represent sequences that are suitable for targeting the above mentioned C8-beta sequences. The invention therefore also provides an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer of between about 8 to 50 nucleotides in length (such as 8 to 20 or 10 to 20 or 16 to 50 nucleotides in length) comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos. Also provided is an oligomer, pharmaceutical composition, method or use according to the present invention, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos.

Reference herein to an «invention compound» or like phrase or «composition of the invention» or like phrase means a composition disclosed herein.

The following examples are given for purposes of illustration only in order that the present invention may be more fully understood. These examples are not intended to limit in any way the scope of the invention unless otherwise specifically indicated.

The disclosures of all references mentioned herein are incorporated herein by reference.

EXAMPLE 1: Antisense inhibitors of complement synthesis in the liver

Complement component C8-beta is mainly expressed in the liver and secreted from this organ into the circulation. Knockdown of the liver expression of C8-beta will substantially reduce ability to form MAC complexes thus reducing the efficacy of the complement system. Many studies have confirmed that systemically administrated antisense oligonucleotides are efficacious in the liver.

Antisense oligonucleotides

The antisense oligomers against complement component C8-beta were designed against sequences with the high homology between rodents and human (See Fig. 3A-3D). The antisense oligonucleotides (15-18mers) were chemically modified with Locked Nucleic Acids (LNA). The LNA protects the oligo against nuclease and increases the affinity (T_m) for complementary mRNA sequences allowing the use of short 15-18 mer oligonucleotides with high efficacy. Oligomers shorter than 18 nucleotides are less prone to activate innate immune responses as

compared to longer oligomers. The oligonucleotide is designed as a gapmer. This means that the three ultimate positions at the 5' end and the penultimate 3 positions at the 3' end of the oligo contain LNA moieties while the center and the 3' ultimate position consists out of DNA analogues. Typical gapmer designs are indicated below:

L=LNA, d=DNA

5' - LLLddddddddddLLLd -3'

or

5' - LLLddddddddddLLL -3'

or

5' - LLddddddddddLL -3'

or

5' - LLddddddddLL -3'

or

5' - LLddddddddLL -3'

in which L= LNA and d=DNA. The whole oligo is phosphorothiolated to reduce renal clearance and increase circulation time *in vivo*. All C residues were converted to methyl-C to reduce immune stimulation.

Table 1, below, shows the structure of LNA modified antisense oligonucleotides made against mouse C8-beta (target sequence and oligo sequence is mouse, bold and large case text=LNA, small case text=DNA):

Oligomer	SEQ ID NO:	LNA modified Oligomer	SEQ ID NO:
Target Position CCAGTGGGATAAATCT 527	335	Oligo5'3' **A G A** t t t a t c c c a c **T G G** Batch No. 1018	336
Target Position CCCAGTTCTCGATCAC 564	337	Oligo5'3' **G T G** a t c g a g a a c t **G G G** Batch No. 1019	338
Target Position GCAGTGACATTATGAA 1208	339	Oligo5'3' **T T C** a t a a t g t c a c **T G C** Batch No. 1020	340
Target Position GGAAGTGGAGTTGCTG 1637	341	Oligo5'3' **C A G** c a a c t c c a c t **T C C** Batch No. 1021	342
Target Position GGACACAAAACAAGAC 1678	343	Oligo5'3' **G T C** t t g t t t t g t g **T C C** Batch No. 1022	344

Table 1

All of the LNA modified oligomers shown in Table 1 were fully phosphorothiolated. All oligomers (ODN's) were synthesized using the phosphoramidite approach on an ÄKTA Oligopilot (GE Healthcare) at 130-185 µmole scales using a polystyrene primer support. The ODN's were purified by ion exchange (IEX) and desalted using a Millipore-membrane. ODN's are characterized by LC/MS (Agilent). The molecular mass of the ODNs was checked by Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) on a Biflex III MALDI (Brucker instruments, Leipzig, Germany).

Target start	Seq ID	oligo start		SEQ ID	Batch
CCAGTGGGATAAATCT	335	527	**A G A** t t t a t c c c a c **T G G**	**336**	**1018**
CCAGTGGGATAAATTT	345		**A A A** t t t a t c c c a c **T G G**	**346**	
CCCAGTTCTCGATCAC	337	564	**G T G** a t c g a g a a c t **G G G**	**338**	**1019**
CCCAGTTCTTGATCAC	347		**G T G** a t c a a g a a c t **G G G**	**348**	
GCAGTGACATTATGAA	339	1208	**T T C** a t a a t g t c a c **T G C**	**340**	**1020**
GCAGAGGTATTCTGAA	349		**T T C** a g a a t a c c t c **T G C**	**350**	
GGAAGTGGAGTTGCTG	341	1637	**C A G** c a a c t c c a c t **T C C**	**342**	**1021**
GGAAGTGGAATTGCTG	351		**C A G** c a a t t c c a c t **T C C**	**352**	
GGACACAAAACAAGAC	343	1678	**G T C** t t g t t t t g t g **T C C**	**344**	**1022**
AGACGTAAGACAAGAC	353		**G T C** t t g t c t t a c g **T C T**	**354**	

Table 2

Table 2 shows the mouse oligomers shown in Table 1 along with preferred corresponding human oligomers without (SEQ ID Nos: 345, 347, 349, 351, and 353) or with LNA monomers

(SEQ ID Nos. 346, 348, 350, 352, and 354). For oligomers with LNA substitutions, LNA monomers are shown in bold uppercase text while DNA is shown in unbold, lower case text.

***In vivo* oligo efficacy test**

Since cell lines in culture do not express (or only at a very low level) complement proteins, the efficacy of the oligonucleotides can be tested directly *in vivo*. The goal of the first screen was to identify from the list of initial designs a set of potential oligos with efficacy *in vivo*. Eight to ten week old mice NMRI strain (Charles River, the Netherlands) were injected (intraperitonally IP or intravenously (IV)) once a day with 5mg/kg of oligo dissolved in PBS. As control we gave PBS injections only in the first screening. For each treatment five mice per group were used. After three days of treatment the mice are sacrificed at day four. Liver samples are taken out and were used to determine the knockdown levels of the protein components using Western blotting for detection of the protein levels and quantative qPCR for mRNA levels.

Western-immuno blots are done after denaturing acryl amide electrophoresis under standard conditions using the mini-protean system (Biorad). Complement proteins are detected using commercially available specific monoclonal and polyclonal antibodies. Immunodection of proteins is done using the Lumi-Light enhanced chemi-luminescence kit (Roche) and the LAS-3000 darkbox imaging system (FujiFilm, Tokyo, Japan). qPCR was done using universal probes (Roche) on the Lightcycler 480 system (Roche)

After selection of potential lead candidates, specific mismatch versions (minimal 3 mismatches) as control will be designed.

Prolonged administration of oligonucleotides (>4 days) was done using osmotic mini pumps (Alzet, Durect Co., Cupertino, Ca, USA). These pumps were implanted dorsally according to the instructions of the manufacturer. The osmotic minipumps were incubated in PBS 20 hours at 37°C prior to implantation to start up the pump, in order to quickly reach a steady delivery rate after implantation. The usage of these pumps reduces the stress in the animals in prolonged experiments since it is not required to perform daily injections. In vitro testing showed that the Alzet minipumps reach a steady pumping rate within 24 hours. The osmotic minipumps were filled with oligonucleotides dissolved in PBS.

Mini tox screen

Blood samples are taken to measure aspartate aminotransferase (ASAT) and alanine aminotransferase (ALAT) levels in the serum. ASAT and ALAT levels in serum are determined using standard diagnostic procedures with the H747 (Hitachi/Roche) with the appropriate kits (Roche Diagnostics). Bodyweight is monitored and body temperature of mice is measured daily for each mouse using IPTT-200 transponder chips and a DAS 5002 chip reader (Biomedic Data Systems, Seaford, Dellaware, USA).

Example 2: *In Vivo* Complement mRNA levels after 3 days of treatment with Oligonucleotides

The LNA oligonucleotides shown in Table 1, above, were used to reduce levels of C8-beta mRNA in NMRI nu/nu mice. Four animals per treatment group were used including one PBS control mouse (15 mice total). Mice received IP injections of each oligo at day 1, 2 and 3 (5mg/kg animal). Mice were sacrificed at day 4 and livers excised. RNA was prepared using conventional approaches. C8-beta mRNA was quantified using qPCR with the Roche lightcycler 480 and universal probes according to the manufacturer's instructions.

Figure 4 shows in vivo complement mRNA levels after 3 days of treatment with the complement antisense LNA oligonucleotides.

Example 3: Oligonucleotide 1018 Improves Nerve Recovery *In Vivo*

The following experiment describes the nerve crush experiment (crush of the n. ischiadicus). The nerve crush is a model for peripheral nerve injury. See WO 2010/005310 (PCT/NL2009/050418); and de Jonge et al 2004, *Hum Mol Genet.* 13(3):295-302.

Outline of experiment.

In this particular experiment we tested two oligonucleotides: 1119 directed against C6 and 1018 directed against C8b (see Table I, above). The C6 compound has been disclosed in the WO 2010/005310 (PCT/NL2009/050418) patent application. Mice were treated for several days before the nerve crush to allow C6 or C8b knockdown. The ischiadic nerve was then crushed in one leg and recovery is monitored over time. Recovery of nerve function was monitored by

measuring sensory function. Sensory function was measured by applying an electric stimulus to the footpad of a mouse. By stepwise increasing the electrical current sensory function was quantified.

Mice

Balb/C, Female, Housed IVC, 5-7 animals per cage

Oligo treatment (start day1)

Mice were treated with 5mg/kg dose of oligo at day 1, 2, 3, 4, 7. At day 7 the nerve crush was done (See below). The mice also received oligo dosing following the injury (day 11, 14, 17). Animals were sacrificed at day 21.

Nerve crush (day 7)

All the surgical procedures were performed aseptically under deep isoflurane anesthesia (2.5 vol% isoflurane, 1 L/min O_2 and 1 L/min N_2O). The left thigh was shaved and the sciatic nerve was exposed via an incision in the upper thigh. The nerve was crushed for three 10 s periods at the level of the sciatic notch using smooth, curved forceps (No.7), resulting in a completely translucent appearance of the crushed area on the nerve. The right leg is used as control. A sham operation was performed on this leg (only exposing the nerve. The muscle and the skin are then closed with sutures.

Footflick assay (start day 9)

Recovery of sensory function was assessed with the foot-flick test according to De Koning et al. *J. Neurol. Sci.* 74 (1986), pp. 237–246. Briefly, a shock source with a variable current of 0.1–0.5 mA was used. The mice were immobilized,two stimulation electrodes were placed at the same point on the foot sole for every animal and stimulation applied by stepwise increasing the current from 0.1 to 0.5 mA. A response was scored positive when the mouse retracted its paw upon stimulation at a given current. The minimum current (mA) needed to elicit a retraction response was recorded. Values are expressed as percentage of normal function and represent the mean ± SEM.

Figure 5 is explained in more detail as follows: Recovery of sensory function after crush of the sciatic nerve. Animals were treated with PBS (control), 1119 or 1018 at a 5mg/kg dose. In the figure, RGS1018 and 1018; RGS1119 and 1119 have the same meaning.

At day 21 (14 days post nerve crush) we sacrificed the animals. We isolated liver and blood samples. Liver samples were stored in RNAlater (Ambion) and blood was left to coagulate After centrifugation serum was isolated to determine alanine aminotransferase (ALT) levels.

Using qPCR we measured C8b mRNA and C6 mRNA levels in the livers of mice treated with 1018 (C8b oligo) or 1119 (C6 oligo) to confirm knockdown of the intended target. RNA was isolated from liver using Trizol according to the instructions of the manufacturer (Invitrogen). cDNA was made using oligodT primer and SuperScriptII enzyme (Invitrogen). qPCR was done using Universal probe primers (Roche) and a Lightcycler 480 (Roche). All data was corrected using mouse Hprt as housekeeping gene /loading control. All reactions were done in triplicate and qPCR conditions were as standard recommended by the manufacturer (Roche). Alanine aminotransferase (ALT) levels in serum were determined using standard diagnostic procedures with the H747 (Hitachi/Roche) with the appropriate kit (Roche Diagnostics).

Specific knockdown of C8b mRNA was confirmed in all mice treated with 1018. While specific knockdown of C6 was confirmed for mice treated with 1119.

Figure 6 is explained in more detail as follows: mRNA levels of C6 (top left and C8b (bottom left) in liver as measured by qPCR. mRNA levels corrected for Hprt expression for individual mice are depicted. Right; ALT levels in serum (U/L37°C depicted as mean per treatment group).

The disclosures of all references mentioned herein (including all patent and scientific documents) are incorporated herein by reference. The invention has been described in detail with reference to preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of this disclosure, may make modifications and improvements within the spirit and scope of the invention.

What is claimed is:

1. An oligomer of between about 10 to 50 nucleotides in length having a contiguous nucleobase sequence with at least 80 % sequence identity to a corresponding region of a nucleic acid which encodes the COMPLEMENT COMPONENT 8-beta (C8-beta) sequence represented by SEQ ID NO: 1 or a naturally occurring allelic variant thereof; the oligomer comprising at least one nucleotide analogue and being capable of reducing the level of C8-beta mRNA expression in a mammal by at least 20% as determined by a qPCR assay.

2. The oligomer of claim 1, wherein the oligomer further comprises at least one of a modified internucleoside linkage and a modified nucleobase.

3. The oligomer of claim 1 or 2, wherein the nucleotide analogue is a modified sugar moiety selected from the group consisting of: 2'-O-methoxyethyl modified sugar moiety, a 2'-methoxy modified sugar moiety, a 2'-O-alkyl modified sugar moiety, and a bicyclic sugar moiety.

4. The oligomer of claim 3, wherein the bicyclic sugar moiety is a locked nucleic acid (LNA) monomer.

5. The oligomer of any one of claims 1-4, wherein the oligomer is a gapmer comprising 2 or 3 LNA momomers at each of the 3' and 5' ends of the oligomer.

6. The oligomer of any one of claims 1-5, wherein the oligomer further comprises 2'-deoxynucleotides positioned between the 5' and 3' wing segments and, optionally, one or both of the 5' and 3' ends of the oligomer.

7. The oligomer of any one of claims 2-6, wherein the modified internucleoside linkage is a phosphorothioate internucleoside linkage.

8. The oligomer of any one of claims 2-7, wherein the modified nucleobase is 5-methylcytosine.

9. The oligomer of any one of claims 1-8, wherein the oligomer is between about 10 to about 20 nucleotides in length.

10. The oligomer of claim 9, wherein the oligomer is between about 11 to about 17 nucleotides in length.

11. The oligomer of any one of claims 1-10, wherein the oligomer is targeted to about nucleotides 55-582, 607-669, 700-830, 887-1098, 1181-1299, 1303-1710 from the ATG start site of SEQ ID NO: 1 (starting at the "A").

12. The oligomer of claim 11, wherein the oligomer is targeted to about nucleotides 116- 582, 607-669, 723-830, 887-1075, 1181-1228, 1303-1466, 1637-1699 from the ATG start site of SEQ ID NO: 1.

13. The oligomer of any one of claims 1-12, wherein the oligomer has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to Complement Component C8-beta sequence represented by SEQ ID NO:1.

14. The oligomer of any one of claims 1-13, wherein the oligomer comprises one, two, or three mismatches with respect to the Complement Component C8-beta sequence represented by SEQ ID NO:1.

15. The oligomer of any one of claims 1-14, wherein the oligomer is an antisense oligonucleotide.

16. A pharmaceutical composition comprising the oligomer of any one of claims 1-15 and a pharmaceutically acceptable diluent, carrier, salt or adjuvant.

17. A method of reducing or inhibiting the expression of COMPLEMENT COMPONENT 8-beta (C8-beta) in a cell or a tissue in vitro or in vivo, the method comprising the step of

contacting said cell or tissue with the oligomer of any one of claims 1-15 so that expression of the COMPLEMENT COMPONENT 8-beta (C8-beta) is reduced or inhibited.

18. The method of claim 17, wherein the method further comprises the step of measuring at least one of the Complement Component 8-beta (C8-beta), mRNA encoding the protein and a membrane attack complex (MAC) following administration of the oligomer.

19. A method of reducing or inhibiting the production of a membrane attack complex (MAC) in a cell or a tissue in vitro or in vivo, the method comprising the step of contacting said cell or tissue with the oligomer of any one of claims 1-15 so that expression of the MAC is reduced or inhibited.

20. The method of claim 19, wherein the method further comprises the step of measuring at least one of the MAC, the Complement Component 8-beta (C8-beta) and mRNA encoding the Complement Component 8-beta following administration of the oligomer.

21. A method for treating, preventing or reducing symptoms of a disorder mediated by undesired activity of the complement system, the method comprising administering the pharmaceutical composition of claim 16 to a mammal in need thereof.

22. The method of claim 21, wherein the disorder is a chronic demyelinating neuropathy.

23. The method of claim 22, wherein the chronic demyelinating neuropathy is multiple sclerosis.

24. The method of claim 23, wherein the method further comprises administering at least one of Rebif® (interferon beta-1a), Avonex® (interferon beta-1a), Betaseron® (interferon beta-1b), Copaxone® (glatiramer acetate), Gilenya® (FTY720, fingolimod), Novantrone® (mitozantrone), and Tysabri® (natalizumab).

25. A method for treating, preventing or reducing symptoms of a disorder mediated by undesired activity of the complement system, the method comprising administering the pharmaceutical

composition of claim 16 to a mammal in need thereof and further comprising the administration of one or more of an anti-inflammatory agent and a complement inhibitor.

26. The method of claim 21, wherein the disorder is neuronal trauma.

27 The method of claim 26, wherein the neuronal trauma is traumatic brain injury (TBI).

28. An oligomer according to any one of claims 1-15 for use as a medicament.

29. An oligomer according to any one of claims 1-15 for use in the treatment of a disorder mediated by undesired activity of the complement system.

30. An oligomer according to any one of claims 1-15 for use in the treatment of a condition requiring axonal regeneration.

31. An oligomer according to any one of claims 1-15 for use in the treatment of a chronic dyemylinating condition.

32. Use of at least one oligomer according to any one of claims 1-15 for the manufacture of a medicament for the treatment of a disorder mediated by undesired activity of the complement system.

33. Use of at least one oligomer according to any one of claims 1-15 for the manufacture of a medicament for the treatment of a condition requiring axonal regeneration.

34. Use of at least one oligomer according to any one of claims 1-15 for the manufacture of a medicament for the treatment of a chronic dyemylinating condition.

35. An oligomer according to claim 31 or the use of claim 34, wherein the chronic dyemylinating condition is multiple sclerosis.

36. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer of between about 10 to 50 nucleotides in length comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos.

37. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 2, 24, 46, 68, 90, 112, 134, 156, 178 and 200 and the complementary sequences of said SEQ ID Nos.

38. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer of between about 10 to 50 nucleotides in length comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos.

39. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 222, 225, 228, 231 and 234 and the complementary sequences of said SEQ ID Nos.

40. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer of between about 10 to 50 nucleotides in length comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100%

sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos.

41. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 335, 337, 339, 341 and 343 and the complementary sequences of said SEQ ID Nos.

42. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer of between about 10 to 50 nucleotides in length comprising a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos.

43. An oligomer, pharmaceutical composition, method or use according to any one of claims 1-35, wherein said oligomer is an oligomer essentially consisting of a contiguous nucleobase sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos. 336, 338, 340, 342 and 344 and the complementary sequences of said SEQ ID Nos.

Human complement component 8-beta (C8-beta) mRNA sequence (Genbank Ref. NM_000066.2)

SEQ ID No: 1

GGCACTCACAGCACAGGCTTGTTATGGGTCTAGCAGCCTCTGTGGCATCTCCTGTCACAT
TGGGAAAATGAAGAATTCCAGGACATGGGCTTGGAGGGCGCCGGTGGAGCTATTTCTTCT
CTGTGCTGCCCTGGGCTGTCTCAGTTTGCCTGGCTCCAGAGGTGAAAGGCCACATTCCTT
TGGGTCAAATGCAGTCAACAAGAGCTTTGCTAAGAGCAGACAGATGCGGAGTGTGGATGT
TACCCTGATGCCCATTGATTGTGAGCTGTCTAGTTGGTCCTCTTGGACCACATGTGACCC
CTGTCAGAAGAAAAGGTACAGGTATGCCTACTTGCTCCAGCCCTCTCAGTTCCATGGGGA
ACCGTGCAACTTCTCTGACAAGGAAGTCGAAGACTGTGTTACCAACAGACCATGCGGAAG
TCAAGTGCGATGTGAAGGCTTTGTGTGTGCACAGACAGGAAGGTGTGTAAACCGCAGACT
TCTTTGCAATGGGGACAATGACTGTGGAGACCAGTCAGATGAAGCAAACTGTAGAAGGAT
TTATAAAAAAATGTCAGCATGAAATGGACCAATACTGGGGAATTGGCAGTCTGGCCAGTGG
GATAAATTTGTTCACAAACAGTTTTGAGGGCCCAGTTCTTGATCACAGGTATTATGCAGG
TGGATGCTCCCCGCATTACATCCTGAACACGAGGTTTAGGAAGCCCTACAATGTGGAAAG
CTACACGCCACAGACCCAAGGCAAATACGAATTCATATTAAAAGAGTATGAATCATACTC
AGATTTTGAACGCAATGTCACAGAGAAAATGGCAAGCAAGTCTGGTTTCAGTTTTGGTTT
TAAAATACCTGGAATATTTGAACTTGGCATCAGTAGTCAAAGTGATCGAGGCAAACACTA
TATTAGGAGAACCAAACGATTCTCTCATACTAAAAGCGTATTTCTGCATGCACGCTCTGA
CCTTGAAGTAGCACATTACAAGCTGAAACCCAGAAGCCTCATGCTCCATTACGAGTTCCT
TCAGAGAGTTAAGCGGCTGCCCCTGGAGTACAGCTACGGGGAATACAGAGATCTCTTCCG
TGATTTTGGGACCCACTACATCACAGAGGCTGTGCTTGGGGGCATTTATGAATACACCCT
CGTTATGAACAAAGAGGCCATGGAGAGAGGAGATTATACTCTTAACAACGTCCATGCCTG
TGCCAAAAATGATTTTAAAATTGGTGGTGCCATTGAAGAGGTCTACGTCAGTCTGGGTGT
GTCTGTAGGCAAATGCAGAGGTATTCTGAATGAAATAAAAGACAGAAACAAGAGGGACAC
CATGGTGGAGGACTTGGTGGTCCTGGTACGAGGAGGGGCAAGTGAGCACATCACCACCCT
GGCATACCAGGAGCTGCCGACGGCGGACCTGATGCAGGAGTGGGGAGACGCTGTGCAGTA
CAACCCAGCCATCATCAAAGTTAAGGTGGAGCCTCTGTATGAACTAGTGACAGCCACAGA
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ATCACGCTGTGACTGCATCTGTCCTGTTGGATCCCAAGGCCTAGCCTGTGAGGTCTCCTA
TCGGAAGAATACCCCCATTGATGGGAAGTGGAATTGCTGGTCAAATTGGTCTTCATGCTC
TGGAAGACGTAAGACAAGACAAAGGCAGTGTAACAATCCACCTCCTCAAAATGGGGGTAG
CCCCTGTTCAGGCCCTGCTTCAGAAACACTTGACTGCTCCTAGCAGATGATACAGCAGTG
GGCTACATACAATGAGAGCCCTGAGCCCTCAAGAACTCATGCCAGCTCAGCCCTACACCA
GTTTCCACCTGGAGTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTTAAAATAA
AGATGTTACCTTGTAAAATGCAAGTTGATTTAAATAAATACTGAGTTAAAGGCTTAAAAA
AAAAAAAAAAAAA

Fig. 1A

C8-beta Oligonucleotides
SEQ ID NOs: 2 - 236

518 GCAGTCTGGCCAGTGGGATAAATTT SEQ ID NO: 2

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
GTCTGGCCAGTGGGATAAA	3	GUCUGGCCAGUGGGAUAAA	10	UUUAUCCCACUGGCCAGAC	17
TCTGGCCAGTGGGATAAAT	4	UCUGGCCAGUGGGAUAAAU	11	AUUUAUCCCACUGGCCAGA	18
CTGGCCAGTGGGATAAATT	5	CUGGCCAGUGGGAUAAAUU	12	AAUUUAUCCCACUGGCCAG	19
TGGCCAGTGGGATAAATTT	6	UGGCCAGUGGGAUAAAUUU	13	AAAUUUAUCCCACUGGCCA	20
AGTCTGGCCAGTGGGATAA	7	AGUCUGGCCAGUGGGAUAA	14	UUAUCCCACUGGCCAGACU	21
CAGTCTGGCCAGTGGGATA	8	CAGUCUGGCCAGUGGGAUA	15	UAUCCCACUGGCCAGACUG	22
GCAGTCTGGCCAGTGGGAT	9	GCAGUCUGGCCAGUGGGAU	16	AUCCCACUGGCCAGACUGC	23

562 GGCCCAGTTCTTGATCACAGGTATT SEQ ID NO: 24

DNA Sequence	SEQ ID NO:	RNA Sequence		Reverse Complement	SEQ ID NO:
CAGTTCTTGATCACAGGTA	25	CAGUUCUUGAUCACAGGUA	32	UACCUGUGAUCAAGAACUG	39
AGTTCTTGATCACAGGTAT	26	AGUUCUUGAUCACAGGUAU	33	AUACCUGUGAUCAAGAACU	40
GTTCTTGATCACAGGTATT	27	GUUCUUGAUCACAGGUAUU	34	AAUACCUGUGAUCAAGAAC	41
GGCCCAGTTCTTGATCACA	28	GGCCCAGUUCUUGAUCACA	35	UGUGAUCAAGAACUGGGCC	42
CCAGTTCTTGATCACAGGT	29	CCAGUUCUUGAUCACAGGU	36	ACCUGUGAUCAAGAACUGG	43
GCCCAGTTCTTGATCACAG	30	GCCCAGUUCUUGAUCACAG	37	CUGUGAUCAAGAACUGGGC	44
CCCAGTTCTTGATCACAGG	31	CCCAGUUCUUGAUCACAGG	38	CCUGUGAUCAAGAACUGGG	45

607 CATTACATCCTGAACACGAGGTTTA SEQ ID NO: 46

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
ATCCTGAACACGAGGTTTA	47	AUCCUGAACACGAGGUUUA	54	UAAACCUCGUGUUCAGGAU	61
ACATCCTGAACACGAGGTT	48	ACAUCCUGAACACGAGGUU	55	AACCUCGUGUUCAGGAUGU	62
CATTACATCCTGAACACGA	49	CAUUACAUCCUGAACACGA	56	UCGUGUUCAGGAUGUAAUG	63
ATTACATCCTGAACACGAG	50	AUUACAUCCUGAACACGAG	57	CUCGUGUUCAGGAUGUAAU	64
TACATCCTGAACACGAGGT	51	UACAUCCUGAACACGAGGU	58	ACCUCGUGUUCAGGAUGUA	65
CATCCTGAACACGAGGTTT	52	CAUCCUGAACACGAGGUUU	59	AAACCUCGUGUUCAGGAUG	66
TTACATCCTGAACACGAGG	53	UUACAUCCUGAACACGAGG	60	CCUCGUGUUCAGGAUGUAA	67

Fig. 2A

811 CAAAGTGATCGAGGCAAACACTATA SEQ ID NO: 68

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
AAAGTGATCGAGGCAAACA	69	AAAGUGAUCGAGGCAAACA	76	UGUUUGCCUCGAUCACUUU	83
TGATCGAGGCAAACACTAT	70	UGAUCGAGGCAAACACUAU	77	AUAGUGUUUGCCUCGAUCA	84
GATCGAGGCAAACACTATA	71	GAUCGAGGCAAACACUAUA	78	UAUAGUGUUUGCCUCGAUC	85
GTGATCGAGGCAAACACTA	72	GUGAUCGAGGCAAACACUA	79	UAGUGUUUGCCUCGAUCAC	86
AGTGATCGAGGCAAACACT	73	AGUGAUCGAGGCAAACACU	80	AGUGUUUGCCUCGAUCACU	87
CAAAGTGATCGAGGCAAAC	74	CAAAGUGAUCGAGGCAAAC	81	GUUUGCCUCGAUCACUUUG	88
AAGTGATCGAGGCAAACAC	75	AAGUGAUCGAGGCAAACAC	82	GUGUUUGCCUCGAUCACUU	89

887 GCTCTGACCTTGAAGTAGCACATTA SEQ ID NO: 90

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
ACCTTGAAGTAGCACATTA	91	ACCUUGAAGUAGCACAUUA	98	UAAUGUGCUACUUCAAGGU	105
CTCTGACCTTGAAGTAGCA	92	CUCUGACCUUGAAGUAGCA	99	UGCUACUUCAAGGUCAGAG	106
TGACCTTGAAGTAGCACAT	93	UGACCUUGAAGUAGCACAU	100	AUGUGCUACUUCAAGGUCA	107
CTGACCTTGAAGTAGCACA	94	CUGACCUUGAAGUAGCACA	101	UGUGCUACUUCAAGGUCAG	108
GACCTTGAAGTAGCACATT	95	GACCUUGAAGUAGCACAUU	102	AAUGUGCUACUUCAAGGUC	109
GCTCTGACCTTGAAGTAGC	96	GCUCUGACCUUGAAGUAGC	103	GCUACUUCAAGGUCAGAGC	110
TCTGACCTTGAAGTAGCAC	97	UCUGACCUUGAAGUAGCAC	104	GUGCUACUUCAAGGUCAGA	111

1054 GGCATTTATGAATACACCCTCGTTA SEQ ID NO: 112

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
TTATGAATACACCCTCGTT	113	UUAUGAAUACACCCUCGUU	120	AACGAGGGUGUAUUCAUAA	127
TATGAATACACCCTCGTTA	114	UAUGAAUACACCCUCGUUA	121	UAACGAGGGUGUAUUCAUA	128
GCATTTATGAATACACCCT	115	GCAUUUAUGAAUACACCCU	122	AGGGUGUAUUCAUAAAUGC	129
TTTATGAATACACCCTCGT	116	UUUAUGAAUACACCCUCGU	123	ACGAGGGUGUAUUCAUAAA	130
ATTTATGAATACACCCTCG	117	AUUUAUGAAUACACCCUCG	124	CGAGGGUGUAUUCAUAAAU	131
GGCATTTATGAATACACCC	118	GGCAUUUAUGAAUACACCC	125	GGGUGUAUUCAUAAAUGCC	132
CATTTATGAATACACCCTC	119	CAUUUAUGAAUACACCCUC	126	GAGGGUGUAUUCAUAAAUG	133

Fig. 2B

1182 CAGTCTGGGTGTGTCTGTAGGCAAA SEQ ID NO: 134

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
GGGTGTGTCTGTAGGCAAA	135	GGGUGUGUCUGUAGGCAAA	142	UUUGCCUACAGACACACCC	149
CAGTCTGGGTGTGTCTGTA	136	CAGUCUGGGUGUGUCUGUA	143	UACAGACACACCCAGACUG	150
TGGGTGTGTCTGTAGGCAA	137	UGGGUGUGUCUGUAGGCAA	144	UUGCCUACAGACACACCCA	151
AGTCTGGGTGTGTCTGTAG	138	AGUCUGGGUGUGUCUGUAG	145	CUACAGACACACCCAGACU	152
CTGGGTGTGTCTGTAGGCA	139	CUGGGUGUGUCUGUAGGCA	146	UGCCUACAGACACACCCAG	153
GTCTGGGTGTGTCTGTAGG	140	GUCUGGGUGUGUCUGUAGG	147	CCUACAGACACACCCAGAC	154
TCTGGGTGTGTCTGTAGGC	141	UCUGGGUGUGUCUGUAGGC	148	GCCUACAGACACACCCAGA	155

1199 TAGGCAAATGCAGAGGTATTCTGAA SEQ ID NO: 156

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
AAATGCAGAGGTATTCTGA	157	AAAUGCAGAGGUAUUCUGA	164	UCAGAAUACCUCUGCAUUU	171
AGGCAAATGCAGAGGTATT	158	AGGCAAAUGCAGAGGUAUU	165	AAUACCUCUGCAUUUGCCU	172
GCAAATGCAGAGGTATTCT	159	GCAAAUGCAGAGGUAUUCU	166	AGAAUACCUCUGCAUUUGC	173
AATGCAGAGGTATTCTGAA	160	AAUGCAGAGGUAUUCUGAA	167	UUCAGAAUACCUCUGCAUU	174
CAAATGCAGAGGTATTCTG	161	CAAAUGCAGAGGUAUUCUG	168	CAGAAUACCUCUGCAUUUG	175
TAGGCAAATGCAGAGGTAT	162	UAGGCAAAUGCAGAGGUAU	169	AUACCUCUGCAUUUGCCUA	176
GGCAAATGCAGAGGTATTC	163	GGCAAAUGCAGAGGUAUUC	170	GAAUACCUCUGCAUUUGCC	177

1445 CCAGCACAGTGAGGCAGAACATGAA SEQ ID NO: 178

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
GCACAGTGAGGCAGAACAT	179	GCACAGUGAGGCAGAACAU	186	AUGUUCUGCCUCACUGUGC	193
ACAGTGAGGCAGAACATGA	180	ACAGUGAGGCAGAACAUGA	187	UCAUGUUCUGCCUCACUGU	194
CAGTGAGGCAGAACATGAA	181	CAGUGAGGCAGAACAUGAA	188	UUCAUGUUCUGCCUCACUG	195
AGCACAGTGAGGCAGAACA	182	AGCACAGUGAGGCAGAACA	189	UGUUCUGCCUCACUGUGCU	196
CCAGCACAGTGAGGCAGAA	183	CCAGCACAGUGAGGCAGAA	190	UUCUGCCUCACUGUGCUGG	197
CACAGTGAGGCAGAACATG	184	CACAGUGAGGCAGAACAUG	191	CAUGUUCUGCCUCACUGUG	198
CAGCACAGTGAGGCAGAAC	185	CAGCACAGUGAGGCAGAAC	192	GUUCUGCCUCACUGUGCUG	199

Fig. 2C

1633 GATGGGAAGTGGAATTGCTGGTCAA SEQ ID NO: 200

DNA Sequence	SEQ ID NO:	RNA Sequence	SEQ ID NO:	Reverse Complement	SEQ ID NO:
GAAGTGGAATTGCTGGTCA	201	GAAGUGGAAUUGCUGGUCA	208	UGACCAGCAAUUCCACUUC	215
AAGTGGAATTGCTGGTCAA	202	AAGUGGAAUUGCUGGUCAA	209	UUGACCAGCAAUUCCACUU	216
GATGGGAAGTGGAATTGCT	203	GAUGGGAAGUGGAAUUGCU	210	AGCAAUUCCACUUCCCAUC	217
GGGAAGTGGAATTGCTGGT	204	GGGAAGUGGAAUUGCUGGU	211	ACCAGCAAUUCCACUUCCC	218
ATGGGAAGTGGAATTGCTG	205	AUGGGAAGUGGAAUUGCUG	212	CAGCAAUUCCACUUCCCAU	219
GGAAGTGGAATTGCTGGTC	206	GGAAGUGGAAUUGCUGGUC	213	GACCAGCAAUUCCACUUCC	220
TGGGAAGTGGAATTGCTGG	207	UGGGAAGUGGAAUUGCUGG	214	CCAGCAAUUCCACUUCCCA	221

Fig. 2D

			SEQ ID NO:
810	TCAAAGTGATCGAGGCAAA	target	222
	UCAAAGUGAUCGAGGCAAA	RNA	223
	UUUGCCUCGAUCACUUUGA	Reverse complement	224
723	ACGCAATGTCACAGAGAAA	target	225
	ACGCAAUGUCACAGAGAAA	RNA	226
	UUUCUCUGUGACAUUGCGU	Reverse complement	227
116	GGTCAAATGCAGTCAACAA	target	228
	GGUCAAAUGCAGUCAACAA	RNA	229
	UUGUUGACUGCAUUUGACC	Reverse complement	230
1200	AGGCAAATGCAGAGGTATT	target	231
	AGGCAAAUGCAGAGGUAUU	RNA	232
	AAUACCUCUGCAUUUGCCU	Reverse complement	233
1678	AGACGTAAGACAAGACAAA	target	234
	AGACGUAAGACAAGACAAA	RNA	235
	UUUGUCUUGUCUUACGUCU	Reverse complement	236

Fig. 2E

Selected C8-beta cross-species oligomers
SEQ ID NOs: 237-332

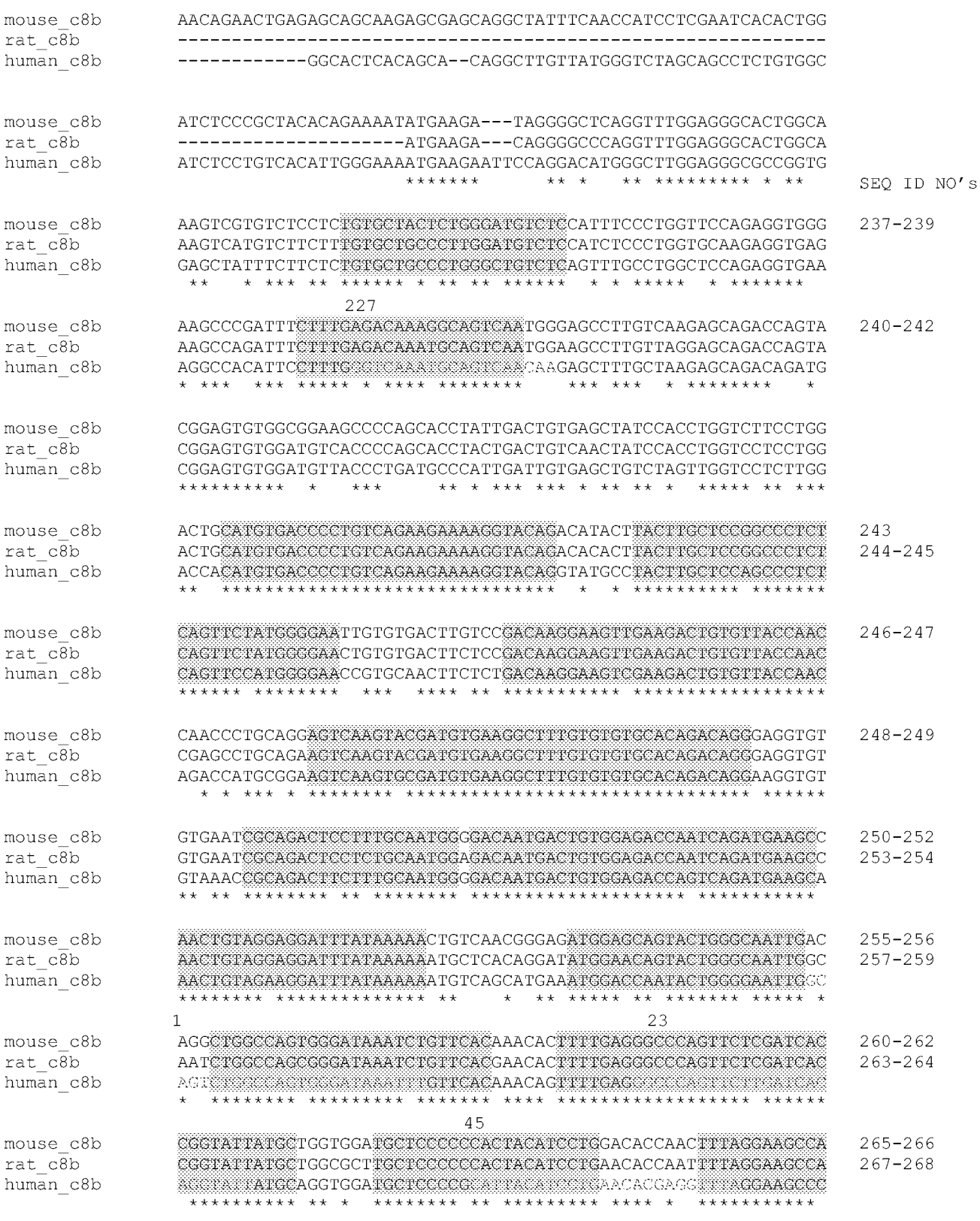
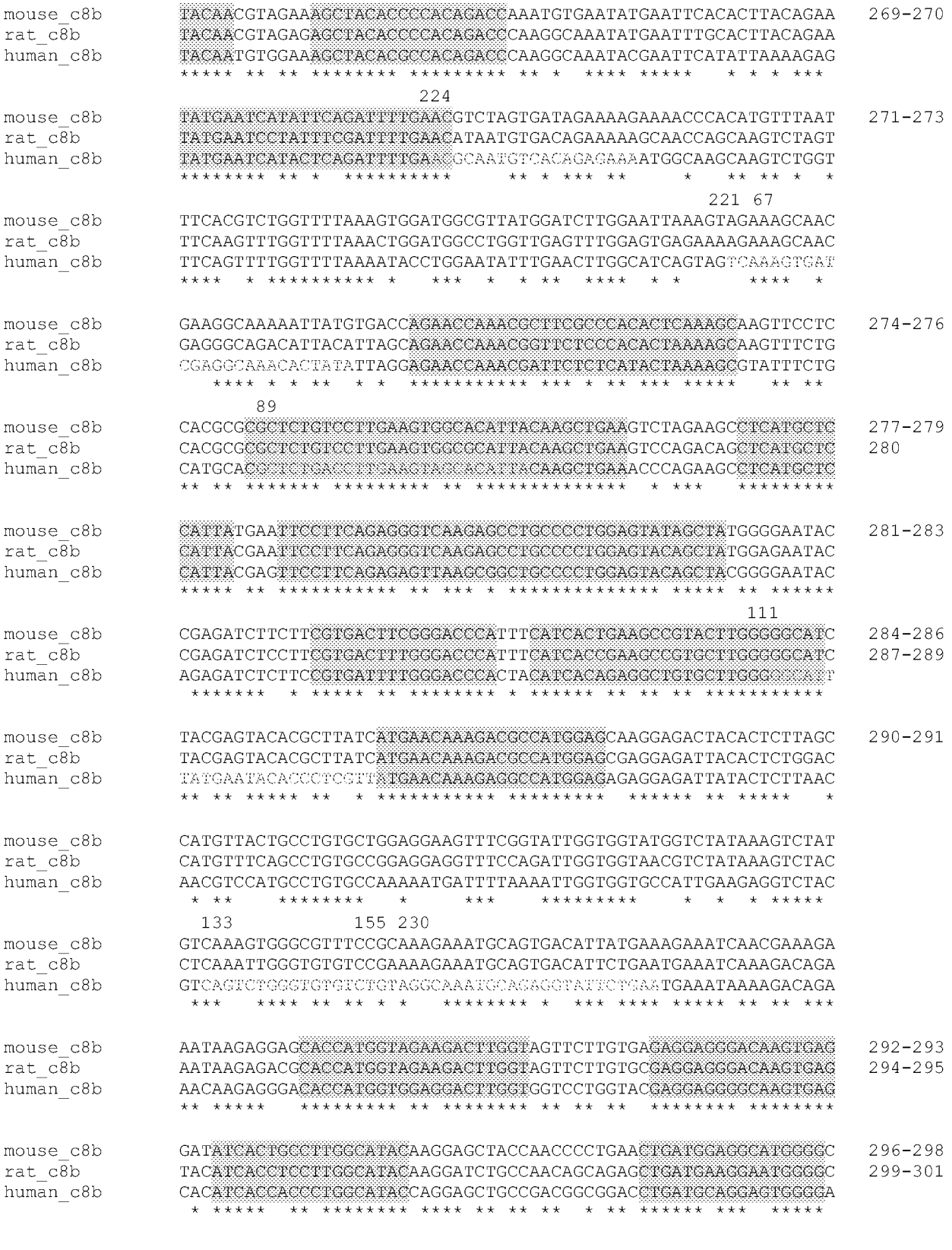


Fig. 3A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rat_c8b
human_c8b
269-270
271-273
274-276
277-279
280
281-283
284-286
287-289
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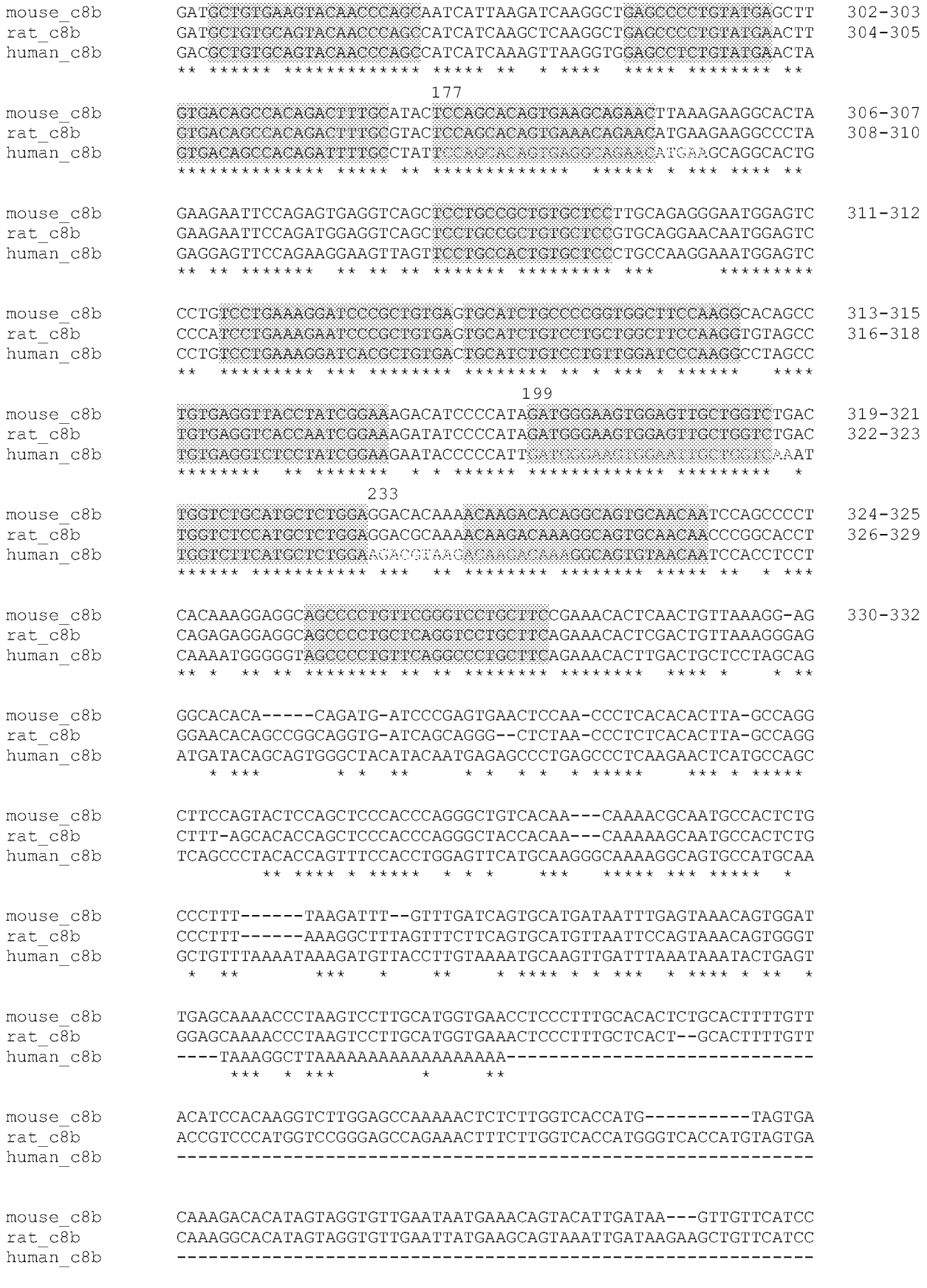
292-293
294-295
296-298
299-301
224
221 67
89
111
133
155 230

Fig. 3B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rat_c8b GATGCTGTGCAGTACAACCCAGCCATCATCAAGCTCAAGGCTGAGCCCCTGTATGAACTT 304-305
human_c8b GACGCTGTGCAGTACAACCCAGCCATCATCAAAGTTAAGGTGGAGCCTCTGTATGAACTA
177
mouse_c8b GTGACAGCCACAGACTTTGCATACTCCAGCACAGTGAAGCAGAACTTAAAGAAGGCACTA 306-307
rat_c8b GTGACAGCCACAGACTTTGCGTACTCCAGCACAGTGAAACAGAACATGAAGAAGGCCCTA 308-310
human_c8b GTGACAGCCACAGATTTTGCCTATTCCAGCACAGTGAGGCAGAACATGAAGCAGGCACTG
mouse_c8b GAAGAATTCCAGAGTGAGGTCAGCTCCTGCCGCTGTGCTCCTTGCAGAGGGAATGGAGTC 311-312
rat_c8b GAAGAATTCCAGATGGAGGTCAGCTCCTGCCGCTGTGCTCCGTGCAGGAACAATGGAGTC
human_c8b GAGGAGTTCCAGAAGGAAGTTAGTTCCTGCCACTGTGCTCCCTGCCAAGGAAATGGAGTC
mouse_c8b CCTGTCCTGAAAGGATCCCGCTGTGAGTGCATCTGCCCCGGTGGCTTCCAAGGCACAGCC 313-315
rat_c8b CCCATCCTGAAAGAATCCCGCTGTGAGTGCATCTGTCCTGCTGGCTTCCAAGGTGTAGCC 316-318
human_c8b CCTGTCCTGAAAGGATCACGCTGTGACTGCATCTGTCCTGTTGGATCCCAAGGCCTAGCC
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mouse_c8b TGTGAGGTTACCTATCGGAAAGACATCCCCATAGATGGGAAGTGGAGTTGCTGGTCTGAC 319-321
rat_c8b TGTGAGGTCACCAATCGGAAAGATATCCCCATAGATGGGAAGTGGAGTTGCTGGTCTGAC 322-323
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mouse_c8b TGGTCTGCATGCTCTGGAGGACACAAAACAAGACACAGGCAGTGCAACAATCCAGCCCCT 324-325
rat_c8b TGGTCTCCATGCTCTGGAGGACGCAAAACAAGACAAAGGCAGTGCAACAACCCGGCACCT 326-329
human_c8b TGGTCTTCATGCTCTGGAAGACGTAACACAACACAAGGCAGTGTAACAATCCACCTCCT
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rat_c8b CAGAGAGGAGGCAGCCCCTGCTCAGGTCCTGCTTCAGAAACACTCGACTGTTAAAGGGAG
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mouse_c8b GGCACACA-----CAGATG-ATCCCGAGTGAACTCCAA-CCCTCACACACTTA-GCCAGG
rat_c8b GGAACACAGCCGGCAGGTG-ATCAGCAGGG--CTCTAA-CCCTCTCACACTTA-GCCAGG
human_c8b ATGATACAGCAGTGGGCTACATACAATGAGAGCCCTGAGCCCTCAAGAACTCATGCCAGC
mouse_c8b CTTCCAGTACTCCAGCTCCCACCCAGGGCTGTCACAA---CAAAACGCAATGCCACTCTG
rat_c8b CTTT-AGCACACCAGCTCCCACCCAGGGCTACCACAA---CAAAAAGCAATGCCACTCTG
human_c8b TCAGCCCTACACCAGTTTCCACCTGGAGTTCATGCAAGGGCAAAAGGCAGTGCCATGCAA
mouse_c8b CCCTTT------TAAGATTT--GTTTGATCAGTGCATGATAATTTGAGTAAACAGTGGAT
rat_c8b CCCTTT------AAAGGCTTTAGTTTCTTCAGTGCATGTTAATTCCAGTAAACAGTGGGT
human_c8b GCTGTTTAAAATAAAGATGTTACCTTGTAAAATGCAAGTTGATTTAAATAAATACTGAGT
mouse_c8b TGAGCAAAACCCTAAGTCCTTGCATGGTGAACCTCCCTTTGCACACTCTGCACTTTTGTT
rat_c8b GGAGCAAAACCCTAAGTCCTTGCATGGTGAAACTCCCTTTGCTCACT--GCACTTTTGTT
human_c8b ----TAAAGGCTTAAAAAAAAAAAAAAAAA----------
mouse_c8b ACATCCACAAGGTCTTGGAGCCAAAAACTCTCTTGGTCACCATG----------TAGTGA
rat_c8b ACCGTCCCATGGTCCGGGAGCCAGAAACTTTCTTGGTCACCATGGGTCACCATGTAGTGA
human_c8b ----------
mouse_c8b CAAAGACACATAGTAGGTGTTGAATAATGAAACAGTACATTGATAA---GTTGTTCATCC
rat_c8b CAAAGGCACATAGTAGGTGTTGAATTATGAAGCAGTAAATTGATAAGAAGCTGTTCATCC
human_c8b ----------

Fig. 3C

```
mouse_c8b       CTTGGTAAGCACAGAGTCTTCTTCAGTAATAAAGACAGCCAATCTCTA-GGAAATG----
rat_c8b         CTTGGTAAGCACAGAGTGTTCTTCAGTAATAAAGACAGCCAATCTCGATAAAAATGATCT
human_c8b       ------------------------------------------------------------

mouse_c8b       ------------------------------------------------------------
rat_c8b         TCTGTGTGCCACCAATCCATCCCCCATGACAACCTTGCAAGACAAATATCTGGGAAACAG
human_c8b       ------------------------------------------------------------

mouse_c8b       ------------------------------------------------------------
rat_c8b         GCTTGGGGGATATAATGACTTGTCCCAGGTCATACAATTAGGAAATGCCAGAATTGTGCA
human_c8b       ------------------------------------------------------------

mouse_c8b       ------------------------------------------------------------
rat_c8b         GCCAACAAGGCTCTGGATTCGATGAGGCTCGTCTTTTTCTGAATGAGCGTGCAGTTAGCA
human_c8b       ------------------------------------------------------------

mouse_c8b       ------------------------------------
rat_c8b         AAGAATTGTTCATGGAATAAAACGCAACAGAAAGCC
human_c8b       ------------------------------------
```

Fig. 3D

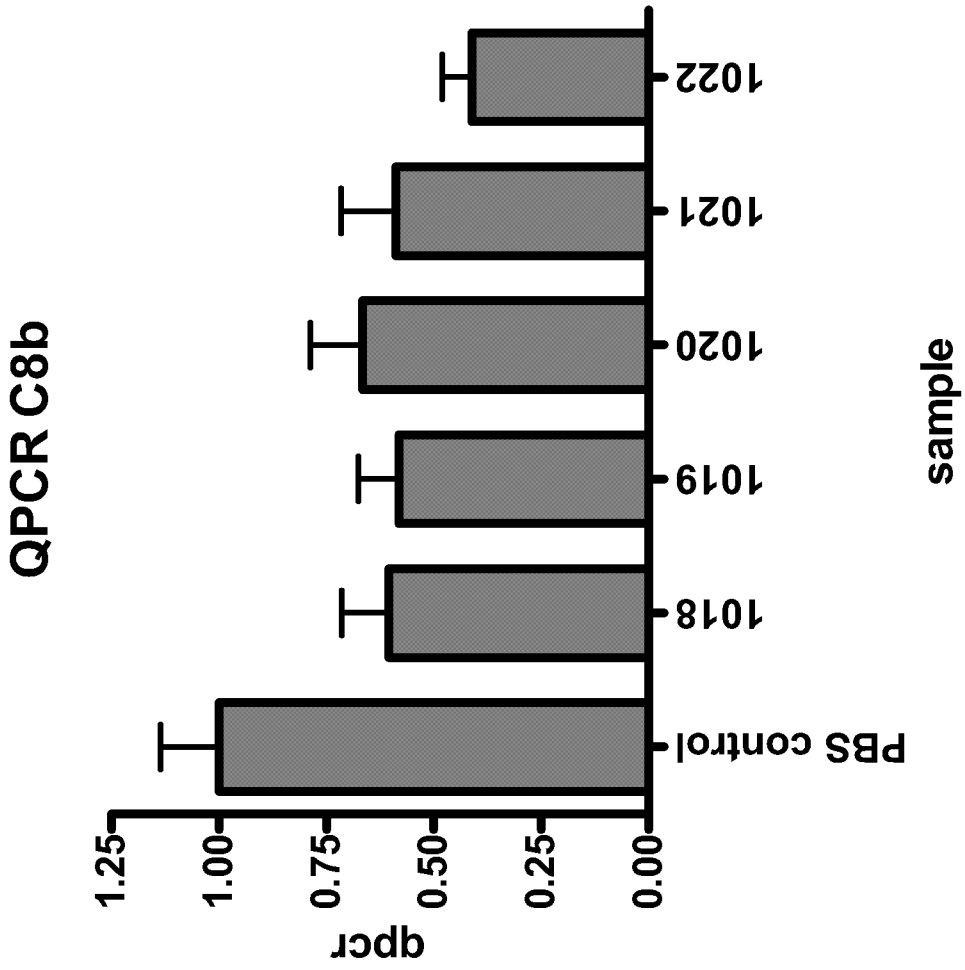
QPCR C8b
qpcr
1.25
1.00
0.75
0.50
0.25
0.00
PBS control
1018
1019
1020
1021
1022
sample

Fig. 4

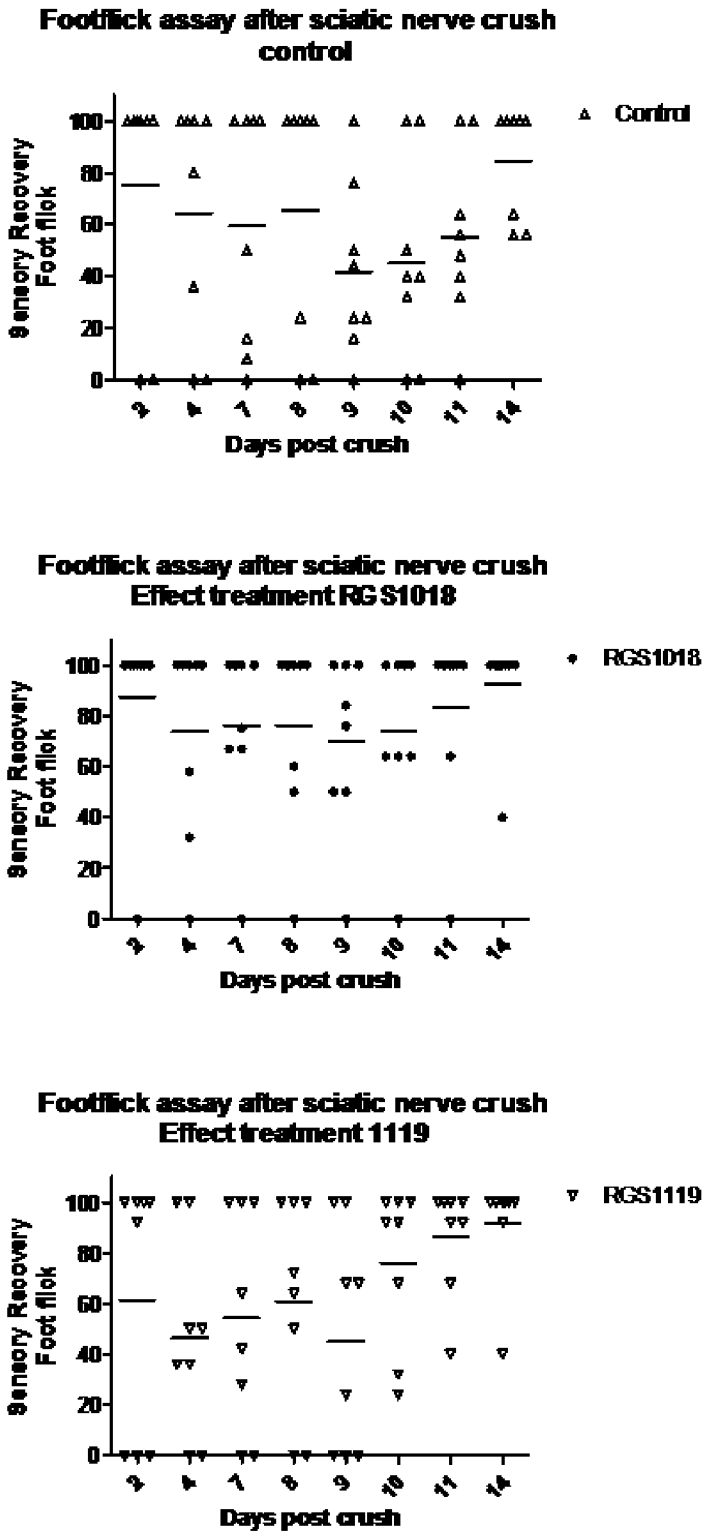
Footflick assay after sciatic nerve crush
control
Control
Sensory Recovery
Foot flick
100
80
60
40
20
0
3
4
7
8
9
10
11
14
Days post crush
Footflick assay after sciatic nerve crush
Effect treatment RGS1018
RGS1018
Sensory Recovery
Foot flick
Days post crush
Footflick assay after sciatic nerve crush
Effect treatment 1119
RGS1119
Sensory Recovery
Foot flick
Days post crush

Figure 5

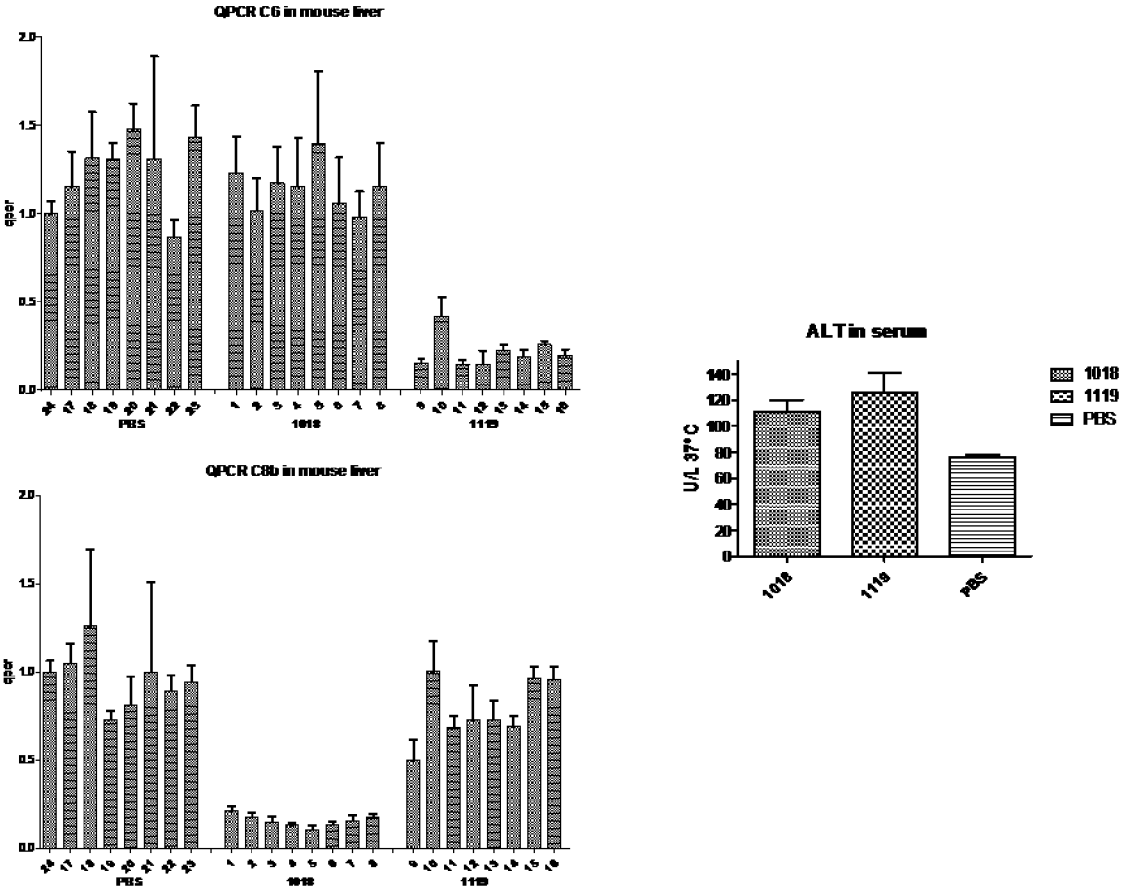
QPCR C6 in mouse liver
QPCR C8b in mouse liver
ALT in serum
U/L 37° C
1018
1119
PBS

Figure 6