COMPOSITIONS FOR MODULATING SOD-1 EXPRESSION

Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0240WOSEQ_ST25.pdf created March 30, 2015, which is 320 Kb in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

Field

Provided are compositions and methods for reducing expression of superoxide dismutase 1, soluble (SOD-1) mRNA and protein in an animal. Such methods are useful to treat, prevent, or ameliorate neurodegenerative diseases, including amyotrophic lateral sclerosis (ALS) by inhibiting expression of SOD-1 in an animal.

Background

The soluble SOD-1 enzyme (also known as Cu/Zn superoxide dismutase) is one of the superoxide dismutases that provide defense against oxidative damage of biomolecules by catalyzing the dismutation of superoxide to hydrogen peroxide (H2O2) (Fridovich, Annu. Rev. Biochem., 1995, 64, 97-112). The superoxide anion (O2-) is a potentially harmful cellular by-product produced primarily by errors of oxidative phosphorylation in mitochondria (Turrens, J. Physiol. 2003, 552, 335-344)

Mutations in the SOD-1 gene are associated with a dominantly-inherited form of amyotrophic lateral sclerosis (ALS, also known as Lou Gehrig's disease) a disorder characterized by a selective degeneration of upper and lower motor neurons (Rowland, N. Engl. J. Med. 2001, 344, 1688-1700). There is a tight genetic linkage between familial ALS and missense mutations in the SOD1 gene (Rosen, Nature, 1993, 362, 59-62). The toxicity of mutant SOD1 is believed to arise from an initial misfolding (gain of function) reducing nuclear protection from the active enzyme (loss of function in the nuclei), a process that may be involved in ALS pathogenesis (Sau, Hum. Mol. Genet. 2007, 16, 1604-1618).

ALS is a devastating progressive neurodegenerative disease affecting as many as 30,000 Americans at any given time. The progressive degeneration of the motor neurons in ALS eventually leads to their death. When the motor neurons die, the ability of the brain to initiate and control muscle movement is lost. With voluntary muscle action progressively affected, patients in the later stages of the disease may become totally

paralyzed.

Currently lacking are acceptable options for treating such neurodegenerative diseases. It is therefore an object herein to provide methods for the treatment of such diseases.

Summary

Provided herein are methods, compounds, and compositions for modulating expression of superoxide dismutase 1, soluble (SOD-1) mRNA and protein. In certain embodiments, compounds useful for modulating expression of SOD-1 mRNA and protein are antisense compounds. In certain embodiments, the antisense compounds are modified oligonucleotides.

In certain embodiments, modulation can occur in a cell or tissue. In certain embodiments, the cell or tissue is in an animal. In certain embodiments, the animal is a human. In certain embodiments, SOD-1 mRNA levels are reduced. In certain embodiments, SOD-1 protein levels are reduced. Such reduction can occur in a time-dependent manner or in a dose-dependent manner.

Also provided are methods, compounds, and compositions useful for preventing, treating, and ameliorating diseases, disorders, and conditions. In certain embodiments, such SOD-1 related diseases, disorders, and conditions are neurodegenerative diseases. In certain embodiments, such neurodegenerative diseases, disorders, and conditions include amyotrophic lateral sclerosis (ALS).

Such diseases, disorders, and conditions can have one or more risk factors, causes, or outcomes in common. Certain risk factors and causes for development of ALS include growing older, having a personal or family history, or genetic predisposition. However, the majority of ALS cases are sporadic and no known risk factors are known. Certain symptoms and outcomes associated with development of ALS include but are not limited to: fasciculations, cramps, tight and stiff muscles (spasticity), muscle weakness affecting an arm or a leg, slurred and nasal speech, difficulty walking, difficulty chewing or swallowing (dysphagia), difficulty speaking or forming words (dysarthria), weakness or atrophy, spasticity, exaggerated reflexes (hyperreflexia), and presence of Babinski's sign. As ALS progresses, symptoms and outcomes by include weakening of other limbs, perhaps accompanied by twitching, muscle cramping, and exaggerated, faster reflexes; problems with chewing, swallowing, and breathing; drooling may occur; eventual paralysis; and death.

In certain embodiments, methods of treatment include administering an SOD-1 antisense compound to an individual in need thereof. In certain embodiments, methods of treatment include administering an SOD-1 modified oligonucleotide to an individual in need thereof.

Detailed Description

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed. Herein, the use of the singular includes the plural unless specifically stated otherwise. As used herein, the use of "or"

means "and/or" unless stated otherwise. Additionally, as used herein, the use of "and" means "and/or" unless stated otherwise. Furthermore, the use of the term "including" as well as other forms, such as "includes" and "included", is not limiting. Also, terms such as "element" or "component" encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated otherwise. Also, all sequences described herein are listed 5' to 3', unless otherwise stated.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this disclosure, including, but not limited to, patents, patent applications, published patent applications, articles, books, treatises, and GENBANK Accession Numbers and associated sequence information obtainable through databases such as National Center for Biotechnology Information (NCBI) and other data referred to throughout in the disclosure herein are hereby expressly incorporated by reference for the portions of the document discussed herein, as well as in their entirety.

Definitions

Unless specific definitions are provided, the nomenclature utilized in connection with, and the procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques may be used for chemical synthesis, and chemical analysis.

Unless otherwise indicated, the following terms have the following meanings:

"2'-deoxynucleoside" (also 2'-deoxyribonucleoside) means a nucleoside comprising 2'-H furanosyl sugar moiety, as found in naturally occurring deoxyribonucleosides (DNA). In certain embodiments, a 2'-deoxynucleoside may comprise a modified nucleobase or may comprise an RNA nucleobase (e.g., uracil).

"2'-deoxyribose sugar" means a 2'-H furanosyl sugar moiety, as found in naturally occurring deoxyribonucleic acids (DNA).

"2'-O-methoxyethyl" (also 2'-MOE and 2'-OCH_2CH_2-OCH_3 and MOE and 2'-O-methoxyethylribose) refers to an O-methoxy-ethyl modification of the 2' position of a furanose ring. A 2'-O-methoxyethylribose modified sugar is a modified sugar.

"2'-O-methoxyethylribose modified nucleoside" (also2'-MOE nucleoside) means a nucleoside comprising a 2'-MOE modified sugar moiety.

"2'-substituted nucleoside" means a nucleoside comprising a substituent at the 2'-position of the furanose ring other than H or OH. In certain embodiments, 2' substituted nucleosides include nucleosides with bicyclic sugar modifications.

"5-methylcytosine" means a cytosine modified with a methyl group attached to the 5 position. A 5-methylcytosine is a modified nucleobase.

"About" means within ±10% of a value. For example, if it is stated, "the compounds affected at least about 50% inhibition of SOD-1", it is implied that the SOD-1 levels are inhibited within a range of 45% and 55%. "Administered concomitantly" refers to the co-administration of two pharmaceutical agents in any manner in which the pharmacological effects of both are manifest in the patient at the same time. Concomitant administration does not require that both pharmaceutical agents be administered in a single pharmaceutical composition, in the same dosage form, or by the same route of administration. The effects of both pharmaceutical agents need not manifest themselves at the same time. The effects need only be overlapping for a period of time and need not be coextensive.

"Administering" means providing a pharmaceutical agent to an animal, and includes, but is not limited to administering by a medical professional and self-administering.

"Amelioration" refers to a lessening, slowing, stopping, or reversing of at least one indicator of the severity of a condition or disease. The severity of indicators may be determined by subjective or objective measures, which are known to those skilled in the art.

"Animal" refers to a human or non-human animal, including, but not limited to, mice, rats, rabbits, dogs, cats, pigs, and non-human primates, including, but not limited to, monkeys and chimpanzees.

"Antibody" refers to a molecule characterized by reacting specifically with an antigen in some way, where the antibody and the antigen are each defined in terms of the other. Antibody may refer to a complete antibody molecule or any fragment or region thereof, such as the heavy chain, the light chain, Fab region, and Fc region.

"Antisense activity" means any detectable or measurable activity attributable to the hybridization of an antisense compound to its target nucleic acid. In certain embodiments, antisense activity is a decrease in the amount or expression of a target nucleic acid or protein encoded by such target nucleic acid.

"Antisense compound" means an oligomeric compound that is capable of undergoing hybridization to a target nucleic acid through hydrogen bonding. Examples of antisense compounds include single-stranded and double-stranded compounds, such as, antisense oligonucleotides, siRNAs, shRNAs, ssRNAs, and occupancy-based compounds.

"Antisense inhibition" means reduction of target nucleic acid levels in the presence of an antisense compound complementary to a target nucleic acid compared to target nucleic acid levels or in the absence of the antisense compound.

"Antisense mechanisms" are all those mechanisms involving hybridization of a compound with a target nucleic acid, wherein the outcome or effect of the hybridization is either target degradation or target occupancy with concomitant stalling of the cellular machinery involving, for example, transcription or splicing.

"Antisense oligonucleotide" means a single-stranded oligonucleotide having a nucleobase sequence that permits hybridization to a corresponding segment of a target nucleic acid.

"Base complementarity" refers to the capacity for the precise base pairing of nucleobases of an oligonucleotide with corresponding nucleobases in a target nucleic acid (i.e., hybridization), and is mediated by Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen binding between corresponding nucleobases.

"Bicyclic sugar" means a furanose ring modified by the bridging of two atoms. A bicyclic sugar is a modified sugar.

"Bicyclic nucleic acid" or "BNA" refers to a nucleoside or nucleotide wherein the furanose portion of the nucleoside or nucleotide includes a bridge connecting two carbon atoms on the furanose ring, thereby forming a bicyclic ring system.

"Cap structure" or "terminal cap moiety" means chemical modifications, which have been incorporated at either terminus of an antisense compound.

"cEt" or "constrained ethyl" or "cEt modified sugar" means a bicyclic nucleoside having a sugar moiety comprising a bridge connecting the 4'-carbon and the 2'-carbon, wherein the bridge has the formula: 4'-$CH(CH_3)$-O-2'. A cEt modified sugar is a modified sugar.

"cEt modified nucleoside" means a bicyclic nucleoside having a sugar moiety comprising a bridge connecting the 4'-carbon and the 2'-carbon, wherein the bridge has the formula: 4'-$CH(CH_3)$-O-2'. A cEt modified sugar is a modified sugar.

"Chemically distinct region" refers to a region of an antisense compound that is in some way chemically different than another region of the same antisense compound. For example, a region having 2'-O-methoxyethyl nucleosides is chemically distinct from a region having nucleosides without 2'-O-methoxyethyl modifications.

"Chimeric antisense compound" means an antisense compound that has at least two chemically distinct regions, each position having a plurality of subunits.

"Co-administration" means administration of two or more pharmaceutical agents to an individual. The two or more pharmaceutical agents may be in a single pharmaceutical composition, or may be in separate pharmaceutical compositions. Each of the two or more pharmaceutical agents may be administered through the same or different routes of administration. Co-administration encompasses parallel or sequential administration.

"Complementarity" means the capacity for pairing between nucleobases of a first nucleic acid and a second nucleic acid.

"Comprise," "comprises," and "comprising" will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

"Contiguous nucleobases" means nucleobases immediately adjacent to each other.

"Designing" or "designed to" refer to the process of designing an oligomeric compound that specifically hybridizes with a selected nucleic acid molecule.

"Diluent" means an ingredient in a composition that lacks pharmacological activity, but is pharmaceutically necessary or desirable. For example, in drugs that are injected, the diluent may be a liquid, e.g. saline solution.

"Dose" means a specified quantity of a pharmaceutical agent provided in a single administration, or in a specified time period. In certain embodiments, a dose may be administered in one, two, or more boluses, tablets, or injections. For example, in certain embodiments where subcutaneous administration is desired, the desired dose requires a volume not easily accommodated by a single injection, therefore, two or more injections may be used to achieve the desired dose. In certain embodiments, the pharmaceutical agent is administered by infusion over an extended period of time or continuously. Doses may be stated as the amount of pharmaceutical agent per hour, day, week, or month.

"Effective amount" in the context of modulating an activity or of treating or preventing a condition means the administration of that amount of pharmaceutical agent to a subject in need of such modulation, treatment, or prophylaxis, either in a single dose or as part of a series, that is effective for modulation of that effect, or for treatment or prophylaxis or improvement of that condition. The effective amount may vary among individuals depending on the health and physical condition of the individual to be treated, the taxonomic group of the individuals to be treated, the formulation of the composition, assessment of the individual's medical condition, and other relevant factors.

"Efficacy" means the ability to produce a desired effect.

"Expression" includes all the functions by which a gene's coded information is converted into structures present and operating in a cell. Such structures include, but are not limited to the products of transcription and translation.

"Fully complementary" or "100% complementary" means each nucleobase of a first nucleic acid has a complementary nucleobase in a second nucleic acid. In certain embodiments, a first nucleic acid is an antisense compound and a target nucleic acid is a second nucleic acid.

"Gapmer" means a chimeric antisense compound in which an internal region having a plurality of nucleosides that support RNase H cleavage is positioned between external regions having one or more nucleosides, wherein the nucleosides comprising the internal region are chemically distinct from the nucleoside or nucleosides comprising the external regions. The internal region may be referred to as a "gap" and the external regions may be referred to as the "wings."

"Gap-narrowed" means a chimeric antisense compound having a gap segment of 9 or fewer contiguous 2'-deoxyribonucleosides positioned between and immediately adjacent to 5' and 3' wing segments having from 1 to 6 nucleosides.

"Gap-widened" means a chimeric antisense compound having a gap segment of 12 or more contiguous 2'-deoxyribonucleosides positioned between and immediately adjacent to 5' and 3' wing segments having from 1 to 6 nucleosides.

"Hybridization" means the annealing of complementary nucleic acid molecules. In certain embodiments, complementary nucleic acid molecules include, but are not limited to, an antisense compound and a target nucleic acid. In certain embodiments, complementary nucleic acid molecules include, but are not limited to, an oligonucleotide and a nucleic acid target.

"Identifying an animal having a SOD-1 associated disease" means identifying an animal having been diagnosed with a SOD-1 associated disease or predisposed to develop a SOD-1 associated disease. Individuals predisposed to develop a SOD-1 associated disease include those having one or more risk factors for developing a SOD-1 associated disease, including, growing older, having a personal or family history, or genetic predisposition of one or more SOD-1 associated diseases. Such identification may be accomplished by any method including evaluating an individual's medical history and standard clinical tests or assessments, such as genetic testing.

"Immediately adjacent" means there are no intervening elements between the immediately adjacent elements.

"Individual" means a human or non-human animal selected for treatment or therapy.

"Inhibiting SOD-1" means reducing the level or expression of a SOD-1 mRNA and/or protein. In certain embodiments, SOD-1 mRNA and/or protein levels are inhibited in the presence of an antisense compound targeting SOD-1, including a modified oligonucleotide targeting SOD-1, as compared to expression of SOD-1 mRNA and/or protein levels in the absence of a SOD-1 antisense compound, such as a modified oligonucleotide.

"Inhibiting the expression or activity" refers to a reduction or blockade of the expression or activity and does not necessarily indicate a total elimination of expression or activity.

"Internucleoside linkage" refers to the chemical bond between nucleosides.

"Linked nucleosides" means adjacent nucleosides linked together by an internucleoside linkage.

"Mismatch" or "non-complementary nucleobase" refers to the case when a nucleobase of a first nucleic acid is not capable of pairing with the corresponding nucleobase of a second or target nucleic acid.

"Mixed backbone" means a pattern of internucleoside linkages including at least two different internucleoside linkages. For example, an oligonucleotide with a mixed backbone may include at least one phosphodiester linkage and at least one phosphorothioate linkage.

"Modified internucleoside linkage" refers to a substitution or any change from a naturally occurring internucleoside bond (*i.e.*, a phosphodiester internucleoside bond).

"Modified nucleobase" means any nucleobase other than adenine, cytosine, guanine, thymidine, or uracil. An "unmodified nucleobase" means the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C), and uracil (U).

A "modified nucleoside" means a nucleoside having, independently, a modified sugar moiety and/or modified nucleobase.

"Modified nucleotide" means a nucleotide having, independently, a modified sugar moiety, modified internucleoside linkage, and/or modified nucleobase.

"Modified oligonucleotide" means an oligonucleotide comprising at least one modified internucleoside linkage, modified sugar, and/or modified nucleobase.

"Modified sugar" means substitution and/or any change from a natural sugar moiety.

"Monomer" means a single unit of an oligomer. Monomers include, but are not limited to, nucleosides and nucleotides, whether naturally occurring or modified.

"Motif" means the pattern of unmodified and modified nucleosides in an antisense compound.

"Natural sugar moiety" means a sugar moiety found in DNA (2'-H) or RNA (2'-OH).

"Naturally occurring internucleoside linkage" means a 3' to 5' phosphodiester linkage.

"Non-complementary nucleobase" refers to a pair of nucleobases that do not form hydrogen bonds with one another or otherwise support hybridization.

"Nucleic acid" refers to molecules composed of monomeric nucleotides. A nucleic acid includes, but is not limited to, ribonucleic acids (RNA), deoxyribonucleic acids (DNA), single-stranded nucleic acids, double-stranded nucleic acids, small interfering ribonucleic acids (siRNA), and microRNAs (miRNA).

"Nucleobase" means a heterocyclic moiety capable of pairing with a base of another nucleic acid.

"Nucleobase complementarity" refers to a nucleobase that is capable of base pairing with another nucleobase. For example, in DNA, adenine (A) is complementary to thymine (T). For example, in RNA, adenine (A) is complementary to uracil (U). In certain embodiments, complementary nucleobase refers to a nucleobase of an antisense compound that is capable of base pairing with a nucleobase of its target nucleic acid. For example, if a nucleobase at a certain position of an antisense compound is capable of hydrogen bonding with a nucleobase at a certain position of a target nucleic acid, then the position of hydrogen bonding between the oligonucleotide and the target nucleic acid is considered to be complementary at that nucleobase pair.

"Nucleobase sequence" means the order of contiguous nucleobases independent of any sugar, linkage, and/or nucleobase modification.

"Nucleoside" means a nucleobase linked to a sugar.

"Nucleoside mimetic" includes those structures used to replace the sugar or the sugar and the base and not necessarily the linkage at one or more positions of an oligomeric compound such as for example nucleoside mimetics having morpholino, cyclohexenyl, cyclohexyl, tetrahydropyranyl, bicyclo, or tricyclo sugar mimetics, *e.g.*, non furanose sugar units. Nucleotide mimetic includes those structures used to replace the nucleoside and the linkage at one or more positions of an oligomeric compound such as for example peptide nucleic acids or morpholinos (morpholinos linked by -N(H)-C(=O)-O- or other non-phosphodiester linkage). Sugar surrogate overlaps with the slightly broader term nucleoside mimetic but is intended to indicate replacement of the sugar unit (furanose ring) only. The tetrahydropyranyl rings provided herein are

illustrative of an example of a sugar surrogate wherein the furanose sugar group has been replaced with a tetrahydropyranyl ring system. "Mimetic" refers to groups that are substituted for a sugar, a nucleobase, and/or internucleoside linkage. Generally, a mimetic is used in place of the sugar or sugar-internucleoside linkage combination, and the nucleobase is maintained for hybridization to a selected target.

"Nucleotide" means a nucleoside having a phosphate group covalently linked to the sugar portion of the nucleoside.

"Off-target effect" refers to an unwanted or deleterious biological effect associated with modulation of RNA or protein expression of a gene other than the intended target nucleic acid.

"Oligomeric compound" or "oligomer" means a polymer of linked monomeric subunits which is capable of hybridizing to at least a region of a nucleic acid molecule.

"Oligonucleotide" means a polymer of linked nucleosides each of which can be modified or unmodified, independent one from another.

"Parenteral administration" means administration through injection (e.g., bolus injection) or infusion. Parenteral administration includes subcutaneous administration, intravenous administration, intramuscular administration, intraarterial administration, intraperitoneal administration, or intracranial administration, e.g., intrathecal or intracerebroventricular administration.

"Peptide" means a molecule formed by linking at least two amino acids by amide bonds. Without limitation, as used herein, peptide refers to polypeptides and proteins.

"Pharmaceutical agent" means a substance that provides a therapeutic benefit when administered to an individual. For example, in certain embodiments, a modified oligonucleotide targeted to SOD-1 is a pharmaceutical agent.

"Pharmaceutical composition" means a mixture of substances suitable for administering to a subject. For example, a pharmaceutical composition may comprise a modified oligonucleotide and a sterile aqueous solution.

"Pharmaceutically acceptable derivative" encompasses pharmaceutically acceptable salts, conjugates, prodrugs or isomers of the compounds described herein.

"Pharmaceutically acceptable salts" means physiologically and pharmaceutically acceptable salts of antisense compounds, *i.e.*, salts that retain the desired biological activity of the parent oligonucleotide and do not impart undesired toxicological effects thereto.

"Phosphorothioate linkage" means a linkage between nucleosides where the phosphodiester bond is modified by replacing one of the non-bridging oxygen atoms with a sulfur atom. A phosphorothioate linkage is a modified internucleoside linkage.

"Portion" means a defined number of contiguous (*i.e.*, linked) nucleobases of a nucleic acid. In certain embodiments, a portion is a defined number of contiguous nucleobases of a target nucleic acid. In certain embodiments, a portion is a defined number of contiguous nucleobases of an antisense compound.

"Prevent" or "preventing" refers to delaying or forestalling the onset or development of a disease, disorder, or condition for a period of time from minutes to days, weeks to months, or indefinitely.

"Prodrug" means a therapeutic agent that is prepared in an inactive form that is converted to an active form (i.e., drug) within the body or cells thereof by the action of endogenous enzymes or other chemicals and/or conditions.

"Prophylactically effective amount" refers to an amount of a pharmaceutical agent that provides a prophylactic or preventative benefit to an animal.

"Region" is defined as a portion of the target nucleic acid having at least one identifiable structure, function, or characteristic.

"Ribonucleotide" means a nucleotide having a hydroxy at the 2' position of the sugar portion of the nucleotide. Ribonucleotides may be modified with any of a variety of substituents.

"Salts" mean a physiologically and pharmaceutically acceptable salts of antisense compounds, i.e., salts that retain the desired biological activity of the parent oligonucleotide and do not impart undesired toxicological effects thereto.

"Segments" are defined as smaller or sub-portions of regions within a target nucleic acid.

"Shortened" or "truncated" versions of oligonucleotides SOD-1ght herein have one, two or more nucleosides deleted.

"Side effects" means physiological responses attributable to a treatment other than desired effects. In certain embodiments, side effects include, without limitation, injection site reactions, liver function test abnormalities, renal function abnormalities, liver toxicity, renal toxicity, central nervous system abnormalities, and myopathies.

"Single-stranded oligonucleotide" means an oligonucleotide which is not hybridized to a complementary strand.

"Sites," as used herein, are defined as unique nucleobase positions within a target nucleic acid.

"Slows progression" means decrease in the development of the disease.

"SOD-1" means the mammalian gene superoxide dismutase 1, soluble (SOD-1), including the human gene superoxide dismutase 1, soluble (SOD-1).

"SOD-1 associated disease" means any disease associated with any SOD-1 nucleic acid or expression product thereof. Such diseases may include a neurodegenerative disease. Such neurodegenerative diseases may include amyotrophic lateral sclerosis (ALS).

"SOD-1 mRNA" means any messenger RNA expression product of a DNA sequence encoding SOD-1.

"SOD-1 nucleic acid" means any nucleic acid encoding SOD-1. For example, in certain embodiments, a SOD-1 nucleic acid includes a DNA sequence encoding SOD-1, an RNA sequence

transcribed from DNA encoding SOD-1 (including genomic DNA comprising introns and exons), and a mRNA sequence encoding SOD-1. "SOD-1 mRNA" means a mRNA encoding a SOD-1 protein.

"SOD-1 protein" means the polypeptide expression product of a SOD-1 nucleic acid.

"Specifically hybridizable" refers to an antisense compound having a sufficient degree of complementarity between an oligonucleotide and a target nucleic acid to induce a desired effect, while exhibiting minimal or no effects on non-target nucleic acids under conditions in which specific binding is desired, *i.e.*, under physiological conditions in the case of *in vivo* assays and therapeutic treatments.

"Stringent hybridization conditions" or "stringent conditions" refer to conditions under which an oligomeric compound will hybridize to its target sequence, but to a minimal number of other sequences.

"Subject" means a human or non-human animal selected for treatment or therapy.

"Sugar chemistry motif" means a pattern of sugar modifications including at least two different sugar modifications. For example, an oligonucleotide with a mixed backbone may include at least one 2'-O-methoxyethyl modified nucleoside, and/or one cEt modified nucleoside, and/or one 2'-deoxynucleoside.

"Target" refers to a protein, the modulation of which is desired.

"Target gene" refers to a gene encoding a target.

"Targeting" or "targeted" means the process of design and selection of an antisense compound that will specifically hybridize to a target nucleic acid and induce a desired effect.

"Target nucleic acid," "target RNA," and "target RNA transcript" and "nucleic acid target" all mean a nucleic acid capable of being targeted by antisense compounds.

"Target region" means a portion of a target nucleic acid to which one or more antisense compounds is targeted.

"Target segment" means the sequence of nucleotides of a target nucleic acid to which an antisense compound is targeted. "5' target site" refers to the 5'-most nucleotide of a target segment. "3' target site" refers to the 3'-most nucleotide of a target segment.

"Therapeutically effective amount" means an amount of a pharmaceutical agent that provides a therapeutic benefit to an individual.

"Treat" or "treating" or "treatment" refers administering a composition to effect an alteration or improvement of the disease or condition.

"Unmodified nucleobases" mean the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U).

"Unmodified nucleotide" means a nucleotide composed of naturally occuring nucleobases, sugar moieties, and internucleoside linkages. In certain embodiments, an unmodified nucleotide is an RNA nucleotide (*i.e.* β-D-ribonucleosides) or a DNA nucleotide (*i.e.* β-D-deoxyribonucleoside).

"Wing segment" means a plurality of nucleosides modified to impart to an oligonucleotide properties such as enhanced inhibitory activity, increased binding affinity for a target nucleic acid, or resistance to

degradation by in vivo nucleases.

Certain Embodiments

Certain embodiments provide methods, compounds, and compositions for inhibiting SOD-1 mRNA and protein expression. Certain embodiments provide methods, compounds, and composition for decreasing SOD-1 mRNA and protein levels.

Certain embodiments provide antisense compounds targeted to a SOD-1 nucleic acid. In certain embodiments, the SOD-1 nucleic acid is the sequence set forth in GENBANK Accession No. NM_000454.4 (incorporated herein as SEQ ID NO: 1), GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000 (incorporated herein as SEQ ID NO: 2), and the complement of GENBANK Accession No. NW_001114168.1 truncated from nucleotides 2258000 to 2271000 (incorporated herein as SEQ ID NO: 3).

Certain embodiments provide methods for the treatment, prevention, or amelioration of diseases, disorders, and conditions associated with SOD-1 in an individual in need thereof. Also contemplated are methods for the preparation of a medicament for the treatment, prevention, or amelioration of a disease, disorder, or condition associated with SOD-1. SOD-1 associated diseases, disorders, and conditions include neurodegenerative diseases. In certain embodiments, SOD-1 associated diseases include amyotrophic lateral sclerosis (ALS).

Embodiment 1. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising 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 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 118-1461.

Embodiment 2. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence comprising 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 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs:15, 21, 23, 47, 54, and 67, wherein at least one internucleoside linkage is a phosphodiester linkage.

Embodiment 3. The compound of any preceding embodiment, wherein the modified oligonucleotide has a mixed backbone.

Embodiment 4. The compound of embodiment 3, wherein the mixed backbone motif is any of the following:

sossssssssoooss,

sooossssssssoss,

sooossssssssssoss,

soossssssssooss,
sooossssssssooss,
sooossssssssooss,
sooossssssssssooss,
sooossssssssssoooos,
soooossssssssssooss,
sooossssssssssssooss,
sosossssssssssosos, and
sooossssssssssoooss, wherein
s = a phosphorothioate internucleoside linkage, and
o = a phosphodiester internucleoside linkage.

Embodiment 5. The compound of any preceding embodiment, wherein the modified oligonucleotide has a sugar chemistry motif of any of the following:
ekddddddddekekee,
kekeddddddddekek,
eeeeddddddddkkee,
eeeeddddddddekeke,
eeeeddddddddkekee,
eeeeddddddddkkeee,
eeeeeddddddddkkee,
eeeekddddddddkeee,
eeeekddddddddkeeee,
eeekddddddddkeeee,
eeekkddddddddkkeee,
eekkddddddddddkkee,
eekkddddddddeeeee,
eekkddddddddkkeee,
ekekddddddddeeeee,
ekekddddddddkekee, and
kekeddddddddeeeee, wherein
e = a 2'-O-methoxyethylribose modified sugar,
k = a cEt modified sugar,
d = a 2'-deoxyribose sugar,

Embodiment 6. The compound of any preceding embodiment, wherein the nucleobase sequence of

the modified oligonucleotide is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to SEQ ID NO: 1 or SEQ ID NO: 2.

Embodiment 7. The compound of any preceding embodiment, consisting of a single-stranded modified oligonucleotide.

Embodiment 8. The compound of any preceding embodiment, wherein at least one internucleoside linkage is a modified internucleoside linkage.

Embodiment 9. The compound of embodiment 8, wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 10. The compound of embodiment 9, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 11. The compound of any preceding embodiment, wherein at least one internucleoside linkage is a phosphodiester internucleoside linkage.

Embodiment 12. The compound of any preceding embodiment, wherein at least one internucleoside linkage is a phosphorothioate linkage and at least one internucleoside linkage is a phosphodiester linkage.

Embodiment 13. The compound of any preceding embodiment, wherein at least one nucleoside comprises a modified nucleobase.

Embodiment 14. The compound of embodiment 13, wherein the modified nucleobase is a 5-methylcytosine.

Embodiment 15. The compound of any preceding embodiment, wherein at least one nucleoside of the modified oligonucleotide comprises a modified sugar.

Embodiment 16. The compound of embodiment 15, wherein the at least one modified sugar is a bicyclic sugar.

Embodiment 17. The compound of embodiment 16, wherein the bicyclic sugar comprises a chemical link between the 2' and 4' position of the sugar 4'-CH_2-N(R)-O-2' bridge wherein R is, independently, H, C_1-C_{12} alkyl, or a protecting group.

Embodiment 18. The compound of embodiment 17, wherein the bicyclic sugar comprises a 4'-CH_2-N(R)-O-2' bridge wherein R is, independently, H, C_1-C_{12} alkyl, or a protecting group.

Embodiment 19. The compound of embodiment 15, wherein at least one modified sugar comprises a

2'-O-methoxyethyl group.

Embodiment 20. The compound of embodiment 15, wherein the modified sugar comprises a 2'-$O(CH_2)_2$-OCH_3 group.

Embodiment 21. The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

a gap segment consisting of 10 linked deoxynucleosides;
a 5' wing segment consisting of 5 linked nucleosides; and
a 3' wing segment consisting of 5 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 22. The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

a gap segment consisting of 9 linked deoxynucleosides;
a 5' wing segment consisting of 5 linked nucleosides; and
a 3' wing segment consisting of 5 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 23. The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

a gap segment consisting of 8 linked deoxynucleosides;
a 5' wing segment consisting of 5 linked nucleosides; and
a 3' wing segment consisting of 5 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 24. The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

a gap segment consisting of 8 linked deoxynucleosides;
a 5' wing segment consisting of 4 linked nucleosides; and
a 3' wing segment consisting of 5 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 25. The compound of any preceding embodiment, wherein the modified oligonucleotide

comprises:

a gap segment consisting of 8 linked deoxynucleosides;
a 5' wing segment consisting of 5 linked nucleosides; and
a 3' wing segment consisting of 7 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 26. The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

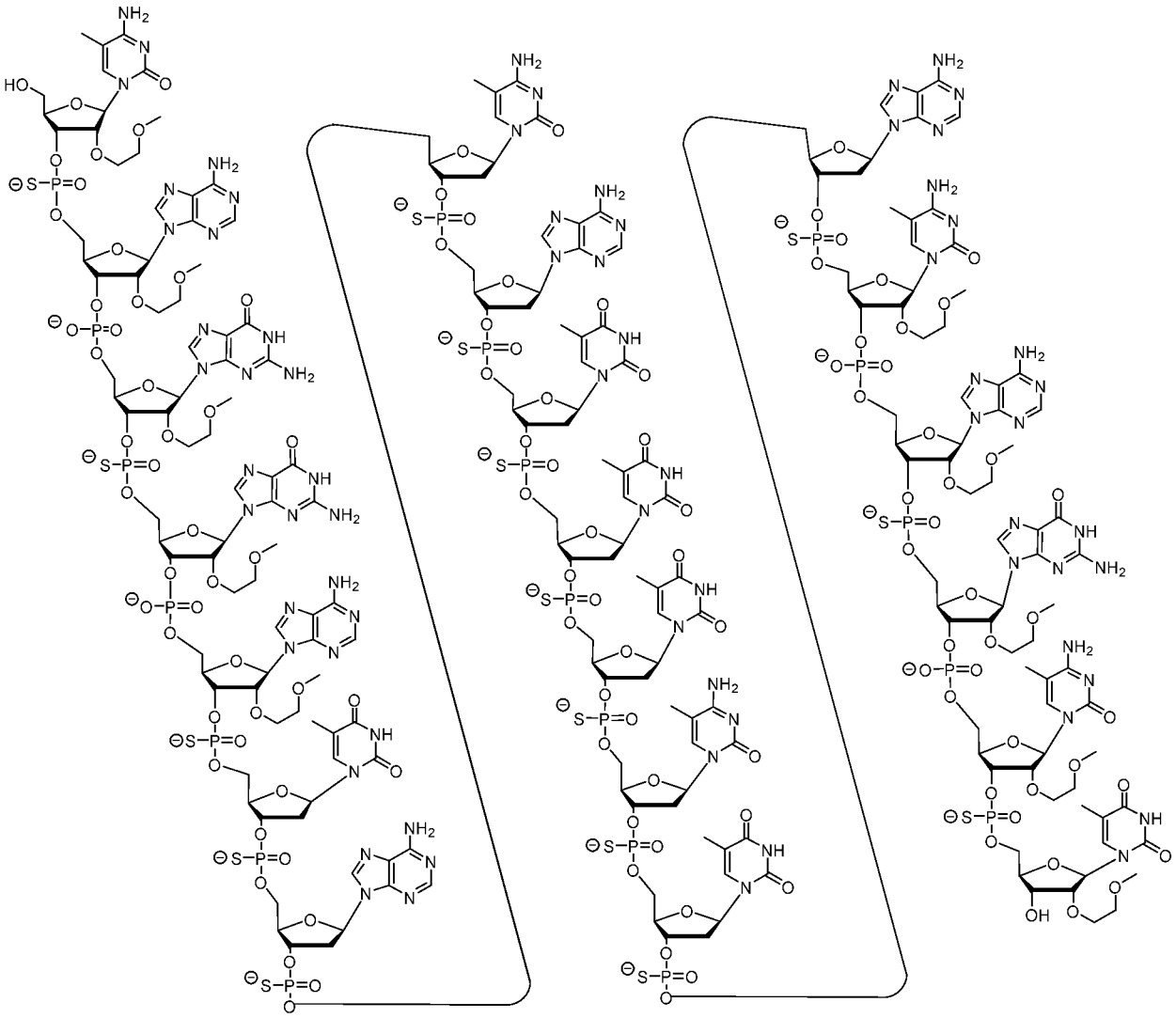
a gap segment consisting of 8 linked deoxynucleosides;
a 5' wing segment consisting of 6 linked nucleosides; and
a 3' wing segment consisting of 6 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 27. The compound of any preceding embodiment, wherein the modified oligonucleotide comprises:

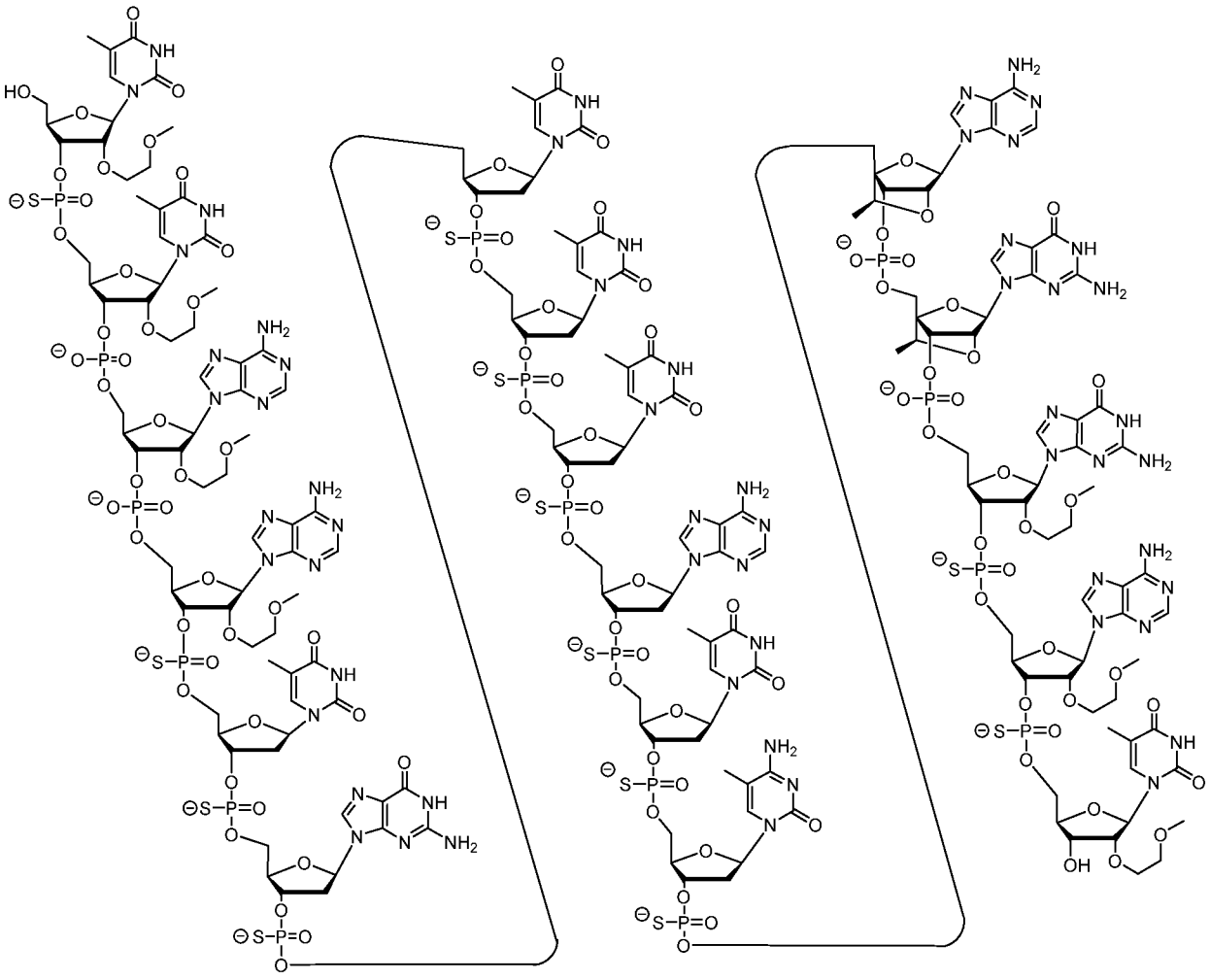
a gap segment consisting of 9 linked deoxynucleosides;
a 5' wing segment consisting of 6 linked nucleosides; and
a 3' wing segment consisting of 5 linked nucleosides;
wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

Embodiment 28. The compound of any preceding embodiment, wherein the modified oligonucleotide consists of 12, 13, 14, 15, 16, 17, 18, 19, or 20 linked nucleosides.

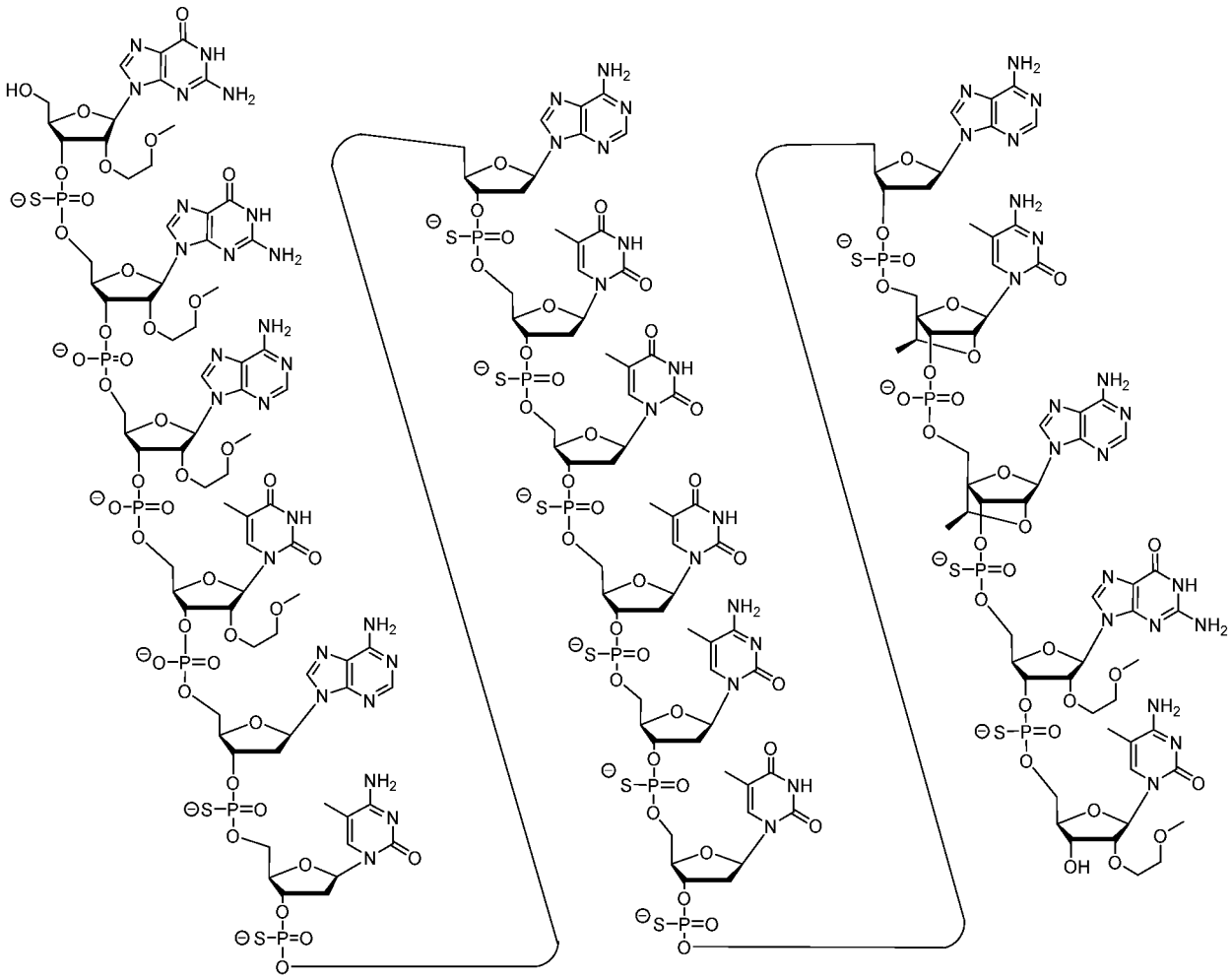
Embodiment 29. A compound consisting of a modified oligonucleotide according to the following formula:



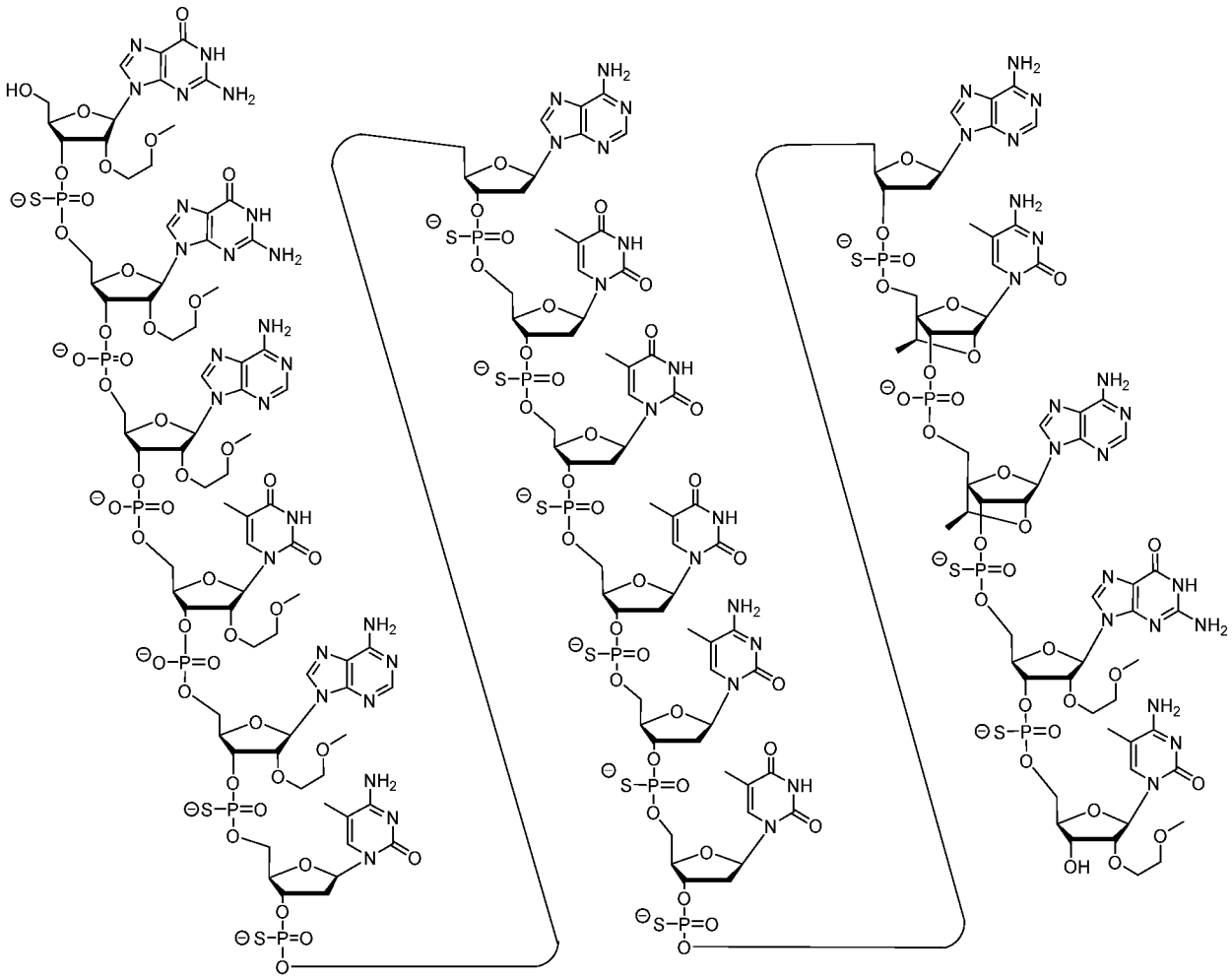
Embodiment 30. A compound consisting of a modified oligonucleotide according to the following formula:



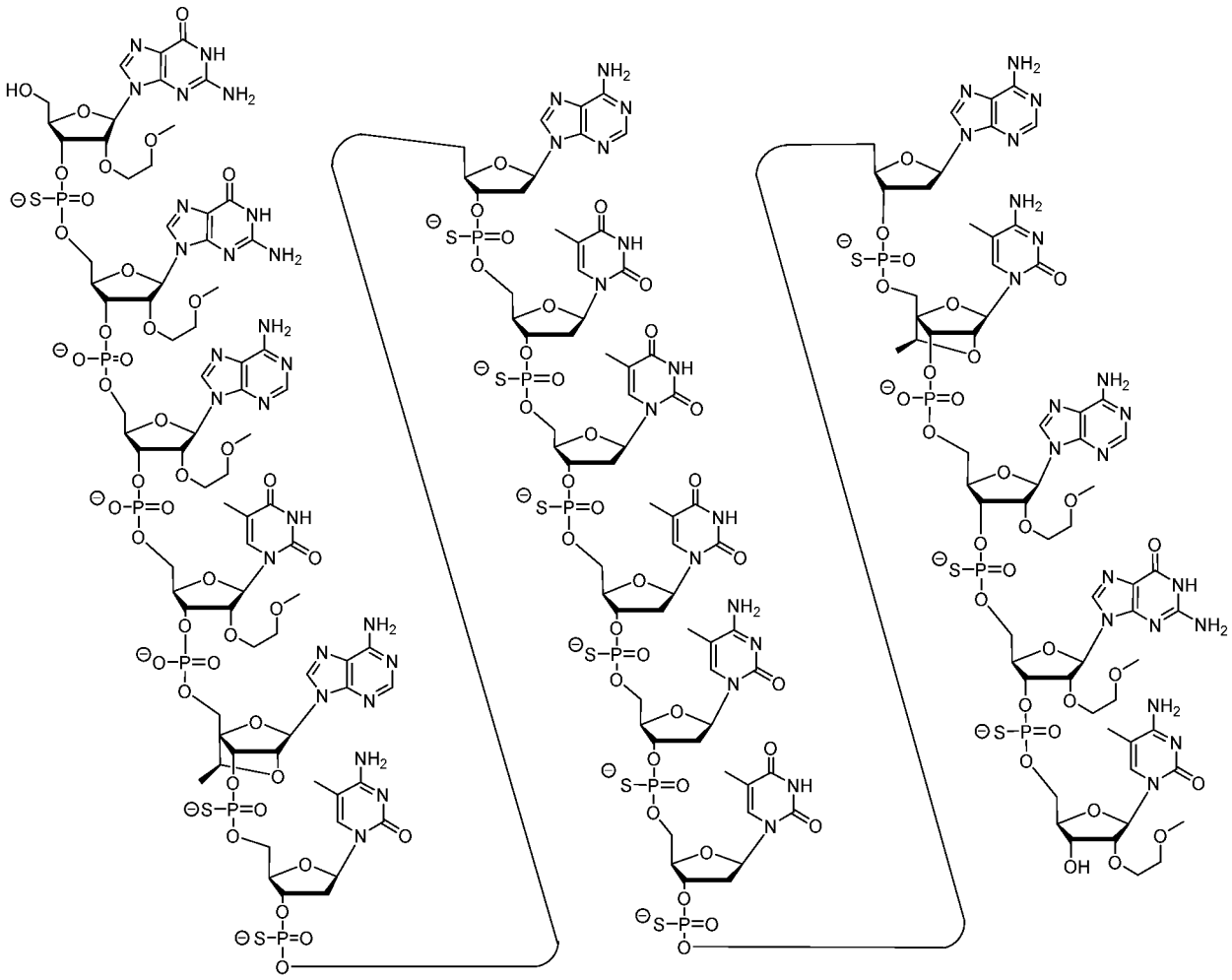
Embodiment 31. A compound consisting of a modified oligonucleotide according to the following formula:



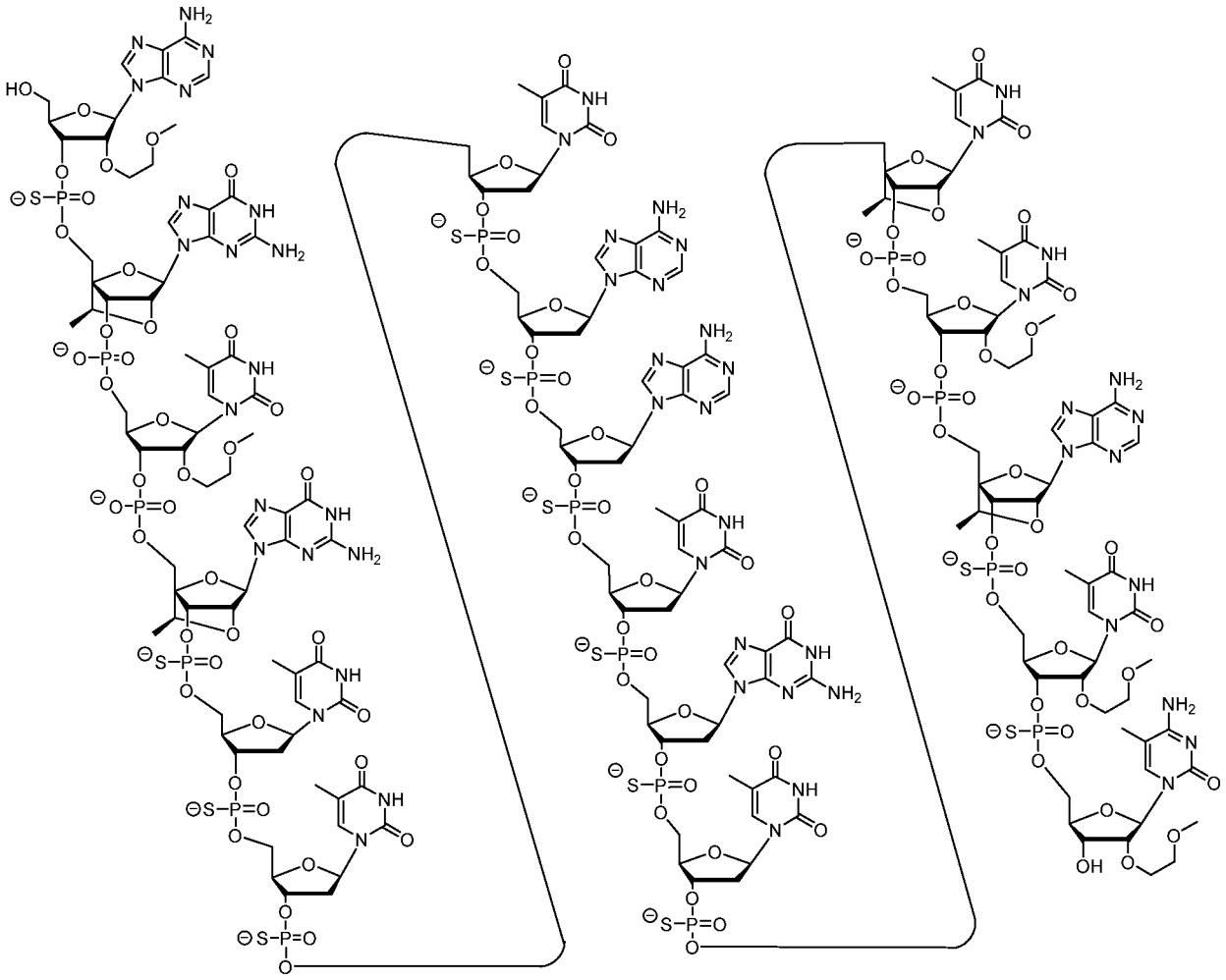
Embodiment 32. A compound consisting of a modified oligonucleotide according to the following formula:



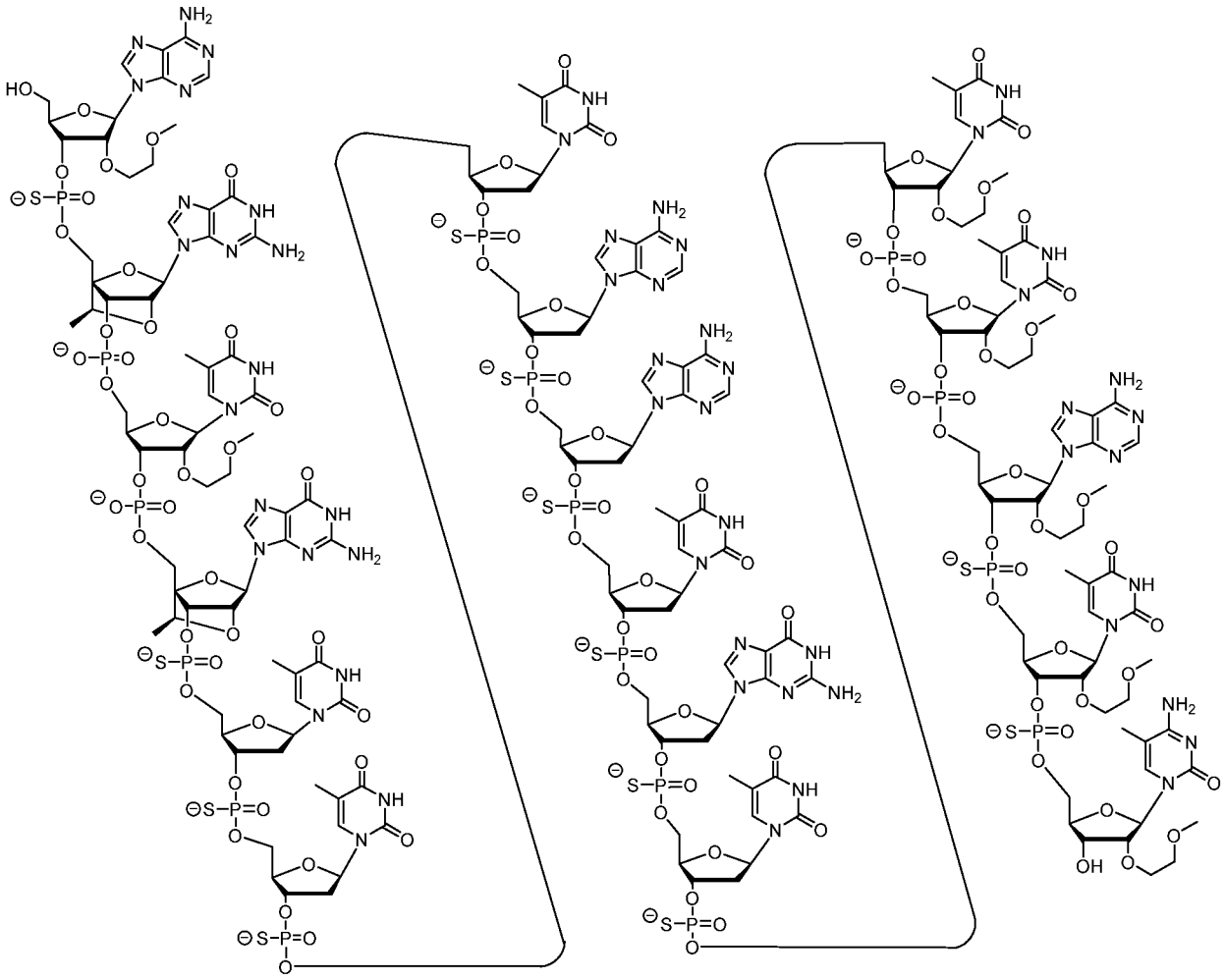
Embodiment 33. A compound consisting of a modified oligonucleotide according to the following formula:



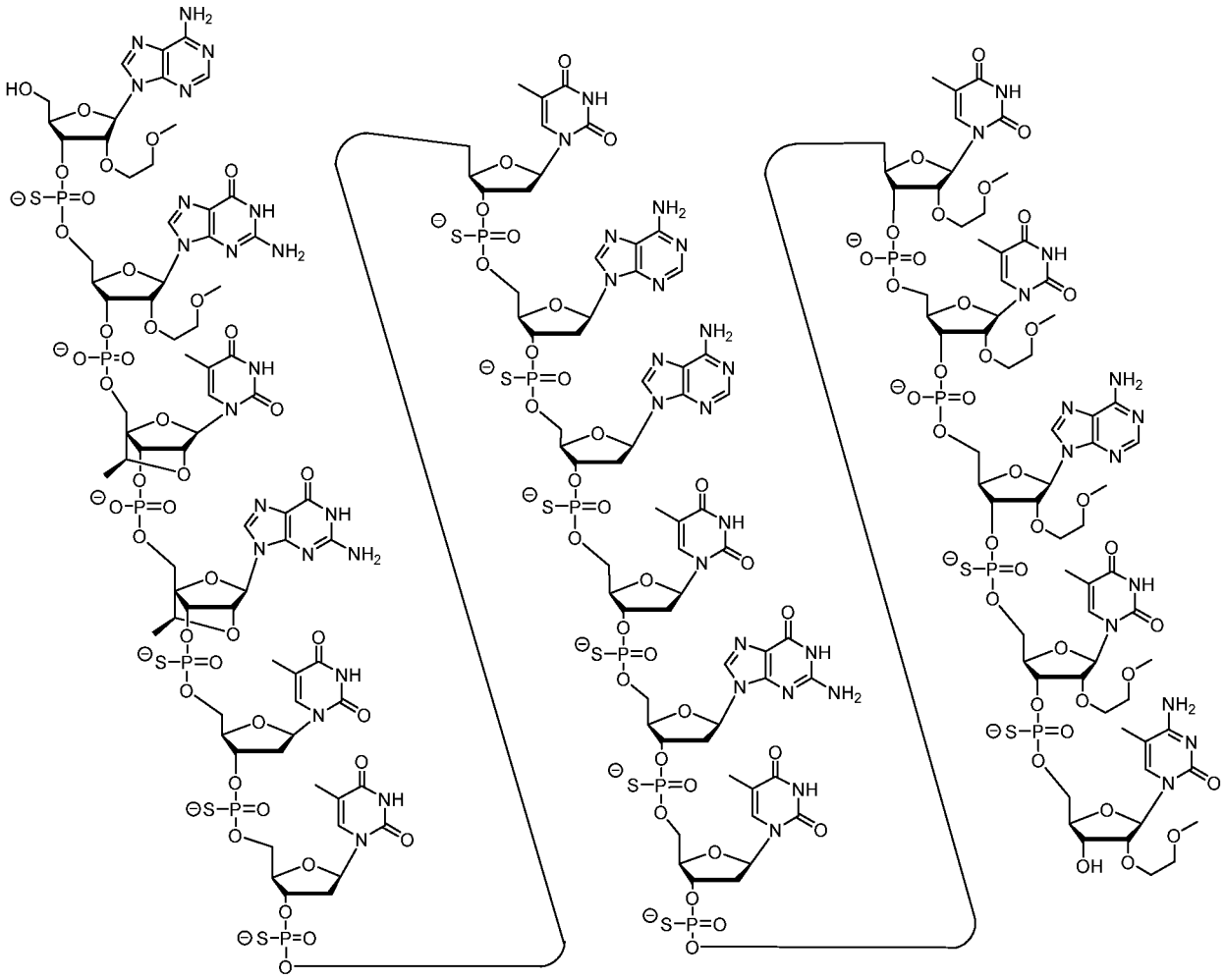
Embodiment 34. A compound consisting of a modified oligonucleotide according to the following formula:



Embodiment 35. A compound consisting of a modified oligonucleotide according to the following formula:



Embodiment 36. A compound consisting of a modified oligonucleotide according to the following formula:



Embodiment 37. A compound consisting of a modified oligonucleotide according to the following formula: mCes Aeo Ges Geo Aes Tds Ads mCds Ads Tds Tds Tds mCds Tds Ads mCeo Aes Geo mCes Te; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 38. A compound consisting of a modified oligonucleotide according to the following formula: Tes Teo Aeo Aes Tds Gds Tds Tds Tds Ads Tds mCds Ako Gko Ges Aes Te; wherein,

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethylribose modified sugar,
k = a cEt modified sugar,
d = a 2'-deoxyribose sugar,
s = a phosphorothioate internucleoside linkage, and
o = a phosphodiester internucleoside linkage.

Embodiment 39. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo Aeo Teo Ads mCds Ads Tds Tds Tds mCds Tds Ads mCko Aks Ges mCe; wherein,

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethylribose modified sugar,
k = a cEt modified sugar,
d = a 2'-deoxyribose sugar,
s = a phosphorothioate internucleoside linkage, and
o = a phosphodiester internucleoside linkage.

Embodiment 40. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo Aeo Teo Aes mCds Ads Tds Tds Tds mCds Tds Ads mCko Aks Ges mCe; wherein,

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethylribose modified sugar,
k = a cEt modified sugar,
d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 41. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo Aeo Teo Aks mCds Ads Tds Tds Tds mCds Tds Ads mCko Aes Ges mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 42. A compound consisting of a modified oligonucleotide according to the following formula: Aes Gko Teo Gks Tds Tds Tds Ads Ads Tds Gds Tds Tko Teo Aks Tes mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 43. A compound consisting of a modified oligonucleotide according to the following formula: Aes Gko Teo Gks Tds Tds Tds Ads Ads Tds Gds Tds Teo Teo Aes Tes mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 44. A compound consisting of a modified oligonucleotide according to the following formula: Aes Geo Tko Gks Tds Tds Tds Ads Ads Tds Gds Tds Teo Teo Aes Tes mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 45. A compound consisting of a modified oligonucleotide according to the following formula: mCes mCeo Geo Teo mCeo Gds mCds mCds mCds Tds Tds mCds Ads Gds mCds Aeo mCeo Ges mCes Ae, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 46. A compound consisting of a modified oligonucleotide according to the following formula: mCes mCeo Geo Teo mCes Gds mCds mCds mCds Tds Tds mCds Ads Ges mCeo Aeo mCeo Ges mCes Ae, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 47. A compound consisting of a modified oligonucleotide according to the following formula: mCes mCeo Geo Teo mCes Gds mCds mCds mCds Tds Tds mCds Ads Gds mCds Aeo mCeo Geo mCes Ae, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 48. A compound consisting of a modified oligonucleotide according to the following formula: Aes mCeo Aeo mCeo mCes Tds Tds mCds Ads mCds Tds Gds Gds Tds mCds mCeo Aeo Teo Tes Ae, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 49. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo mCeo Geo Aes Tds mCds mCds mCds Ads Ads Tds Tds Ads mCds Aeo mCeo mCeo Aes mCe, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 50. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo mCeo Geo Aes Tes mCds mCds mCds Ads Ads Tds Tds Ads mCeo Aeo mCeo mCes Aes mCe, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 51. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo mCeo Geo Aes Tds mCds mCds mCds Ads Ads Tds Tds Aes mCeo Aeo mCeo mCes Aes mCe, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Embodiment 52. A compound consisting of a modified oligonucleotide according to the following formula: Ges Geo mCeo Geo Aeo Tes mCds mCds mCds Ads Ads Tds Tds Ads mCds Aeo mCeo mCes Aes mCe, wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,
d = a 2'-deoxyribose sugar,
s = a phosphorothioate internucleoside linkage, and
o = a phosphodiester internucleoside linkage.

Embodiment 53. A compound consisting of a modified oligonucleotide according to the following formula: Ges Teo mCeo Geo mCes mCds mCds Tds Tds mCds Ads Gds mCds Ads mCds Geo mCeo Aeo mCes Ae, wherein,

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethylribose modified sugar,
d = a 2'-deoxyribose sugar,
s = a phosphorothioate internucleoside linkage, and
o = a phosphodiester internucleoside linkage.

Embodiment 54. A compound consisting of a modified oligonucleotide according to the following formula: Tes mCeo Geo mCeo mCes mCds Tds Tds mCds Ads Gds mCds Ads mCds Gds mCeo Aeo mCeo Aes mCe, wherein,

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethylribose modified sugar,
d = a 2'-deoxyribose sugar,
s = a phosphorothioate internucleoside linkage, and
o = a phosphodiester internucleoside linkage.

Embodiment 55. A compound consisting of a modified oligonucleotide according to the following formula: Ges Aes Aes Aes Tes Tds Gds Ads Tds Gds Ads Tds Gds mCds mCds mCes Tes Ges mCes Ae, wherein,

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar, and

s = a phosphorothioate internucleoside linkage.

Embodiment 56. A composition comprising the compound of any preceding embodiment or salt thereof and at least one of a pharmaceutically acceptable carrier or diluent.

Embodiment 57. A method comprising administering to an animal the compound or composition of any preceding embodiment.

Embodiment 58. The method of embodiment 57, wherein the animal is a human.

Embodiment 59. The method of embodiment 57, wherein administering the compound prevents, treats, ameliorates, or slows progression of a SOD-1 associated disease.

Embodiment 60. The method of embodiment 59, wherein the SOD-1 associated disease is a neurodegenerative disease.

Embodiment 61. The method of embodiment 60, wherein the SOD-1 associated disease is ALS.

Embodiment 62. Use of the compound or composition of any preceding embodiment for the manufacture of a medicament for treating a neurodegenerative disorder.

Embodiment 63. Use of the compound or composition of any preceding embodiment for the manufacture of a medicament for treating ALS.

Embodiment 64. The compound or composition of any preceding embodiment wherein the modified oligonucleotide does not have the nucleobase sequence of SEQ ID NO: 21.

Embodiment 65. The compound or composition of any preceding embodiment wherein the modified oligonucleotide does not have the nucleobase sequence of any of SEQ ID NOs: 21-118.

Embodiment 66. A compound comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and having a nucleobase sequence, wherein the nucleobase sequence comprises an at least 12 consecutive nucleobase portion complementary to an equal number of nucleobases of nucleotides 665 to 684 of SEQ ID NO: 1, wherein the modified oligonucleotide is at least 80% complementary to SEQ ID NO: 1.

Embodiment 67. The compound of embodiment 66, wherein the modified oligonucleotide is 100% complementary to SEQ ID NO: 1.

Embodiment 68. The compound of embodiment 66, wherein the modified oligonucleotide is a single-stranded modified oligonucleotide.

Embodiment 69. The compound of embodiments 66-68 wherein at least one internucleoside linkage is

a modified internucleoside linkage.

Embodiment 70. The compound of embodiment 69, wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 71. The compound of embodiment 70, wherein each modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 72. The compound of embodiments 66-69, wherein at least one internucleoside linkage is a phosphodiester internucleoside linkage.

Embodiment 73. The compound of embodiments 66-71 and 72-73, wherein at least one internucleoside linkage is a phosphorothioate linkage and at least one internucleoside linkage is a phosphodiester linkage.

Embodiment 74. The compound of embodiments 66-73, wherein at least one nucleoside comprises a modified nucleobase.

Embodiment 75. The compound of embodiment 74, wherein the modified nucleobase is a 5-methylcytosine.

Embodiment 76. The compound of embodiments 66-75, wherein at least one nucleoside of the modified oligonucleotide comprises a modified sugar.

Embodiment 77. The compound of embodiment 76, wherein the at least one modified sugar is a bicyclic sugar.

Embodiment 78. The compound of embodiment 77, wherein the bicyclic sugar comprises a 4'-CH(R)-O-2' bridge wherein R is, independently, H, C_1-C_{12} alkyl, or a protecting group.

Embodiment 79. The compound of embodiment 78, wherein R is methyl.

Embodiment 80. The compound of embodiment 78, wherein R is H.

Embodiment 81. The compound of embodiment 76, wherein the at least one modified sugar comprises a 2'-O-methoxyethyl group.

Antisense Compounds

Oligomeric compounds include, but are not limited to, oligonucleotides, oligonucleosides, oligonucleotide analogs, oligonucleotide mimetics, antisense compounds, antisense oligonucleotides, modified oligonucleotides, and siRNAs. An oligomeric compound may be "antisense" to a target nucleic acid, meaning that is is capable of undergoing hybridization to a target nucleic acid through hydrogen bonding.

In certain embodiments, an antisense compound has a nucleobase sequence that, when written in the 5' to 3' direction, comprises the reverse complement of the target segment of a target nucleic acid to which it is targeted. In certain such embodiments, an oligonucleotide has a nucleobase sequence that, when written in the 5' to 3' direction, comprises the reverse complement of the target segment of a target nucleic acid to which it is targeted.

In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 12 to 30 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 12 to 25 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 12 to 22 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 14 to 20 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 15 to 25 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 18 to 22 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 19 to 21 subunits in length. In certain embodiments, the antisense compound is 8 to 80, 12 to 50, 13 to 30, 13 to 50, 14 to 30, 14 to 50, 15 to 30, 15 to 50, 16 to 30, 16 to 50, 17 to 30, 17 to 50, 18 to 30, 18 to 50, 19 to 30, 19 to 50, or 20 to 30 linked subunits in length.

In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 12 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 13 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 14 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 15 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 16 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 17 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 18 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 19 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 20 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 21 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 22 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 23 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 24 subunits in

length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 25 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 26 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 27 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 28 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 29 subunits in length. In certain embodiments, an antisense compound targeted to a SOD-1 nucleic acid is 30 subunits in length. In certain embodiments, the antisense compound targeted to a SOD-1 nucleic acid is 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or 80 linked subunits in length, or a range defined by any two of the above values. In certain embodiments the antisense compound is a modified oligonucleotide, and the linked subunits are nucleosides.

In certain embodiments, oligonucleotides targeted to a SOD-1 nucleic acid may be shortened or truncated. For example, a single subunit may be deleted from the 5' end (5' truncation), or alternatively from the 3' end (3' truncation). A shortened or truncated antisense compound targeted to a SOD-1 nucleic acid may have two subunits deleted from the 5' end, or alternatively may have two subunits deleted from the 3' end, of the antisense compound. Alternatively, the deleted nucleosides may be dispersed throughout the antisense compound, for example, in an antisense compound having one nucleoside deleted from the 5' end and one nucleoside deleted from the 3' end.

When a single additional subunit is present in a lengthened antisense compound, the additional subunit may be located at the 5' or 3' end of the antisense compound. When two or more additional subunits are present, the added subunits may be adjacent to each other, for example, in an antisense compound having two subunits added to the 5' end (5' addition), or alternatively to the 3' end (3' addition), of the antisense compound. Alternatively, the added subunits may be dispersed throughout the antisense compound, for example, in an antisense compound having one subunit added to the 5' end and one subunit added to the 3' end.

It is possible to increase or decrease the length of an antisense compound, such as a modified oligonucleotide, and/or introduce mismatch bases without eliminating activity. For example, in Woolf et al. (Proc. Natl. Acad. Sci. USA 89:7305-7309, 1992), a series of oligonucleotides 13-25 nucleobases in length were tested for their ability to induce cleavage of a target RNA in an oocyte injection model. Oligonucleotides 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the oligonucleotides were able to direct specific cleavage of the target mRNA, albeit to a lesser extent than oligonucleotides that contained no mismatches. Similarly, target specific cleavage was achieved using 13 nucleobase oligonucleotides, including those with 1 or 3 mismatches.

Gautschi et al (J. Natl. Cancer Inst. 93:463-471, March 2001) demonstrated the ability of an oligonucleotide having 100% complementarity to the bcl-2 mRNA and having 3 mismatches to the bcl-xL

mRNA to reduce the expression of both bcl-2 and bcl-xL *in vitro* and *in vivo*. Furthermore, this oligonucleotide demonstrated potent anti-tumor activity *in vivo*.

Maher and Dolnick (Nuc. Acid. Res. 16:3341-3358,1988) tested a series of tandem 14 nucleobase oligonucleotides, and a 28 and 42 nucleobase oligonucleotides comprised of the sequence of two or three of the tandem oligonucleotides, respectively, for their ability to arrest translation of human DHFR in a rabbit reticulocyte assay. Each of the three 14 nucleobase oligonucleotides alone was able to inhibit translation, albeit at a more modest level than the 28 or 42 nucleobase oligonucleotides.

Antisense Compound Motifs

In certain embodiments, antisense compounds targeted to a SOD-1 nucleic acid have chemically modified subunits arranged in patterns, or motifs, to confer to the antisense compounds properties such as enhanced inhibitory activity, increased binding affinity for a target nucleic acid, or resistance to degradation by *in vivo* nucleases.

Chimeric antisense compounds typically contain at least one region modified so as to confer increased resistance to nuclease degradation, increased cellular uptake, increased binding affinity for the target nucleic acid, and/or increased inhibitory activity. A second region of a chimeric antisense compound may optionally serve as a substrate for the cellular endonuclease RNase H, which cleaves the RNA strand of an RNA:DNA duplex.

Antisense compounds having a gapmer motif are considered chimeric antisense compounds. In a gapmer an internal region having a plurality of nucleotides that supports RNaseH cleavage is positioned between external regions having a plurality of nucleotides that are chemically distinct from the nucleosides of the internal region. In the case of an oligonucleotide having a gapmer motif, the gap segment generally serves as the substrate for endonuclease cleavage, while the wing segments comprise modified nucleosides. In certain embodiments, the regions of a gapmer are differentiated by the types of sugar moieties comprising each distinct region. The types of sugar moieties that are used to differentiate the regions of a gapmer may in some embodiments include β-D-ribonucleosides, β-D-deoxyribonucleosides, 2'-modified nucleosides (such 2'-modified nucleosides may include 2'-MOE, and 2'-O-CH_3, among others), and bicyclic sugar modified nucleosides (such bicyclic sugar modified nucleosides may include those having a 4'-(CH_2)n-O-2' bridge, where n=1 or n=2 and 4'-CH_2-O-CH_2-2'). In certain embodiments, wings may include several modified sugar moieties, including, for example 2'-MOE. In certain embodiments, wings may include several modified and unmodified sugar moieties. In certain embodiments, wings may include various combinations of 2'-MOE nucleosides and 2'-deoxynucleosides.

Each distinct region may comprise uniform sugar moieties, variant, or alternating sugar moieties. The wing-gap-wing motif is frequently described as "X-Y-Z", where "X" represents the length of the 5' wing, "Y" represents the length of the gap, and "Z" represents the length of the 3' wing. "X" and "Z" may

comprise uniform, variant, or alternating sugar moieties. In certain embodiments, "X" and "Y" may include one or more 2'-deoxynucleosides. "Y" may comprise 2'-deoxynucleosides. As used herein, a gapmer described as "X-Y-Z" has a configuration such that the gap is positioned immediately adjacent to each of the 5' wing and the 3' wing. Thus, no intervening nucleotides exist between the 5' wing and gap, or the gap and the 3' wing. Any of the antisense compounds described herein can have a gapmer motif. In certain embodiments, "X" and "Z" are the same; in other embodiments they are different.

In certain embodiments, gapmers provided herein include, for example 20-mers having a motif of 5-10-5.

In certain embodiments, gapmers provided herein include, for example 19-mers having a motif of 5-9-5.

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 5-8-5.

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 4-8-5.

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 5-8-7.

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 6-8-6.

In certain embodiments, gapmers provided herein include, for example 18-mers having a motif of 6-8-5.

In certain embodiments, the modified oligonucleotide contains at least one 2'-O-methoxyethyl modified nucleoside , at least one cEt modified nucleoside , and at least one 2'-deoxynucleoside. In certain embodiments, the modified oligonucleotide has a sugar chemistry motif of any of the following:

ekddddddddekekee

kekedddddddekek

eeeeddddddddkkee

eeeeddddddddekeke

eeeeddddddddkekee

eeeeddddddddkkeee

eeeeeddddddddkkee

eeeekddddddddkeee

eeeekddddddddkeeee

eeekddddddddkeeee

eeekkddddddddkkeee

eekkddddddddddkkee

eekkddddddddeeeee

eekkddddddddkkeee

ekekddddddddeeeee

ekekddddddddkekee

kekeddddddddeeeee, wherein

e = a 2'-O-methoxyethylribose modified sugar,

k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

Target Nucleic Acids, Target Regions and Nucleotide Sequences

Nucleotide sequences that encode SOD-1 include, without limitation, the following: GENBANK Accession No. NM_000454.4 (incorporated herein as SEQ ID NO: 1), GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000 (incorporated herein as SEQ ID NO: 2), and the complement of GENBANK Accession No. NW_001114168.1 truncated from nucleotides 2258000 to 2271000 (incorporated herein as SEQ ID NO: 3).

It is understood that the sequence set forth in each SEQ ID NO in the Examples contained herein is independent of any modification to a sugar moiety, an internucleoside linkage, or a nucleobase. As such, antisense compounds defined by a SEQ ID NO may comprise, independently, one or more modifications to a sugar moiety, an internucleoside linkage, or a nucleobase. Antisense compounds described by Isis Number (Isis No) indicate a combination of nucleobase sequence and motif.

In certain embodiments, a target region is a structurally defined region of the target nucleic acid. For example, a target region may encompass a 3' UTR, a 5' UTR, an exon, an intron, an exon/intron junction, a coding region, a translation initiation region, translation termination region, or other defined nucleic acid region. The structurally defined regions for SOD-1 can be obtained by accession number from sequence databases such as NCBI and such information is incorporated herein by reference. In certain embodiments, a target region may encompass the sequence from a 5' target site of one target segment within the target region to a 3' target site of another target segment within the same target region.

Targeting includes determination of at least one target segment to which an antisense compound hybridizes, such that a desired effect occurs. In certain embodiments, the desired effect is a reduction in mRNA target nucleic acid levels. In certain embodiments, the desired effect is reduction of levels of protein encoded by the target nucleic acid or a phenotypic change associated with the target nucleic acid.

A target region may contain one or more target segments. Multiple target segments within a target region may be overlapping. Alternatively, they may be non-overlapping. In certain embodiments, target segments within a target region are separated by no more than about 300 nucleotides. In certain emodiments, target segments within a target region are separated by a number of nucleotides that is, is about, is no more

than, is no more than about, 250, 200, 150, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 nucleotides on the target nucleic acid, or is a range defined by any two of the preceeding values. In certain embodiments, target segments within a target region are separated by no more than, or no more than about, 5 nucleotides on the target nucleic acid. In certain embodiments, target segments are contiguous. Contemplated are target regions defined by a range having a starting nucleic acid that is any of the 5' target sites or 3' target sites listed herein.

Suitable target segments may be found within a 5' UTR, a coding region, a 3' UTR, an intron, an exon, or an exon/intron junction. Target segments containing a start codon or a stop codon are also suitable target segments. A suitable target segment may specifcally exclude a certain structurally defined region such as the start codon or stop codon.

The determination of suitable target segments may include a comparison of the sequence of a target nucleic acid to other sequences throughout the genome. For example, the BLAST algorithm may be used to identify regions of similarity amongst different nucleic acids. This comparison can prevent the selection of antisense compound sequences that may hybridize in a non-specific manner to sequences other than a selected target nucleic acid (i.e., non-target or off-target sequences).

There may be variation in activity (e.g., as defined by percent reduction of target nucleic acid levels) of the antisense compounds within an active target region. In certain embodiments, reductions in SOD-1 mRNA levels are indicative of inhibition of SOD-1 expression. Reductions in levels of a SOD-1 protein are also indicative of inhibition of target mRNA expression. Phenotypic changes are indicative of inhibition of SOD-1 expression. Improvement in neurological function is indicative of inhibition of SOD-1 expression. Improved motor function is indicative of inhibition of SOD-1 expression.

Hybridization

In some embodiments, hybridization occurs between an antisense compound disclosed herein and a SOD-1 nucleic acid. The most common mechanism of hybridization involves hydrogen bonding (e.g., Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding) between complementary nucleobases of the nucleic acid molecules.

Hybridization can occur under varying conditions. Stringent conditions are sequence-dependent and are determined by the nature and composition of the nucleic acid molecules to be hybridized.

Methods of determining whether a sequence is specifically hybridizable to a target nucleic acid are well known in the art. In certain embodiments, the antisense compounds provided herein are specifically hybridizable with a SOD-1 nucleic acid.

Complementarity

An antisense compound and a target nucleic acid are complementary to each other when a sufficient number of nucleobases of the antisense compound can hydrogen bond with the corresponding nucleobases of the target nucleic acid, such that a desired effect will occur (e.g., antisense inhibition of a target nucleic acid, such as a SOD-1 nucleic acid).

Non-complementary nucleobases between an antisense compound and a SOD-1 nucleic acid may be tolerated provided that the antisense compound remains able to specifically hybridize to a target nucleic acid. Moreover, an antisense compound may hybridize over one or more segments of a SOD-1 nucleic acid such that intervening or adjacent segments are not involved in the hybridization event (e.g., a loop structure, mismatch or hairpin structure).

In certain embodiments, the antisense compounds provided herein, or a specified portion thereof, are, or are at least, 70%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% complementary to a SOD-1 nucleic acid, a target region, target segment, or specified portion thereof. Percent complementarity of an antisense compound with a target nucleic acid can be determined using routine methods.

For example, an antisense compound in which 18 of 20 nucleobases of the antisense compound are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In this example, the remaining noncomplementary nucleobases may be clustered or interspersed with complementary nucleobases and need not be contiguous to each other or to complementary nucleobases. As such, an antisense compound which is 18 nucleobases in length having 4 (four) noncomplementary nucleobases which are flanked by two regions of complete complementarity with the target nucleic acid would have 77.8% overall complementarity with the target nucleic acid and would thus fall within the scope of the present invention. Percent complementarity of an antisense compound with a region of a target nucleic acid can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs known in the art (Altschul et al., J. Mol. Biol., 1990, 215, 403 410; Zhang and Madden, Genome Res., 1997, 7, 649 656). Percent homology, sequence identity or complementarity, can be determined by, for example, the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison Wis.), using default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2, 482 489).

In certain embodiments, the antisense compounds provided herein, or specified portions thereof, are fully complementary (*i.e.*, 100% complementary) to a target nucleic acid, or specified portion thereof. For example, an antisense compound may be fully complementary to a SOD-1 nucleic acid, or a target region, or a target segment or target sequence thereof. As used herein, "fully complementary" means each nucleobase of an antisense compound is capable of precise base pairing with the corresponding nucleobases of a target nucleic acid. For example, a 20 nucleobase antisense compound is fully complementary to a target sequence

that is 400 nucleobases long, so long as there is a corresponding 20 nucleobase portion of the target nucleic acid that is fully complementary to the antisense compound. Fully complementary can also be used in reference to a specified portion of the first and /or the second nucleic acid. For example, a 20 nucleobase portion of a 30 nucleobase antisense compound can be "fully complementary" to a target sequence that is 400 nucleobases long. The 20 nucleobase portion of the 30 nucleobase oligonucleotide is fully complementary to the target sequence if the target sequence has a corresponding 20 nucleobase portion wherein each nucleobase is complementary to the 20 nucleobase portion of the antisense compound. At the same time, the entire 30 nucleobase antisense compound may or may not be fully complementary to the target sequence, depending on whether the remaining 10 nucleobases of the antisense compound are also complementary to the target sequence.

The location of a non-complementary nucleobase may be at the 5' end or 3' end of the antisense compound. Alternatively, the non-complementary nucleobase or nucleobases may be at an internal position of the antisense compound. When two or more non-complementary nucleobases are present, they may be contiguous (i.e., linked) or non-contiguous. In one embodiment, a non-complementary nucleobase is located in the wing segment of a gapmer oligonucleotide.

In certain embodiments, antisense compounds that are, or are up to 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleobases in length comprise no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a SOD-1 nucleic acid, or specified portion thereof.

In certain embodiments, antisense compounds that are, or are up to 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length comprise no more than 6, no more than 5, no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a SOD-1 nucleic acid, or specified portion thereof.

The antisense compounds provided herein also include those which are complementary to a portion of a target nucleic acid. As used herein, "portion" refers to a defined number of contiguous (i.e. linked) nucleobases within a region or segment of a target nucleic acid. A "portion" can also refer to a defined number of contiguous nucleobases of an antisense compound. In certain embodiments, the antisense compounds, are complementary to at least an 8 nucleobase portion of a target segment. In certain embodiments, the antisense compounds are complementary to at least a 9 nucleobase portion of a target segment. In certain embodiments, the antisense compounds are complementary to at least a 10 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least an 11 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 12 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 13 nucleobase portion of a target segment. In certain embodiments, the antisense compounds, are complementary to at least a 14 nucleobase portion of a target

segment. In certain embodiments, the antisense compounds, are complementary to at least a 15 nucleobase portion of a target segment. Also contemplated are antisense compounds that are complementary to at least a 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more nucleobase portion of a target segment, or a range defined by any two of these values.

Identity

The antisense compounds provided herein may also have a defined percent identity to a particular nucleotide sequence, SEQ ID NO, or compound represented by a specific Isis number, or portion thereof. As used herein, an antisense compound is identical to the sequence disclosed herein if it has the same nucleobase pairing ability. For example, a RNA which contains uracil in place of thymidine in a disclosed DNA sequence would be considered identical to the DNA sequence since both uracil and thymidine pair with adenine. Shortened and lengthened versions of the antisense compounds described herein as well as compounds having non-identical bases relative to the antisense compounds provided herein also are contemplated. The non-identical bases may be adjacent to each other or dispersed throughout the antisense compound. Percent identity of an antisense compound is calculated according to the number of bases that have identical base pairing relative to the sequence to which it is being compared.

In certain embodiments, the antisense compounds, or portions thereof, are at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to one or more of the antisense compounds or SEQ ID NOs, or a portion thereof, disclosed herein.

In certain embodiments, a portion of the antisense compound is compared to an equal length portion of the target nucleic acid. In certain embodiments, an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleobase portion is compared to an equal length portion of the target nucleic acid.

In certain embodiments, a portion of the oligonucleotide is compared to an equal length portion of the target nucleic acid. In certain embodiments, an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleobase portion is compared to an equal length portion of the target nucleic acid.

Modifications

A nucleoside is a base-sugar combination. The nucleobase (also known as base) portion of the nucleoside is normally a heterocyclic base moiety. 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. Oligonucleotides are formed through the covalent linkage of adjacent nucleosides to one another, to form a linear polymeric oligonucleotide. Within the oligonucleotide structure, the phosphate groups are commonly referred to as forming the internucleoside linkages of the oligonucleotide.

Modifications to antisense compounds encompass substitutions or changes to internucleoside linkages, sugar moieties, or nucleobases. Modified antisense compounds are often preferred over native forms because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for nucleic acid target, increased stability in the presence of nucleases, or increased inhibitory activity.

Chemically modified nucleosides may also be employed to increase the binding affinity of a shortened or truncated oligonucleotide for its target nucleic acid. Consequently, comparable results can often be obtained with shorter antisense compounds that have such chemically modified nucleosides.

Modified Internucleoside Linkages

The naturally occuring internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. Antisense compounds having one or more modified, i.e. non-naturally occurring, internucleoside linkages are often selected over antisense compounds having naturally occurring internucleoside linkages because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for target nucleic acids, and increased stability in the presence of nucleases.

Oligonucleotides having modified internucleoside linkages include internucleoside linkages that retain a phosphorus atom as well as internucleoside linkages that do not have a phosphorus atom. Representative phosphorus containing internucleoside linkages include, but are not limited to, phosphodiesters, phosphotriesters, methylphosphonates, phosphoramidate, and phosphorothioates. Methods of preparation of phosphorous-containing and non-phosphorous-containing linkages are well known.

In certain embodiments, modified oligonucleotides targeted to a SOD-1 nucleic acid comprise one or more modified internucleoside linkages. In certain embodiments, the modified internucleoside linkages are interspersed throughout the antisense compound. In certain embodiments, the modified internucleoside linkages are phosphorothioate linkages. In certain embodiments, each internucleoside linkage of a modified oligonucleotide is a phosphorothioate internucleoside linkage.

In certain embodiments, the modified oligonucleotides targeted to a SOD-1 nucleic acid comprise one or more phosphodiester internucleoside linkages. In certain embodiments, modified oligonucleotides targeted to a SOD-1 nucleic acid comprise at least one phosphorothioate internucleoside linkage and at least one phosphodiester internucleoside linkage. In certain embodiments, the modified oligonucleotide has a mixed backbone motif of the following:

sosssssssssooss,

sooossssssssoss,

sooossssssssoss,

soossssssssooss,

sooossssssssooss,

sooossssssssooss,

sooosssssssssooss,

sooosssssssssssooos,

soooossssssssssooss,

sooossssssssssooss,

sosossssssssssosos, and

sooossssssssssoooss, wherein

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

Modified Sugar Moieties

Antisense compounds of the invention can optionally contain one or more nucleosides wherein the sugar group has been modified. Such sugar modified nucleosides may impart enhanced nuclease stability, increased binding affinity, or some other beneficial biological property to the antisense compounds. In certain embodiments, nucleosides comprise chemically modified ribofuranose ring moieties. Examples of chemically modified ribofuranose rings include without limitation, addition of substitutent groups (including 5' and 2' substituent groups, bridging of non-geminal ring atoms to form bicyclic nucleic acids (BNA), replacement of the ribosyl ring oxygen atom with S, N(R), or $C(R_1)(R_2)$ (R, R_1 and R_2 are each independently H, C_1-C_{12} alkyl or a protecting group) and combinations thereof. Examples of chemically modified sugars include 2'-F-5'-methyl substituted nucleoside (see PCT International Application WO 2008/101157 Published on 8/21/08 for other disclosed 5',2'-bis substituted nucleosides) or replacement of the ribosyl ring oxygen atom with S with further substitution at the 2'-position (see published U.S. Patent Application US2005-0130923, published on June 16, 2005) or alternatively 5'-substitution of a BNA (see PCT International Application WO 2007/134181 Published on 11/22/07 wherein LNA is substituted with for example a 5'-methyl or a 5'-vinyl group).

Examples of nucleosides having modified sugar moieties include without limitation nucleosides comprising 5'-vinyl, 5'-methyl (*R* or *S*), 4'-S, 2'-F, 2'-OCH_3, 2'-OCH_2CH_3, 2'-OCH_2CH_2F and 2'-$O(CH_2)_2OCH_3$ substituent groups. The substituent at the 2' position can also be selected from allyl, amino, azido, thio, O-allyl, O-C_1-C_{10} alkyl, OCF_3, OCH_2F, $O(CH_2)_2SCH_3$, $O(CH_2)_2$-O-$N(R_m)(R_n)$, O-CH_2-C(=O)-$N(R_m)(R_n)$, and O-CH_2-C(=O)-$N(R_l)$-$(CH_2)_2$-$N(R_m)(R_n)$, where each R_l, R_m and R_n is, independently, H or substituted or unsubstituted C_1-C_{10} alkyl.

As used herein, "bicyclic nucleosides" refer to modified nucleosides comprising a bicyclic sugar moiety. Examples of bicyclic nucleic acids (BNAs) include without limitation nucleosides

comprising a bridge between the 4' and the 2' ribosyl ring atoms. In certain embodiments, antisense compounds provided herein include one or more BNA nucleosides wherein the bridge comprises one of the formulas: 4'-(CH_2)-O-2' (LNA); 4'-(CH_2)-S-2'; 4'-(CH_2)$_2$-O-2' (ENA); 4'-CH(CH_3)-O-2' and 4'-CH(CH_2OCH_3)-O-2' (and analogs thereof see U.S. Patent 7,399,845, issued on July 15, 2008); 4'-C(CH_3)(CH_3)-O-2' (and analogs thereof see PCT/US2008/068922 published as WO/2009/006478, published January 8, 2009); 4'-CH_2-N(OCH_3)-2' (and analogs thereof see PCT/US2008/064591 published as WO/2008/150729, published December 11, 2008); 4'-CH_2-O-N(CH_3)-2' (see published U.S. Patent Application US2004-0171570, published September 2, 2004); 4'-CH_2-N(R)-O-2', wherein R is H, C_1-C_{12} alkyl, or a protecting group (see U.S. Patent 7,427,672, issued on September 23, 2008); 4'-CH_2-C(H)(CH_3)-2' (see Chattopadhyaya *et al., J. Org. Chem.,* 2009, *74*, 118-134); and 4'-CH_2-C(=CH_2)-2' (and analogs thereof see PCT/US2008/066154 published as WO 2008/154401, published on December 8, 2008).

Further bicyclic nucleosides have been reported in published literature (see for example: Srivastava et al., *J. Am. Chem. Soc.*, 2007, *129(26)* 8362-8379; Frieden *et al., Nucleic Acids Research,* 2003, *21*, 6365-6372; Elayadi *et al., Curr. Opinion Invens. Drugs,* 2001, *2*, 558-561; Braasch *et al., Chem. Biol.,* 2001, *8*, 1-7; Orum *et al., Curr. Opinion Mol. Ther.,* 2001, *3*, 239-243; Wahlestedt et al., *Proc. Natl. Acad. Sci. U. S. A.*, 2000, *97*, 5633-5638; Singh et al., *Chem. Commun.*, 1998, *4*, 455-456; Koshkin et al., *Tetrahedron*, 1998, *54*, 3607-3630; Kumar et al., *Bioorg. Med. Chem. Lett.*, 1998, *8*, 2219-2222; Singh et al., *J. Org. Chem.*, 1998, *63*, 10035-10039; U.S. Patents Nos.: 7,399,845; 7,053,207; 7,034,133; 6,794,499; 6,770,748; 6,670,461; 6,525,191; 6,268,490; U.S. Patent Publication Nos.: US2008-0039618; US2007-0287831; US2004-0171570; U.S. Patent Applications, Serial Nos.: 12/129,154; 61/099,844; 61/097,787; 61/086,231; 61/056,564; 61/026,998; 61/026,995; 60/989,574; International applications WO 2007/134181; WO 2005/021570; WO 2004/106356; WO 94/14226; and PCT International Applications Nos.: PCT/US2008/068922; PCT/US2008/066154; and PCT/US2008/064591). Each of the foregoing bicyclic nucleosides can be prepared having one or more stereochemical sugar configurations including for example α-L-ribofuranose and β-D-ribofuranose (see PCT international application PCT/DK98/00393, published on March 25, 1999 as WO 99/14226).

As used herein, "monocylic nucleosides" refer to nucleosides comprising modified sugar moieties that are not bicyclic sugar moieties. In certain embodiments, the sugar moiety, or sugar moiety analogue, of a nucleoside may be modified or substituted at any position.

As used herein, "4'-2' bicyclic nucleoside" or "4' to 2' bicyclic nucleoside" refers to a bicyclic nucleoside comprising a furanose ring comprising a bridge connecting two carbon atoms of the furanose ring connects the 2' carbon atom and the 4' carbon atom of the sugar ring.

In certain embodiments, bicyclic sugar moieties of BNA nucleosides include, but are not limited to, compounds having at least one bridge between the 4' and the 2' carbon atoms of the pentofuranosyl sugar moiety including without limitation, bridges comprising 1 or from 1 to 4 linked groups independently selected from $-[C(R_a)(R_b)]_n-$, $-C(R_a)=C(R_b)-$, $-C(R_a)=N-$, $-C(=NR_a)-$, $-C(=O)-$, $-C(=S)-$, $-O-$, $-Si(R_a)_2-$, $-S(=O)_x-$, and $-N(R_a)-$; wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1, NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O)-H), substituted acyl, CN, sulfonyl ($S(=O)_2$-J_1), or sulfoxyl (S(=O)-J_1); and

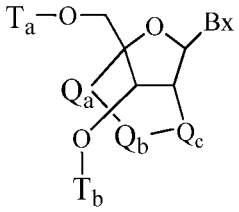
each J_1 and J_2 is, independently, H, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1-C_{12} aminoalkyl, substituted C_1-C_{12} aminoalkyl or a protecting group.

In certain embodiments, the bridge of a bicyclic sugar moiety is , $-[C(R_a)(R_b)]_n-$, $-[C(R_a)(R_b)]_n-O-$, $-C(R_aR_b)-N(R)-O-$ or $-C(R_aR_b)-O-N(R)-$. In certain embodiments, the bridge is 4'-CH_2-2', 4'-$(CH_2)_2$-2', 4'-$(CH_2)_3$-2', 4'-CH_2-O-2', 4'-$(CH_2)_2$-O-2', 4'-CH_2-O-N(R)-2' and 4'-CH_2-N(R)-O-2'- wherein each R is, independently, H, a protecting group or C_1-C_{12} alkyl.

In certain embodiments, bicyclic nucleosides are further defined by isomeric configuration. For example, a nucleoside comprising a 4'-(CH_2)-O-2' bridge, may be in the α-L configuration or in the β-D configuration. Previously, α-L-methyleneoxy (4'-CH_2-O-2') BNA's have been incorporated into antisense oligonucleotides that showed antisense activity (Frieden *et al., Nucleic Acids Research,* 2003, *21*, 6365-6372).

In certain embodiments, bicyclic nucleosides include those having a 4' to 2' bridge wherein such bridges include without limitation, α-L-4'-(CH_2)-O-2', β-D-4'-CH_2-O-2', 4'-$(CH_2)_2$-O-2', 4'-CH_2-O-N(R)-2', 4'-CH_2-N(R)-O-2', 4'-$CH(CH_3)$-O-2', 4'-CH_2-S-2', 4'-CH_2-N(R)-2', 4'-CH_2-$CH(CH_3)$-2', and 4'-$(CH_2)_3$-2', wherein R is H, a protecting group or C_1-C_{12} alkyl.

In certain embodiment, bicyclic nucleosides have the formula:



wherein:

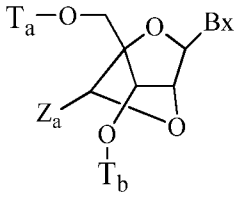
Bx is a heterocyclic base moiety;

$-Q_a-Q_b-Q_c-$ is $-CH_2-N(R_c)-CH_2-$, $-C(=O)-N(R_c)-CH_2-$, $-CH_2-O-N(R_c)-$, $-CH_2-N(R_c)-O-$ or $-N(R_c)-O-CH_2$;

R_c is C_1-C_{12} alkyl or an amino protecting group; and

T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium.

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

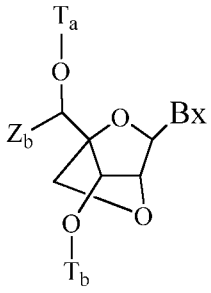
Bx is a heterocyclic base moiety;

T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium;

Z_a is C_1-C_6 alkyl, C_2-C_6 alkenyl, C_2-C_6 alkynyl, substituted C_1-C_6 alkyl, substituted C_2-C_6 alkenyl, substituted C_2-C_6 alkynyl, acyl, substituted acyl, substituted amide, thiol or substituted thiol.

In one embodiment, each of the substituted groups, is, independently, mono or poly substituted with substituent groups independently selected from halogen, oxo, hydroxyl, OJ_c, NJ_cJ_d, SJ_c, N_3, $OC(=X)J_c$, and $NJ_eC(=X)NJ_cJ_d$, wherein each J_c, J_d and J_e is, independently, H, C_1-C_6 alkyl, or substituted C_1-C_6 alkyl and X is O or NJ_c.

In certain embodiments, bicyclic nucleosides have the formula:



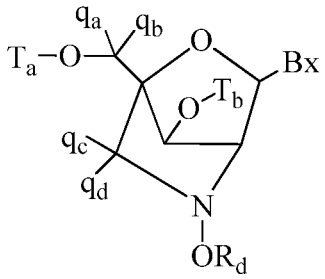
wherein:

Bx is a heterocyclic base moiety;

T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium;

Z_b is C_1-C_6 alkyl, C_2-C_6 alkenyl, C_2-C_6 alkynyl, substituted C_1-C_6 alkyl, substituted C_2-C_6 alkenyl, substituted C_2-C_6 alkynyl or substituted acyl (C(=O)-).

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

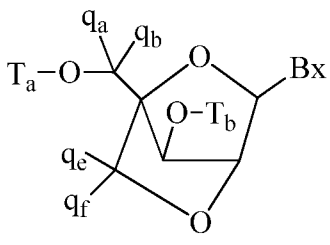
Bx is a heterocyclic base moiety;

T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium;

R_d is C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl or substituted C_2-C_6 alkynyl;

each q_a, q_b, q_c and q_d is, independently, H, halogen, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl or substituted C_2-C_6 alkynyl, C_1-C_6 alkoxyl, substituted C_1-C_6 alkoxyl, acyl, substituted acyl, C_1-C_6 aminoalkyl or substituted C_1-C_6 aminoalkyl;

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

Bx is a heterocyclic base moiety;

T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium;

q_a, q_b, q_e and q_f are each, independently, hydrogen, halogen, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_1-C_{12} alkoxy, substituted C_1-C_{12} alkoxy, OJ_j, SJ_j, SOJ_j, SO_2J_j, NJ_jJ_k, N_3, CN, $C(=O)OJ_j$, $C(=O)NJ_jJ_k$, $C(=O)J_j$, $O\text{-}C(=O)NJ_jJ_k$, $N(H)C(=NH)NJ_jJ_k$, $N(H)C(=O)NJ_jJ_k$ or $N(H)C(=S)NJ_jJ_k$;

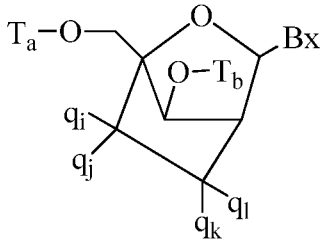
or q_e and q_f together are $=C(q_g)(q_h)$;

q_g and q_h are each, independently, H, halogen, C_1-C_{12} alkyl or substituted C_1-C_{12} alkyl.

The synthesis and preparation of adenine, cytosine, guanine, 5-methyl-cytosine, thymine and uracil bicyclic nucleosides having a 4'-CH_2-O-2' bridge, along with their oligomerization, and nucleic acid recognition properties have been described (Koshkin et al., *Tetrahedron*, 1998, *54*, 3607-3630). The synthesis of bicyclic nucleosides has also been described in WO 98/39352 and WO 99/14226.

Analogs of various bicyclic nucleosides that have 4' to 2' bridging groups such as 4'-CH_2-O-2' and 4'-CH_2-S-2', have also been prepared (Kumar *et al., Bioorg. Med. Chem. Lett.*, 1998, *8*, 2219-2222). Preparation of oligodeoxyribonucleotide duplexes comprising bicyclic nucleosides for use as substrates for nucleic acid polymerases has also been described (Wengel et al., WO 99/14226). Furthermore, synthesis of 2'-amino-BNA, a novel conformationally restricted high-affinity oligonucleotide analog has been described in the art (Singh et al., *J. Org. Chem.*, 1998, *63*, 10035-10039). In addition, 2'-amino- and 2'-methylamino-BNA's have been prepared and the thermal stability of their duplexes with complementary RNA and DNA strands has been previously reported.

In certain embodiments, bicyclic nucleosides have the formula:



wherein:

Bx is a heterocyclic base moiety;

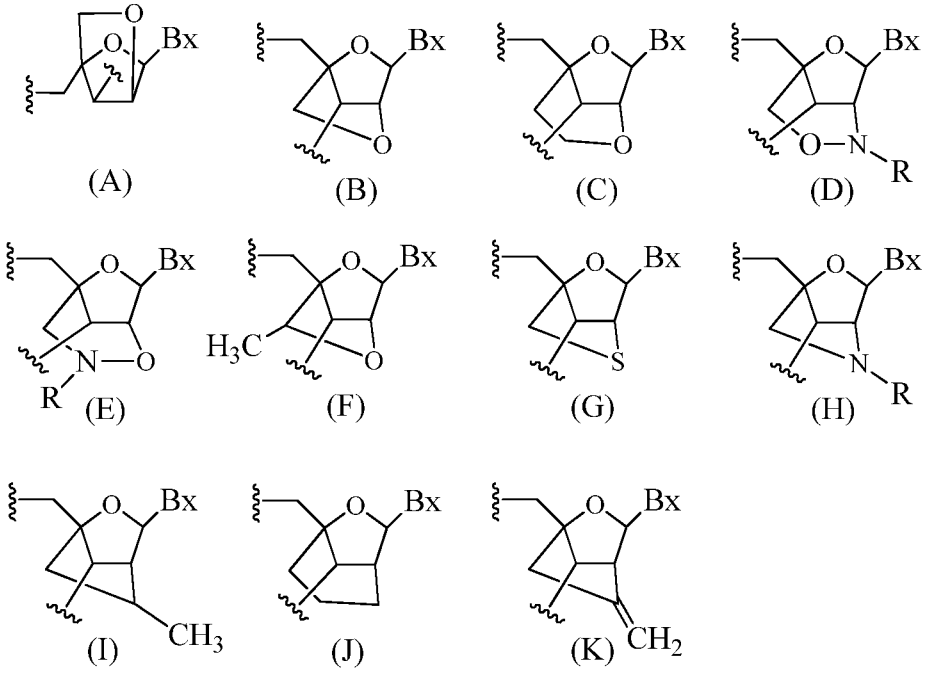
T_a and T_b are each, independently H, a hydroxyl protecting group, a conjugate group, a reactive phosphorus group, a phosphorus moiety or a covalent attachment to a support medium;

each q_i, q_j, q_k and q_l is, independently, H, halogen, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_1-C_{12} alkoxyl, substituted C_1-C_{12} alkoxyl, OJ_j, SJ_j, SOJ_j, SO_2J_j, NJ_jJ_k, N_3, CN, $C(=O)OJ_j$, $C(=O)NJ_jJ_k$, $C(=O)J_j$, O-$C(=O)NJ_jJ_k$, $N(H)C(=NH)NJ_jJ_k$, $N(H)C(=O)NJ_jJ_k$ or $N(H)C(=S)NJ_jJ_k$; and

q_i and q_j or q_l and q_k together are $=C(q_g)(q_h)$, wherein q_g and q_h are each, independently, H, halogen, C_1-C_{12} alkyl or substituted C_1-C_{12} alkyl.

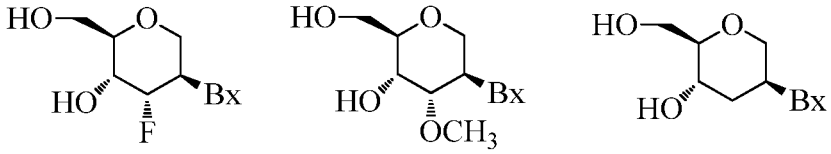
One carbocyclic bicyclic nucleoside having a 4'-$(CH_2)_3$-2' bridge and the alkenyl analog bridge 4'-CH=CH-CH_2-2' have been described (Frier *et al., Nucleic Acids Research*, 1997, *25*(*22*), 4429-4443 and Albaek *et al., J. Org. Chem.*, 2006, *71*, 7731-7740). The synthesis and preparation of carbocyclic bicyclic nucleosides along with their oligomerization and biochemical studies have also been described (Srivastava *et al., J. Am. Chem. Soc.* 2007, *129(26)*, 8362-8379).

In certain embodiments, bicyclic nucleosides include, but are not limited to, (A) α-L-methyleneoxy (4'-CH_2-O-2') BNA , (B) β-D-methyleneoxy (4'-CH_2-O-2') BNA , (C) ethyleneoxy (4'-$(CH_2)_2$-O-2') BNA, (D) aminooxy (4'-CH_2-O-N(R)-2') BNA, (E) oxyamino (4'-CH_2-N(R)-O-2') BNA, (F) methyl(methyleneoxy) (4'-$CH(CH_3)$-O-2') BNA (also referred to as constrained ethyl or cEt), (G) methylene-thio (4'-CH_2-S-2') BNA, (H) methylene-amino (4'-CH_2-N(R)-2') BNA, (I) methyl carbocyclic (4'-CH_2-$CH(CH_3)$-2') BNA, (J) propylene carbocyclic (4'-$(CH_2)_3$-2') BNA, and (K) vinyl BNA as depicted below.

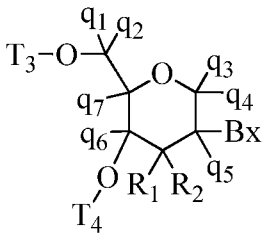


wherein Bx is the base moiety and R is, independently, H, a protecting group, C_1-C_6 alkyl or C_1-C_6 alkoxy.

As used herein, the term "modified tetrahydropyran nucleoside" or "modified THP nucleoside" means a nucleoside having a six-membered tetrahydropyran "sugar" substituted for the pentofuranosyl residue in normal nucleosides and can be referred to as a sugar surrogate. Modified THP nucleosides include, but are not limited to, what is referred to in the art as hexitol nucleic acid (HNA), anitol nucleic acid (ANA), manitol nucleic acid (MNA) (see Leumann, *Bioorg. Med. Chem.*, 2002, *10*, 841-854) or fluoro HNA (F-HNA) having a tetrahydropyranyl ring system as illustrated below.



In certain embodiment, sugar surrogates are selected having the formula:



wherein:

Bx is a heterocyclic base moiety;

T_3 and T_4 are each, independently, an internucleoside linking group linking the tetrahydropyran nucleoside analog to the oligomeric compound or one of T_3 and T_4 is an internucleoside linking group linking the tetrahydropyran nucleoside analog to an oligomeric compound or oligonucleotide and the other of T_3 and T_4 is H, a hydroxyl protecting group, a linked conjugate group or a 5' or 3'-terminal group;

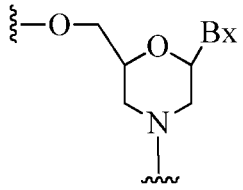
q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each independently, H, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl or substituted C_2-C_6 alkynyl; and

one of R_1 and R_2 is hydrogen and the other is selected from halogen, substituted or unsubstituted alkoxy, NJ_1J_2, SJ_1, N_3, $OC(=X)J_1$, $OC(=X)NJ_1J_2$, $NJ_3C(=X)NJ_1J_2$ and CN, wherein X is O, S or NJ_1 and each J_1, J_2 and J_3 is, independently, H or C_1-C_6 alkyl.

In certain embodiments, q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is other than H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is methyl. In certain embodiments, THP nucleosides are provided wherein one of R_1 and R_2 is F. In certain embodiments, R_1 is fluoro and R_2 is H; R_1 is methoxy and R_2 is H, and

R_1 is methoxyethoxy and R_2 is H.

In certain embodiments, sugar surrogates comprise rings having more than 5 atoms and more than one heteroatom. For example nucleosides comprising morpholino sugar moieties and their use in oligomeric compounds has been reported (see for example: Braasch *et al.*, *Biochemistry*, 2002, *41*, 4503-4510; and U.S. Patents 5,698,685; 5,166,315; 5,185,444; and 5,034,506). As used here, the term "morpholino" means a sugar surrogate having the following formula:

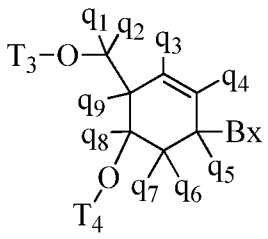


In certain embodiments, morpholinos may be modified, for example by adding or altering various substituent groups from the above morpholino structure. Such sugar surrogates are referred to herein as "modifed morpholinos."

Combinations of modifications are also provided without limitation, such as 2'-F-5'-methyl substituted nucleosides (see PCT International Application WO 2008/101157 published on 8/21/08 for other disclosed 5', 2'-bis substituted nucleosides) and replacement of the ribosyl ring oxygen atom with S and further substitution at the 2'-position (see published U.S. Patent Application US2005-0130923, published on June 16, 2005) or alternatively 5'-substitution of a bicyclic nucleic acid (see PCT International Application WO 2007/134181, published on 11/22/07 wherein a 4'-CH_2-O-2' bicyclic nucleoside is further substituted at the 5' position with a 5'-methyl or a 5'-vinyl group). The synthesis and preparation of carbocyclic bicyclic nucleosides along with their oligomerization and biochemical studies have also been described (*see, e.g.,* Srivastava *et al., J. Am. Chem. Soc.* 2007, *129(26)*, 8362-8379).

In certain embodiments, antisense compounds comprise one or more modified cyclohexenyl nucleosides, which is a nucleoside having a six-membered cyclohexenyl in place of the pentofuranosyl residue in naturally occurring nucleosides. Modified cyclohexenyl nucleosides include, but are not limited to those described in the art (see for example commonly owned, published PCT Application WO 2010/036696, published on April 10, 2010, Robeyns *et al., J. Am. Chem. Soc.,* 2008, *130(6)*, 1979-1984; Horváth *et al., Tetrahedron Letters,* 2007, *48*, 3621-3623; Nauwelaerts *et al., J. Am. Chem. Soc.*, 2007, *129(30)*, 9340-9348; Gu *et al.,*, *Nucleosides, Nucleotides & Nucleic Acids*, 2005, *24(5-7)*, 993-998; Nauwelaerts *et al., Nucleic Acids Research,* 2005, *33(8)*, 2452-2463; Robeyns et al., *Acta Crystallographica, Section F: Structural Biology and*

Crystallization Communications, 2005, *F61(6)*, 585-586; Gu *et al., Tetrahedron*, 2004, *60(9)*, 2111-2123; Gu *et al., Oligonucleotides*, 2003, *13(6)*, 479-489; Wang *et al., J. Org. Chem.,* 2003, *68*, 4499-4505; Verbeure *et al., Nucleic Acids Research*, 2001, *29(24)*, 4941-4947; Wang *et al., J. Org. Chem.,* 2001, *66*, 8478-82; Wang *et al., Nucleosides, Nucleotides & Nucleic Acids*, 2001, *20(4-7)*, 785-788; Wang *et al., J. Am. Chem.,* 2000, *122*, 8595-8602; Published PCT application, WO 06/047842; and Published PCT Application WO 01/049687; the text of each is incorporated by reference herein, in their entirety). Certain modified cyclohexenyl nucleosides have Formula X.



X

wherein independently for each of said at least one cyclohexenyl nucleoside analog of Formula X:

Bx is a heterocyclic base moiety;

T_3 and T_4 are each, independently, an internucleoside linking group linking the cyclohexenyl nucleoside analog to an antisense compound or one of T_3 and T_4 is an internucleoside linking group linking the tetrahydropyran nucleoside analog to an antisense compound and the other of T_3 and T_4 is H, a hydroxyl protecting group, a linked conjugate group, or a 5'-or 3'-terminal group; and

q_1, q_2, q_3, q_4, q_5, q_6, q_7, q_8 and q_9 are each, independently, H, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl, substituted C_2-C_6 alkynyl or other sugar substituent group.

Many other monocyclic, bicyclic and tricyclic ring systems are known in the art and are suitable as sugar surrogates that can be used to modify nucleosides for incorporation into oligomeric compounds as provided herein (see for example review article: Leumann, Christian J. *Bioorg. & Med. Chem.*, 2002, *10*, 841-854). Such ring systems can undergo various additional substitutions to further enhance their activity.

As used herein, "2'-modified sugar" means a furanosyl sugar modified at the 2' position. In certain embodiments, such modifications include substituents selected from: a halide, including, but not limited to substituted and unsubstituted alkoxy, substituted and unsubstituted thioalkyl, substituted and unsubstituted amino alkyl, substituted and unsubstituted alkyl, substituted and unsubstituted allyl, and substituted and unsubstituted alkynyl. In certain embodiments, 2'

modifications are selected from substituents including, but not limited to: $O[(CH_2)_nO]_mCH_3$, $O(CH_2)_nNH_2$, $O(CH_2)_nCH_3$, $O(CH_2)_nF$, $O(CH_2)_nONH_2$, $OCH_2C(=O)N(H)CH_3$, and $O(CH_2)_nON[(CH_2)_nCH_3]_2$, where n and m are from 1 to about 10. Other 2'- substituent groups can also be selected from: C_1-C_{12} alkyl, substituted alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH_3, OCN, Cl, Br, CN, F, CF_3, OCF_3, $SOCH_3$, SO_2CH_3, ONO_2, NO_2, N_3, NH_2, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, an RNA cleaving group, a reporter group, an intercalator, a group for improving pharmacokinetic properties, or a group for improving the pharmacodynamic properties of an antisense compound, and other substituents having similar properties. In certain embodiments, modifed nucleosides comprise a 2'-MOE side chain (Baker *et al.*, *J. Biol. Chem.*, 1997, *272*, 11944-12000). Such 2'-MOE substitution have been described as having improved binding affinity compared to unmodified nucleosides and to other modified nucleosides, such as 2'- *O*-methyl, *O*-propyl, and *O*-aminopropyl. Oligonucleotides having the 2'-MOE substituent also have been shown to be antisense inhibitors of gene expression with promising features for *in vivo* use (Martin, *Helv. Chim. Acta*, 1995, *78*, 486-504; Altmann *et al.*, *Chimia*, 1996, *50*, 168-176; Altmann *et al.*, *Biochem. Soc. Trans.*, 1996, *24*, 630-637; and Altmann *et al.*, *Nucleosides Nucleotides*, 1997, *16*, 917-926).

As used herein, "2'-modified" or "2'-substituted" refers to a nucleoside comprising a sugar comprising a substituent at the 2' position other than H or OH. 2'-modified nucleosides, include, but are not limited to, bicyclic nucleosides wherein the bridge connecting two carbon atoms of the sugar ring connects the 2' carbon and another carbon of the sugar ring; and nucleosides with non-bridging 2'substituents, such as allyl, amino, azido, thio, O-allyl, O-C_1-C_{10} alkyl, $-OCF_3$, O-$(CH_2)_2$-O-CH_3, 2'-$O(CH_2)_2SCH_3$, O-$(CH_2)_2$-O-$N(R_m)(R_n)$, or O-CH_2-C(=O)-$N(R_m)(R_n)$, where each R_m and R_n is, independently, H or substituted or unsubstituted C_1-C_{10} alkyl. 2'-modifed nucleosides may further comprise other modifications, for example at other positions of the sugar and/or at the nucleobase.

As used herein, "2'-F" refers to a nucleoside comprising a sugar comprising a fluoro group at the 2' position of the sugar ring.

As used herein, "2'-OMe" or "2'-OCH_3", "2'-O-methyl" or "2'-methoxy" each refers to a nucleoside comprising a sugar comprising an $-OCH_3$ group at the 2' position of the sugar ring.

As used herein, "MOE" or "2'-MOE" or "2'-$OCH_2CH_2OCH_3$" or "2'-O-methoxyethyl" each refers to a nucleoside comprising a sugar comprising a $-OCH_2CH_2OCH_3$ group at the 2' position of the sugar ring.

Methods for the preparations of modified sugars are well known to those skilled in the art. Some representative U.S. patents that teach the preparation of such modified sugars include without limitation, U.S.: 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; 5,670,633; 5,700,920; 5,792,847 and 6,600,032 and International Application PCT/US2005/019219, filed June 2, 2005 and published as WO 2005/121371 on December 22, 2005, and each of which is herein incorporated by reference in its entirety.

As used herein, "oligonucleotide" refers to a compound comprising a plurality of linked nucleosides. In certain embodiments, one or more of the plurality of nucleosides is modified. In certain embodiments, an oligonucleotide comprises one or more ribonucleosides (RNA) and/or deoxyribonucleosides (DNA).

In nucleotides having modified sugar moieties, the nucleobase moieties (natural, modified or a combination thereof) are maintained for hybridization with an appropriate nucleic acid target.

In certain embodiments, antisense compounds comprise one or more nucleosides having modified sugar moieties. In certain embodiments, the modified sugar moiety is 2'-MOE. In certain embodiments, the 2'-MOE modified nucleosides are arranged in a gapmer motif. In certain embodiments, the modified sugar moiety is a bicyclic nucleoside having a (4'-$CH(CH_3)$-O-2') bridging group. In certain embodiments, the (4'-$CH(CH_3)$-O-2') modified nucleosides are arranged throughout the wings of a gapmer motif.

Compositions and Methods for Formulating Pharmaceutical Compositions

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

An antisense compound targeted to a SOD-1 nucleic acid can be utilized in pharmaceutical compositions by combining the antisense compound with a suitable pharmaceutically acceptable diluent or carrier. A pharmaceutically acceptable diluent includes phosphate-buffered saline (PBS). PBS is a diluent suitable for use in compositions to be delivered parenterally. Accordingly, in one embodiment, employed in the methods described herein is a pharmaceutical composition comprising an antisense compound targeted to a SOD-1 nucleic acid and a pharmaceutically acceptable diluent. In certain embodiments, the pharmaceutically acceptable diluent is PBS. In certain embodiments, the antisense compound is a modified oligonucleotide.

Pharmaceutical compositions comprising antisense compounds encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other oligonucleotide which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of antisense compounds, prodrugs, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. Suitable pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts.

A prodrug can include the incorporation of additional nucleosides at one or both ends of an antisense compound which are cleaved by endogenous nucleases within the body, to form the active antisense compound.

Conjugated Antisense Compounds

Antisense compounds may be covalently linked to one or more moieties or conjugates which enhance the activity, cellular distribution or cellular uptake of the resulting oligonucleotides. Typical conjugate groups include cholesterol moieties and lipid moieties. Additional conjugate groups include carbohydrates, phospholipids, biotin, phenazine, folate, phenanthridine, anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes.

Antisense compounds can also be modified to have one or more stabilizing groups that are generally attached to one or both termini of antisense compounds to enhance properties such as, for example, nuclease stability. Included in stabilizing groups are cap structures. These terminal modifications protect the antisense compound having terminal nucleic acid from exonuclease degradation, and can help in delivery and/or localization within a cell. The cap can be present at the 5'-terminus (5'-cap), or at the 3'-terminus (3'-cap), or can be present on both termini. Cap structures are well known in the art and include, for example, inverted deoxy abasic caps. Further 3' and 5'-stabilizing groups that can be used to cap one or both ends of an antisense compound to impart nuclease stability include those disclosed in WO 03/004602 published on January 16, 2003.

Cell culture and antisense compounds treatment

The effects of antisense compounds on the level, activity or expression of SOD-1 nucleic acids can be tested *in vitro* in a variety of cell types. Cell types used for such analyses are available from commerical vendors (*e.g.* American Type Culture Collection, Manassus, VA; Zen-Bio, Inc., Research Triangle Park, NC; Clonetics Corporation, Walkersville, MD) and are cultured according to the vendor's instructions using commercially available reagents (e.g. Invitrogen Life Technologies, Carlsbad, CA). Illustrative cell types include, but are not limited to, HepG2 cells, Hep3B cells, primary hepatocytes, A431 cells, and SH-SY5Y cells.

In vitro testing of oligonucleotides

Described herein are methods for treatment of cells with oligonucleotides, which can be modified appropriately for treatment with other antisense compounds.

Cells may be treated with oligonucleotides when the cells reach approximately 60-80% confluency in culture.

One reagent commonly used to introduce oligonucleotides into cultured cells includes the cationic lipid transfection reagent LIPOFECTIN (Invitrogen, Carlsbad, CA). Oligonucleotides may be mixed with LIPOFECTIN in OPTI-MEM 1 (Invitrogen, Carlsbad, CA) to achieve the desired final concentration of oligonucleotide and a LIPOFECTIN concentration that may range from 2 to 12 ug/mL per 100 nM oligonucleotide.

Another reagent used to introduce oligonucleotides into cultured cells includes LIPOFECTAMINE (Invitrogen, Carlsbad, CA). Oligonucleotide is mixed with LIPOFECTAMINE in OPTI-MEM 1 reduced serum medium (Invitrogen, Carlsbad, CA) to achieve the desired concentration of oligonucleotide and a LIPOFECTAMINE concentration that may range from 2 to 12 ug/mL per 100 nM oligonucleotide.

Another technique used to introduce oligonucleotides into cultured cells includes electroporation.

Cells are treated with oligonucleotides by routine methods. Cells may be harvested 16-24 hours after oligonucleotide treatment, at which time RNA or protein levels of target nucleic acids are measured by methods known in the art and described herein. In general, when treatments are performed in multiple replicates, the data are presented as the average of the replicate treatments.

The concentration of oligonucleotide used varies from cell line to cell line. Methods to determine the optimal oligonucleotide concentration for a particular cell line are well known in the art. Oligonucleotides are typically used at concentrations ranging from 1 nM to 300 nM when transfected with LIPOFECTAMINE. Oligonucleotides are used at higher concentrations ranging from 625 to 20,000 nM when transfected using electroporation.

RNA Isolation

RNA analysis can be performed on total cellular RNA or poly(A)+ mRNA. Methods of RNA isolation are well known in the art. RNA is prepared using methods well known in the art, for example, using the TRIZOL Reagent (Invitrogen, Carlsbad, CA) according to the manufacturer's recommended protocols.

Analysis of inhibition of target levels or expression

Inhibition of levels or expression of a SOD-1 nucleic acid can be assayed in a variety of ways known in the art. For example, target nucleic acid levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or quantitaive real-time PCR. RNA analysis can be performed

on total cellular RNA or poly(A)+ mRNA. Methods of RNA isolation are well known in the art. Northern blot analysis is also routine in the art. Quantitative real-time PCR can be conveniently accomplished using the commercially available ABI PRISM 7600, 7700, or 7900 Sequence Detection System, available from PE-Applied Biosystems, Foster City, CA and used according to manufacturer's instructions.

Quantitative Real-Time PCR Analysis of Target RNA Levels

Quantitation of target RNA levels may be accomplished by quantitative real-time PCR using the ABI PRISM 7600, 7700, or 7900 Sequence Detection System (PE-Applied Biosystems, Foster City, CA) according to manufacturer's instructions. Methods of quantitative real-time PCR are well known in the art.

Prior to real-time PCR, the isolated RNA is subjected to a reverse transcriptase (RT) reaction, which produces complementary DNA (cDNA) that is then used as the substrate for the real-time PCR amplification. The RT and real-time PCR reactions are performed sequentially in the same sample well. RT and real-time PCR reagents may be obtained from Invitrogen (Carlsbad, CA). RT real-time-PCR reactions are carried out by methods well known to those skilled in the art.

Gene (or RNA) target quantities obtained by real time PCR are normalized using either the expression level of a gene whose expression is constant, such as cyclophilin A, or by quantifying total RNA using RIBOGREEN (Invitrogen, Inc. Carlsbad, CA). Cyclophilin A expression is quantified by real time PCR, by being run simultaneously with the target, multiplexing, or separately. Total RNA is quantified using RIBOGREEN RNA quantification reagent (Invetrogen, Inc. Eugene, OR). Methods of RNA quantification by RIBOGREEN are SOD-1ght in Jones, L.J., et al, (Analytical Biochemistry, 1998, 265, 368-374). A CYTOFLUOR 4000 instrument (PE Applied Biosystems) is used to measure RIBOGREEN fluorescence.

Probes and primers are designed to hybridize to a SOD-1 nucleic acid. Methods for designing real-time PCR probes and primers are well known in the art, and may include the use of software such as PRIMER EXPRESS Software (Applied Biosystems, Foster City, CA).

Analysis of Protein Levels

Antisense inhibition of SOD-1 nucleic acids can be assessed by measuring SOD-1 protein levels. Protein levels of SOD-1 can be evaluated or quantitated in a variety of ways well known in the art, such as immunoprecipitation, Western blot analysis (immunoblotting), enzyme-linked immunosorbent assay (ELISA), quantitative protein assays, protein activity assays (for example, caspase activity assays), immunohistochemistry, immunocytochemistry or fluorescence-activated cell sorting (FACS). Antibodies directed to a target can be identified and obtained from a variety of sources, such as the MSRS catalog of antibodies (Aerie Corporation, Birmingham, MI), or can be prepared via conventional monoclonal or polyclonal antibody generation methods well known in the art. In certain embodiments, the compounds herein provide improved reduction in protein levels.

In vivo testing of antisense compounds

Antisense compounds, for example, modified oligonucleotides, are tested in animals to assess their ability to inhibit expression of SOD-1 and produce phenotypic changes, such as, improved motor function. In certain embodiments, motor function is measured by walking initiation analysis, rotarod, grip strength, pole climb, open field performance, balance beam, hindpaw footprint testing in the animal. Testing may be performed in normal animals, or in experimental disease models. For administration to animals, oligonucleotides are formulated in a pharmaceutically acceptable diluent, such as phosphate-buffered saline. Administration includes parenteral routes of administration, such as intraperitoneal, intravenous, and subcutaneous. Oligonucleotide dosage and dosing frequency depends upon multiple factors such as, but not limited to, route of administration and animal body weight. Following a period of treatment with oligonucleotides, RNA is isolated from CNS tissue or CSF and changes in SOD-1 nucleic acid expression are measured.

Certain Indications

In certain embodiments, provided herein are methods, compounds, and compositions of treating an individual comprising administering one or more pharmaceutical compositions described herein. In certain embodiments, the individual has a neurodegenerative disease. In certain embodiments, the individual is at risk for developing a neurodegenerative disease, including, but not limited to, amyotrophic lateral sclerosis (ALS). In certain embodiments, the individual has been identified as having a SOD-1 associated disease. In certain embodiments, provided herein are methods for prophylactically reducing SOD-1 expression in an individual. Certain embodiments include treating an individual in need thereof by administering to an individual a therapeutically effective amount of an antisense compound targeted to a SOD-1 nucleic acid.

In one embodiment, administration of a therapeutically effective amount of an antisense compound targeted to a SOD-1 nucleic acid is accompanied by monitoring of SOD-1 levels in an individual, to determine an individual's response to administration of the antisense compound. An individual's response to administration of the antisense compound may be used by a physician to determine the amount and duration of therapeutic intervention.

In certain embodiments, administration of an antisense compound targeted to a SOD-1 nucleic acid results in reduction of SOD-1 expression by at least 15, 20, 25, 30, 35, 40, 45, 50, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%, or a range defined by any two of these values. In certain embodiments, administration of an antisense compound targeted to a SOD-1 nucleic acid results in improved motor function in an animal. In certain embodiments, administration of a SOD-1 antisense compound improves motor function by at least 15, 20, 25, 30, 35, 40, 45, 50, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65,

66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100%, or a range defined by any two of these values.

In certain embodiments, pharmaceutical compositions comprising an antisense compound targeted to SOD-1 are used for the preparation of a medicament for treating a patient suffering or susceptible to a neurodegenerative disease including amyotrophic lateral sclerosis (ALS).

Certain Comparator Compositions

Antisense oligonucleotides targeting human SOD-1 were described in an earlier publication (see WO 2005/040180, incorporated by reference herein, in its entirety). Several oligonucleotides (ISIS 333611, ISIS 146144, ISIS 146145, ISIS 150437, ISIS 150441, ISIS 150443, ISIS 150444, ISIS 150445, ISIS 150446, ISIS 150447, ISIS 150448, ISIS 150449, ISIS 150452, ISIS 150454, ISIS 150458, ISIS 150460, ISIS 150462-150467, ISIS 150470, ISIS 150472, ISIS 150474, ISIS 150475, ISIS 150476, ISIS 150479-150483, ISIS 150488, ISIS 150489, ISIS 150490, ISIS 150491-150493, ISIS 150495-150498, ISIS 150511, ISIS 333605, ISIS 333606, ISIS 333609-333617, ISIS 333619, ISIS 333620-333636, ISIS 333638, and ISIS 333640) described therein, were used as comparator compounds throughout select screens for new antisense compounds described herein.

In certain embodiments, ISIS 333611, a 5-10-5 MOE gapmer, having a sequence of (from 5' to 3') CCGTCGCCCTTCAGCACGCA (incorporated herein as SEQ ID NO: 21), wherein each internucleoside linkage is a phosphorothioate linkage, each cytosine is a 5-methylcytosine, and each of nucleosides 1-5 and 16-20 (from 5' to 3') comprise a 2'-O-methoxyethyl moiety was used as a comparator compound. ISIS 333611 was selected as a comparator compound because it exhibited high levels of dose-dependent inhibition in various studies as described in WO 2005/040180. Additionally, phase 1 human clinical trials were completed using ISIS 333611. See, MILLER et al., "An antisense oligonucleotide against SOD1 delivered intrathecally for patients with SOD1 familial amyotrophic lateral sclerosis: a phase 1, randomised, first-in-man study" Lancet Neurol. (2013) 12(5): 435-442. Thus, ISIS 333611 was deemed a highly efficacious and potent compound with an acceptable safety profile (such that it was tested in human patients).

In certain embodiments, the compounds described herein benefit from one or more improved properties relative to the antisense compounds described in WO 2005/040180. Some of the improved properties are demonstrated in the examples provided herein. In certain embodiments, compounds described herein are more efficacious, potent, and/or tolerable in various in vitro and in vivo studies than comparator compounds described herein, including ISIS 333611. In certain embodiments, ISIS 666853, ISIS 666859, ISIS 666919, ISIS 666921, ISIS 666922, ISIS 666869, ISIS 666870, and ISIS 666867 are more efficacious and/or potent in various in vitro and in vivo studies than comparator compounds described herein, including ISIS 333611. In certain embodiments, ISIS 666853, ISIS 666859, ISIS 666919, ISIS 666921, ISIS 666922, ISIS 666869, ISIS 666870, and ISIS 666867 are more tolerable in one or more tolerability assays in animals

than comparator compounds described herein, including ISIS 333611. This is despite 333611 being sufficiently well tolerated to progress to human clinical trials.

In certain embodiments, certain compounds described herein are more efficacious than comparator compounds by virtue of an *in vitro* IC50 of less than 2 μM, less than 1.9 μM, less than 1.8 μM, less than 1.7μM, less than 1.6 μM, less than 1.5 μM, less than 1.4 μM, less than 1.3 μM, less than 1.2 μM, less than 1.1 μM, less than 1 μM, less than 0.9 μM, less than 0.8 μM, less than 0.7 μM, less than 0.6 μM, or less than 0.5 μM less than 0.4 μM, less than 0.3 μM, less than 0.2 μM, less than 0.1 μM, when tested in human cells, for example, in the HepG2 A431 or SH-SY5Y cell lines (For example, see Examples 6-11).

In certain embodiments, certain compounds described herein are more efficacious than comparator compounds by virtue of their ability to inhibit SOD-1 expression in vivo. In certain embodiments, the compounds inhibit SOD-1 in lumbar spinal cord and cervical spinal cord by at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90% or at least 95% in, for example, a transgenic animal model.

In certain embodiments, certain compounds described herein are more tolerable than comparator compounds on the basis of reduced microglial marker levels (e.g.,IBA1), reduced astrocytic marker levels (e.g., GFAP), and/or FOB scores in rats, mice, and/or monkeys. See, for example, Examples 14, 15, 18, and 19.

ISIS 666853

For example, as provided in Example 12 (hereinbelow), ISIS 666853 achieved 81% inhibition in lumbar spinal cord and 74% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

For example, as provided in Example 14 (hereinbelow), ISIS 666853 achieved a FOB score of 0 whereas ISIS 333611 achieved a FOB score of 4 in Sprague-Dawley rats after 3 hours when treated with 3 mg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666853 treated rats as compared to ISIS 333611 treated rats.

For example, as provided in Example 15 (hereinbelow), ISIS 666853 achieved an ED_{50} of 81.3 and 242.6 in lumbar tissue and cervical tissue (respectively) in SOD-1 transgenic rats when treated intrathecally with 10, 30, 100, 300, or 3000 μg of oligonucleotide. ED_{50} in lumbar and cervical tissues could not be calculated in ISIS 333611 treated transgenic rats because the highest concentration tested (3000 μg) filed to inhibit human SOD-1 mRNA greater than 55-65%.

For example, as provided in Example 16 (hereinbelow), at doses of 1 mg and 3 mg ISIS 666853 achieved 3 hour FOB scores of 0.0 and 0.5 (respectively) whereas ISIS 333611 achieved FOB scores of 3.0 and 4.9 (respectively). At doses of 1 mg and 3 mg ISIS 666853 achieved 8 week FOB scores of 0.0 and 0.0 (respectively) whereas ISIS 333611 achieved FOB scores of 0.0 and 1.2 (respectively).

For example, as provided in Example 17 (hereinbelow), ISIS 666853 achieved an ED_{50} of 136 and 188 in lumbar tissue and cortex tissue (respectively) whereas ISIS 333611 achieved an ED_{50} of 401 and 786 in lumbar tissue and cortex tissue (respectively) in SOD-1 transgenic mice when treated with an intracerebral ventricular bolus of 10, 30, 100, 300, or 700 μg of oligonucleotide.

For example, as provided in Example 18 (hereinbelow), ISIS 666853 achieved a FOB score of 1.25 whereas ISIS 333611 achieved a FOB score of 6.5 in C57bl6 mice after 3 hours when treated with 700 μg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666853 treated mice as compared to ISIS 333611 treated mice.

ISIS 666859

For example, as provided in Example 12 (hereinbelow), ISIS 666859 achieved 79% inhibition in lumbar spinal cord and 64% inhibition in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

For example, as provided in Example 14 (hereinbelow), ISIS 666859 achieved a FOB score of 1 whereas ISIS 333611 achieved a FOB score of 4 in Sprague-Dawley rats after 3 hours when treated with 3 mg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666859 treated rats as compared to ISIS 333611 treated rats.

For example, as provided in Example 15 (hereinbelow), ISIS 666859 achieved an ED_{50} of 74.0 and 358.8 in lumbar tissue and cervical tissue (respectively) in SOD-1 transgenic rats when treated intrathecally with 10, 30, 100, 300, or 3000 μg of oligonucleotide. ED_{50} in lumbar and cervical tissues could not be calculated in ISIS 333611 treated transgenic rats because the highest concentration tested (3000 μg) filed to inhibit human SOD-1 mRNA greater than 55-65%.

For example, as provided in Example 16 (hereinbelow), at doses of 1 mg and 3 mg ISIS 666859 achieved 3 hour FOB scores of 0.0 and 2.1 (respectively) whereas ISIS 333611 achieved FOB scores of 3.0 and 4.9 (respectively). At doses of 1 mg and 3 mg ISIS 666859 achieved 8 week FOB scores of 0.0 and 0.3 (respectively) whereas ISIS 333611 achieved FOB scores of 0.0 and 1.2 (respectively).

For example, as provided in Example 17 (hereinbelow), ISIS 666859 achieved an ED_{50} of 106 and 206 in lumbar tissue and cortex tissue (respectively) whereas ISIS 333611 achieved an ED_{50} of 401 and 786 in lumbar tissue and cortex tissue (respectively) in SOD-1 transgenic mice when treated with an intracerebral ventricular bolus of 10, 30, 100, 300, or 700 μg of oligonucleotide.

For example, as provided in Example 18 (hereinbelow), ISIS 666859 achieved a FOB score of 1.75 whereas ISIS 333611 achieved a FOB score of 6.5 in C57bl6 mice after 3 hours when treated with 700 μg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666859 treated mice as compared to ISIS 333611 treated mice.

ISIS 666919

For example, as provided in Example 12 (hereinbelow), ISIS 666919 achieved 76% inhibition in lumbar spinal cord and 68% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

For example, as provided in Example 14 (hereinbelow), ISIS 666919 achieved a FOB score of 2 whereas ISIS 333611 achieved a FOB score of 4 in Sprague-Dawley rats after 3 hours when treated with 3 mg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666919 treated rats as compared to ISIS 333611 treated rats.

For example, as provided in Example 15 (hereinbelow), ISIS 666919 achieved an ED_{50} of 104.1 and 613.5 in lumbar tissue and cervical tissue (respectively) in SOD-1 transgenic rats when treated intrathecally with 10, 30, 100, 300, or 3000 μg of oligonucleotide. ED_{50} in lumbar and cervical tissues could not be calculated in ISIS 333611 treated transgenic rats because the highest concentration tested (3000 μg) filed to inhibit human SOD-1 mRNA greater than 55-65%.

For example, as provided in Example 16 (hereinbelow), at doses of 1 mg and 3 mg ISIS 666919 achieved 3 hour FOB scores of 1.3 and 3.5 (respectively) whereas ISIS 333611 achieved FOB scores of 3.0 and 4.9 (respectively). At doses of 1 mg and 3 mg ISIS 666919 achieved 8 week FOB scores of 0.0 and 0.1 (respectively) whereas ISIS 333611 achieved FOB scores of 0.0 and 1.2 (respectively).

For example, as provided in Example 17 (hereinbelow), ISIS 666919 achieved an ED_{50} of 168 in lumbar tissue whereas ISIS 333611 achieved an ED_{50} of 401 in lumbar tissue in SOD-1 transgenic mice when treated with an intracerebral ventricular bolus of 10, 30, 100, 300, or 700 μg of oligonucleotide.

For example, as provided in Example 18 (hereinbelow), ISIS 666919 achieved a FOB score of 0.0 whereas ISIS 333611 achieved a FOB score of 6.5 in C57bl6 mice after 3 hours when treated with 700 μg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666919 treated mice as compared to ISIS 333611 treated mice.

ISIS 666921

For example, as provided in Example 12 (hereinbelow), ISIS 66621 achieved 71% inhibition in lumbar spinal cord and 65% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

For example, as provided in Example 14 (hereinbelow), ISIS 666921 achieved a FOB score of 2 whereas ISIS 333611 achieved a FOB score of 4 in Sprague-Dawley rats after 3 hours when treated with 3 mg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666919 treated rats as compared to ISIS 333611 treated rats.

ISIS 666922

For example, as provided in Example 12 (hereinbelow), ISIS 666922 achieved 67% inhibition in lumbar spinal cord and 62% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

For example, as provided in Example 14 (hereinbelow), ISIS 666922 achieved a FOB score of 3 whereas ISIS 333611 achieved a FOB score of 4 in Sprague-Dawley rats after 3 hours when treated with 3 mg of oligonucleotide. Microglial marker (IBA1) levels and astrocytic marker (GFAP) levels were also reduced in ISIS 666919 treated rats as compared to ISIS 333611 treated rats.

ISIS 666869

For example, as provided in Example 12 (hereinbelow), ISIS 666869 achieved 82% inhibition in lumbar spinal cord and 81% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

ISIS 666870

For example, as provided in Example 12 (hereinbelow), ISIS 666870 achieved 76% inhibition in lumbar spinal cord and 68% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

For example, as provided in Example 15 (hereinbelow), ISIS 666870 achieved an ED_{50} of 139.4 and 1111 in lumbar tissue and cervical tissue (respectively) in SOD-1 transgenic rats when treated intrathecally with 10, 30, 100, 300, or 3000 μg of oligonucleotide. ED_{50} in lumbar and cervical tissues could not be calculated in ISIS 333611 treated transgenic rats because the highest concentration tested (3000 μg) filed to inhibit human SOD-1 mRNA greater than 55-65%.

For example, as provided in Example 17 (hereinbelow), ISIS 666870 achieved an ED_{50} of 148 and 409 in lumbar tissue and cortex tissue (respectively) whereas ISIS 333611 achieved an ED_{50} of 401 and 786 in lumbar tissue and cortex tissue (respectively) in SOD-1 transgenic mice when treated with an intracerebral ventricular bolus of 10, 30, 100, 300, or 700 μg of oligonucleotide.

For example, as provided in Example 18 (hereinbelow), ISIS 666870 achieved a FOB score of 4.75 whereas ISIS 333611 achieved a FOB score of 6.5 in C57bl6 mice after 3 hours when treated with 700 μg of oligonucleotide.

ISIS 666867

For example, as provided in Example 12 (hereinbelow), ISIS 666867 achieved 59% inhibition in lumbar spinal cord and 48% in cervical spinal cord of an SOD-1 transgenic rat model when dosed with 30 μL of 16.67 mg/ml solution of oligonucleotide diluted in PBS (500 μg final dose), whereas ISIS 333611 achieved 51% inhibition in lumbar spinal cord and 47% inhibition in cervical spinal cord.

Certain Compositions

1. ISIS 666853

In certain embodiments, ISIS 666853 is characterized as a 5-10-5 MOE gapmer, having a sequence of (from 5' to 3') CAGGATACATTTCTACAGCT (incorporated herein as SEQ ID NO: 725), wherein each of nucleosides 1-5 and 16-20 are 2'-O-methoxyethylribose modified nucleosides, and each of nucleosides 6-15 are 2'-deoxynucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 4 to 5, 16 to 17, and 18 to 19 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 3 to 4, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 13 to 14, 14 to 15, 15 to 16, 17 to 18, and 19 to 20 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666853 is described by the following chemical notation: mCes Aeo Ges Geo Aes Tds Ads mCds Ads Tds Tds Tds mCds Tds Ads mCeo Aes Geo mCes Te; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

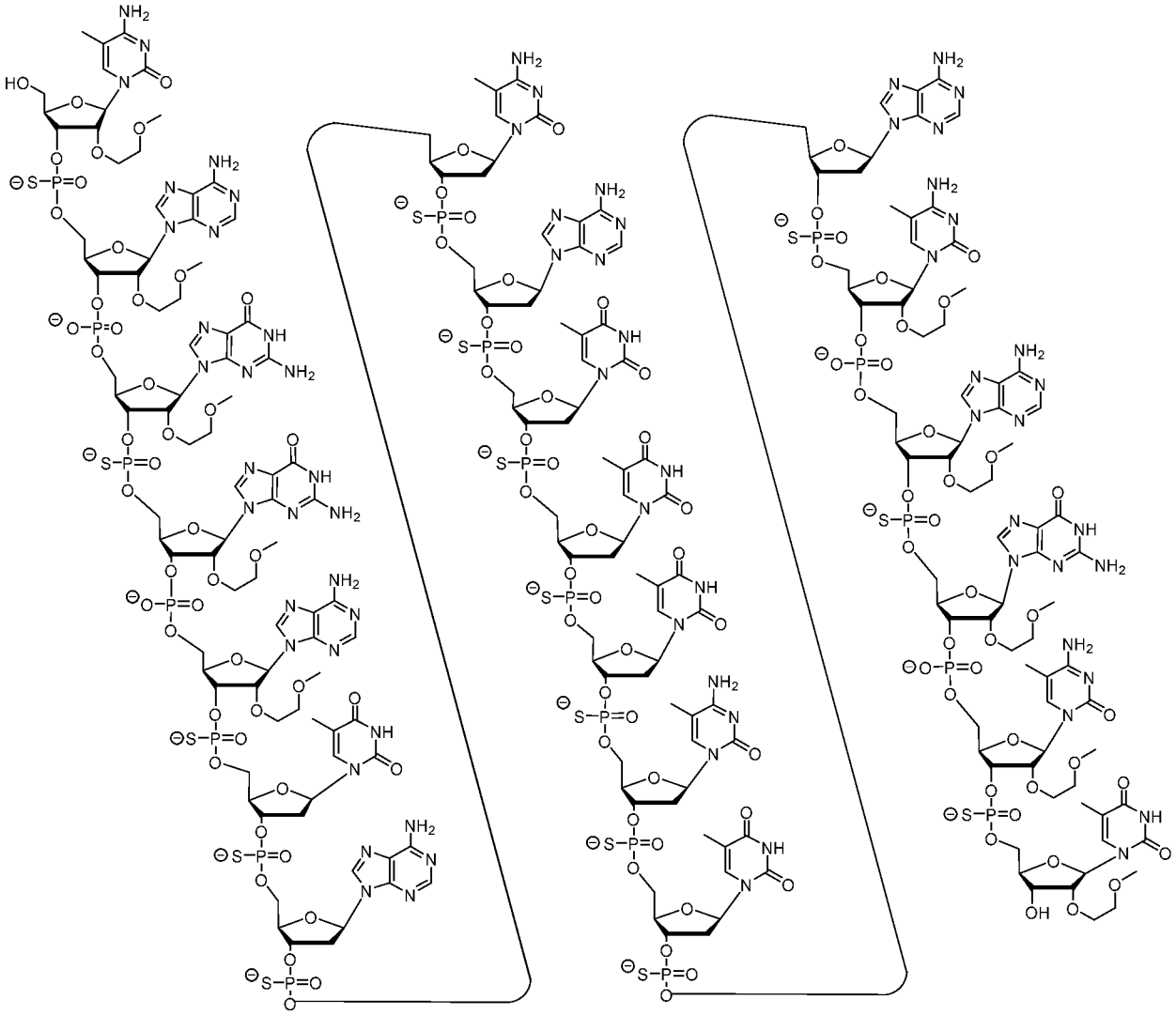
e = a 2'-O-methoxyethylribose modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666853 is described by the following chemical structure:



Structure 1. ISIS 666853

2. ISIS 666859

In certain embodiments, ISIS 666859 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') TTAATGTTTATCAGGAT (incorporated herein as SEQ ID NO: 1351), consisting of seventeen nucleosides, wherein each of nucleosides 1-4 and 15-17 are 2'-O-methoxyethylribose nucleosides, wherein each of nucleosides 13 and 14 are cEt modified nucleosides, wherein each of nucleosides 5-12 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 13 to 14, 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 4 to 5, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666859 is described by the following chemical notation: Tes Teo Aeo Aes Tds Gds Tds Tds Tds Ads Tds mCds Ako Gko Ges Aes Te; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

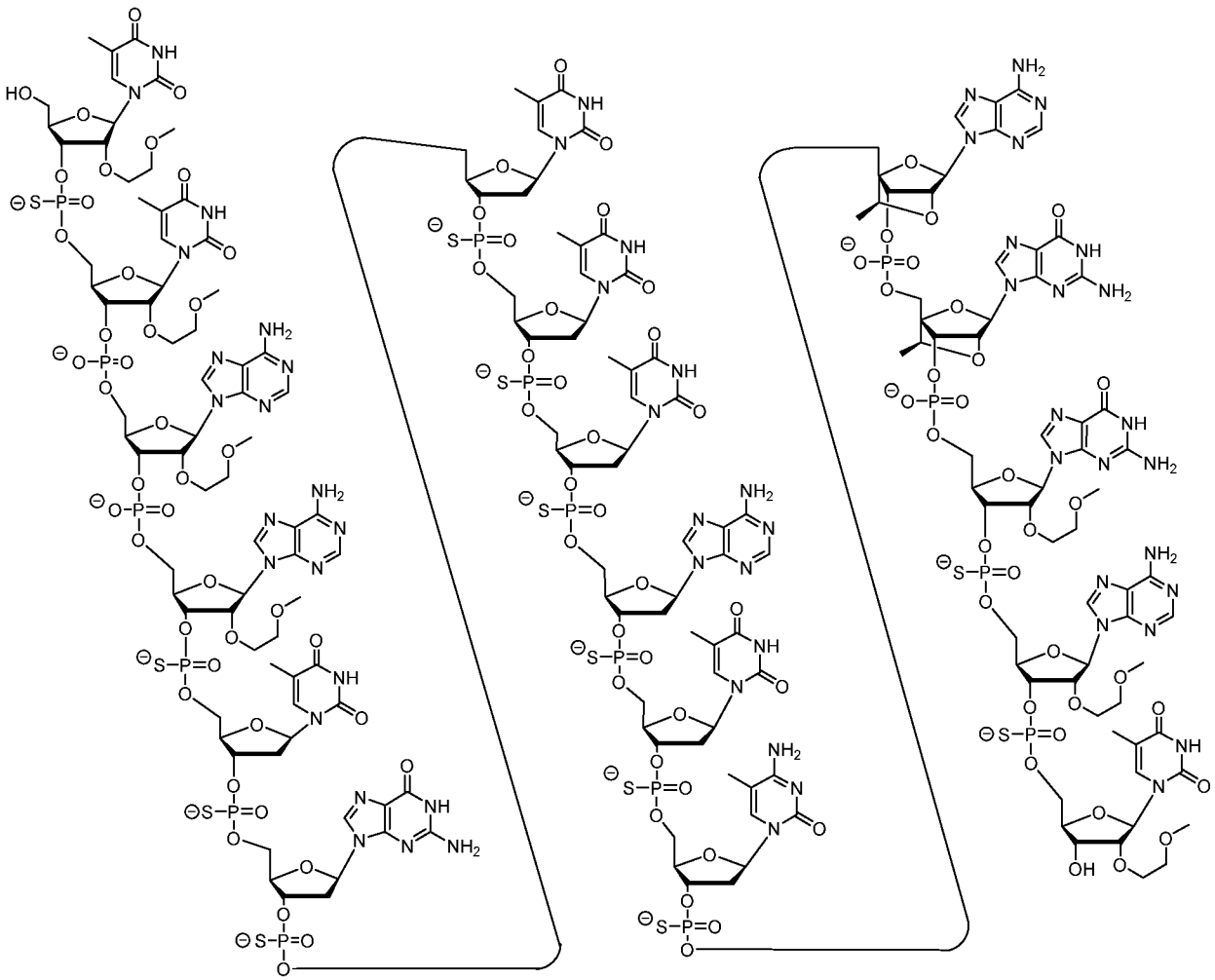
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666859 is described by the following chemical structure:



Structure 2. ISIS 666859

3. ISIS 666919

In certain embodiments, ISIS 666919 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') GGATACATTTCTACAGC (incorporated herein as SEQ

ID NO: 1342), consisting of seventeen nucleosides, wherein each of nucleosides 1-4 and 16-17 are 2'-O-methoxyethylribose modified nucleosides, wherein each of nucleosides 14 and 15 are cEt modified nucleosides, wherein each of nucleosides 5-13 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 4 to 5, and 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 13 to 14, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666919 is described by the following chemical notation: Ges Geo Aeo Teo Ads mCds Ads Tds Tds Tds mCds Tds Ads mCko Aks Ges mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

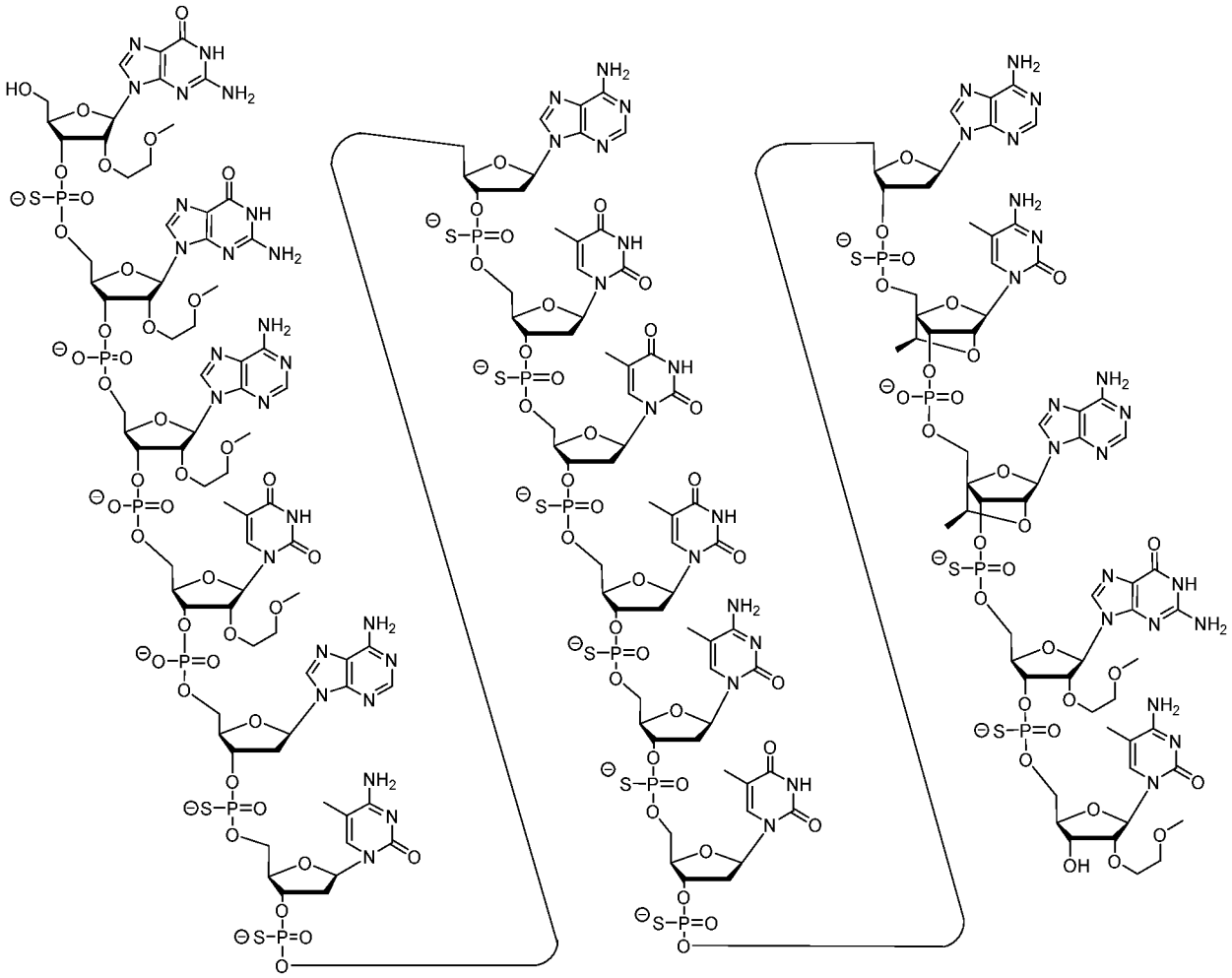
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666919 is described by the following chemical structure:



Structure 3. ISIS 666919

4. ISIS 666921

In certain embodiments, ISIS 666921 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') GGATACATTTCTACAGC (incorporated herein as SEQ ID NO: 1342), consisting of seventeen nucleosides, wherein each of nucleosides 1-5 and 16-17 are 2'-O-methoxyethylribose modified nucleosides, wherein each of nucleosides 14-15 are cEt modified nucleosides, wherein each of nucleosides 6-13 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 4 to 5, and 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 13 to 14, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666921 is described by the following chemical notation: Ges Geo Aeo Teo Aes mCds Ads Tds Tds Tds mCds Tds Ads mCko Aks Ges mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

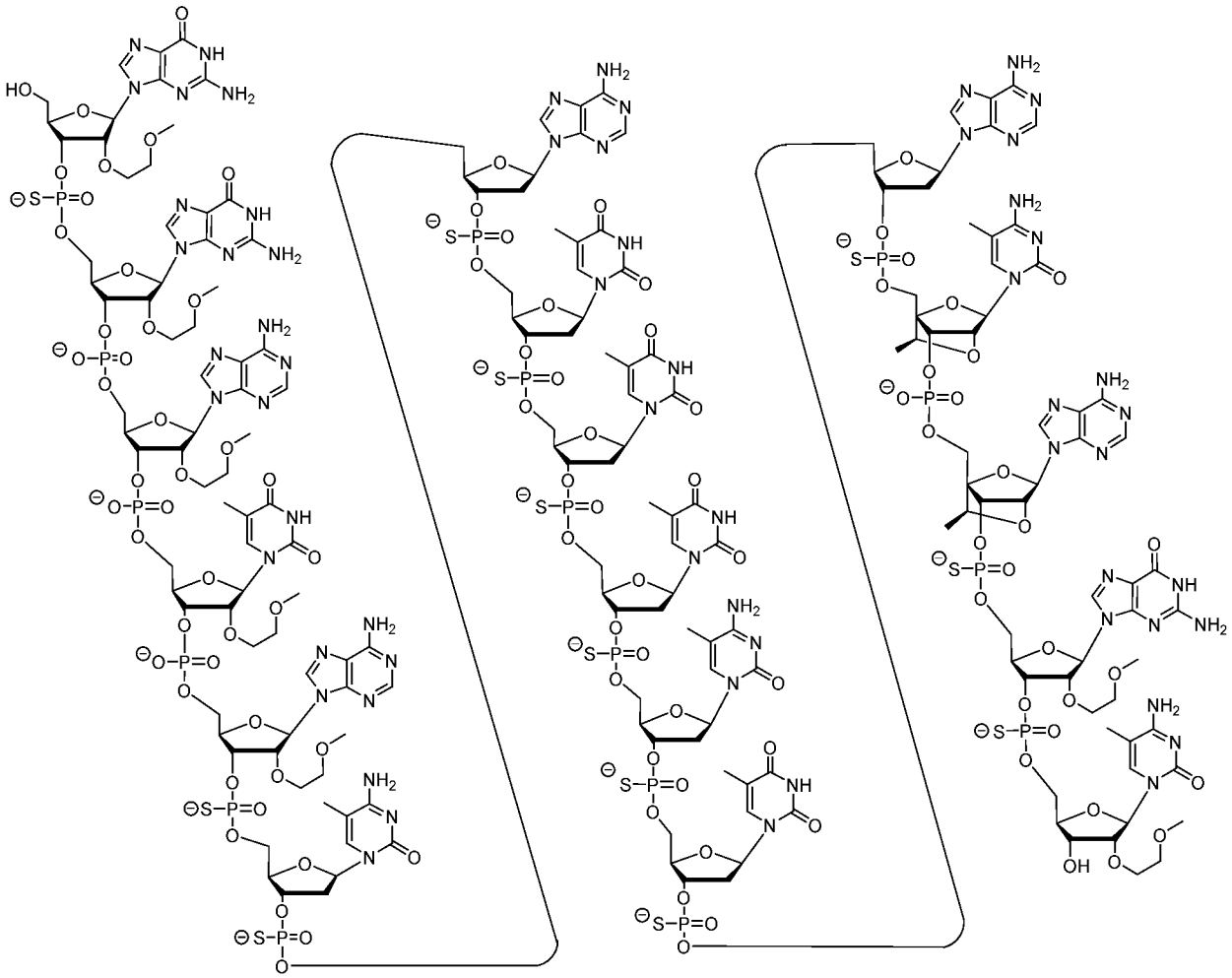
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666921 is described by the following chemical structure:



Structure 4. ISIS 666921

5. ISIS 666922

In certain embodiments, ISIS 666922 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') GGATACATTTCTACAGC (incorporated herein as SEQ ID NO: 1342), consisting of seventeen nucleosides, wherein each of nucleosides 1-4 and 15-17 are 2'-O-methoxyethylribose modified nucleosides, wherein each of nucleosides 5 and 14 are cEt modified nucleosides, wherein each of

nucleosides 6-13 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 4 to 5, and 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 13 to 14, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666922 is described by the following chemical notation: Ges Geo Aeo Teo Aks mCds Ads Tds Tds Tds mCds Tds Ads mCko Aes Ges mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

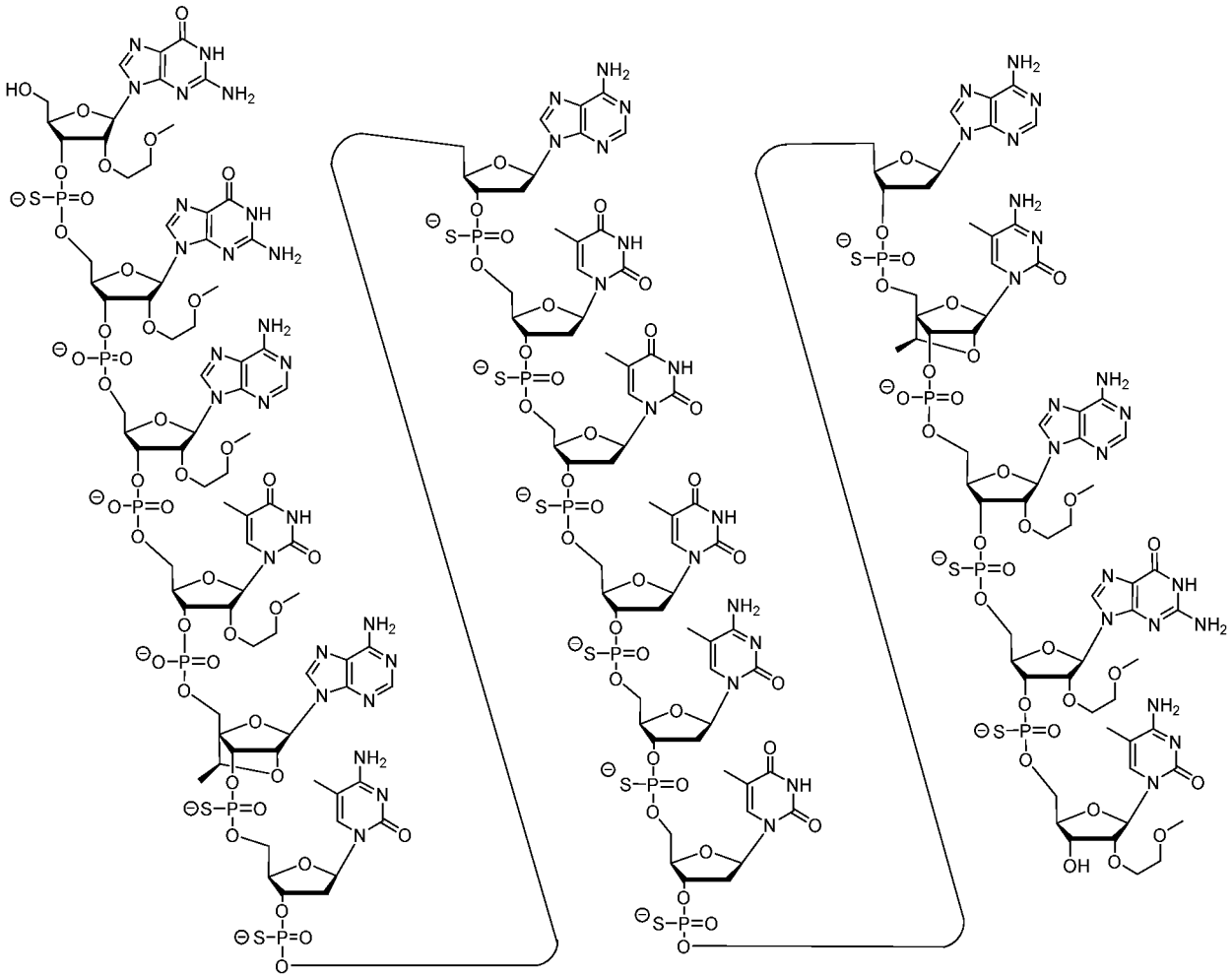
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666922 is described by the following chemical structure:



Structure 5. ISIS 666922

6. ISIS 666869

In certain embodiments, ISIS 666869 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') AGTGTTTAATGTTTATC (incorporated herein as SEQ ID NO: 1173), consisting of seventeen nucleosides, wherein each of nucleosides 1, 3, 14, and 16-17 are 2'-O-methoxyethylribose modified nucleosides, wherein each of nucleosides 2, 4, 13, and 15 are cEt modified nucleosides, wherein each of nucleosides 5-12 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 13 to14, and 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 4 to 5, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666869 is described by the following chemical notation: Aes Gko Teo Gks Tds Tds Tds Ads Ads Tds Gds Tds Tko Teo Aks Tes mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

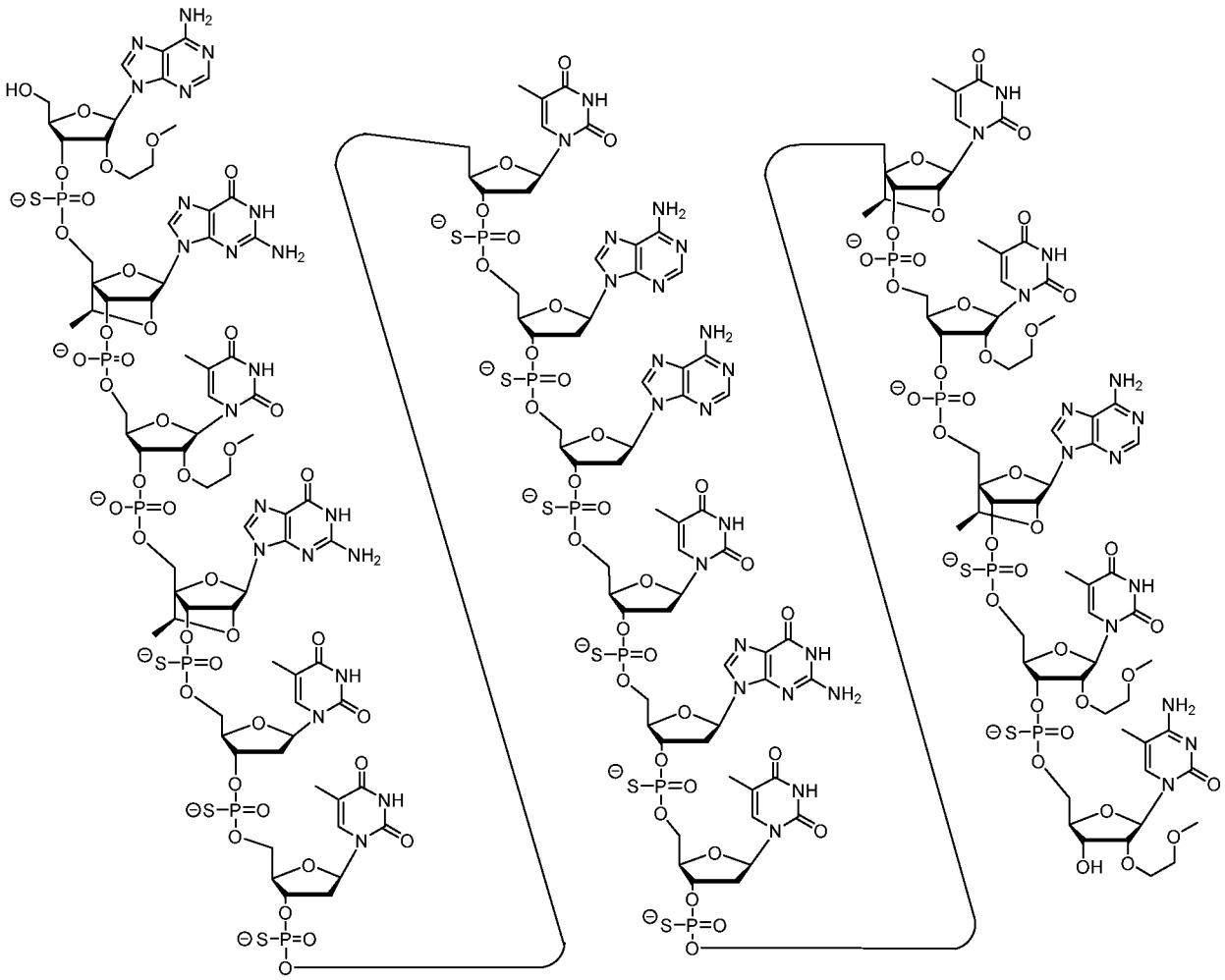
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666869 is described by the following chemical structure:



Structure 6. ISIS 666869

7. ISIS 666870

In certain embodiments, ISIS 666870 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') AGTGTTTAATGTTTATC (incorporated herein as SEQ ID NO: 1173),

consisting of seventeen nucleosides, wherein each of nucleosides 1, 3, 13-17 are 2'-O-methoxyethylribose modified nucleosides, wherein each of nucleosides 2 and 4 are cEt modified nucleosides, wherein each of nucleosides 5-12 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 13 to14, and 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 4 to 5, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666870 is described by the following chemical notation: Aes Gko Teo Gks Tds Tds Tds Ads Ads Tds Gds Tds Teo Teo Aes Tes mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

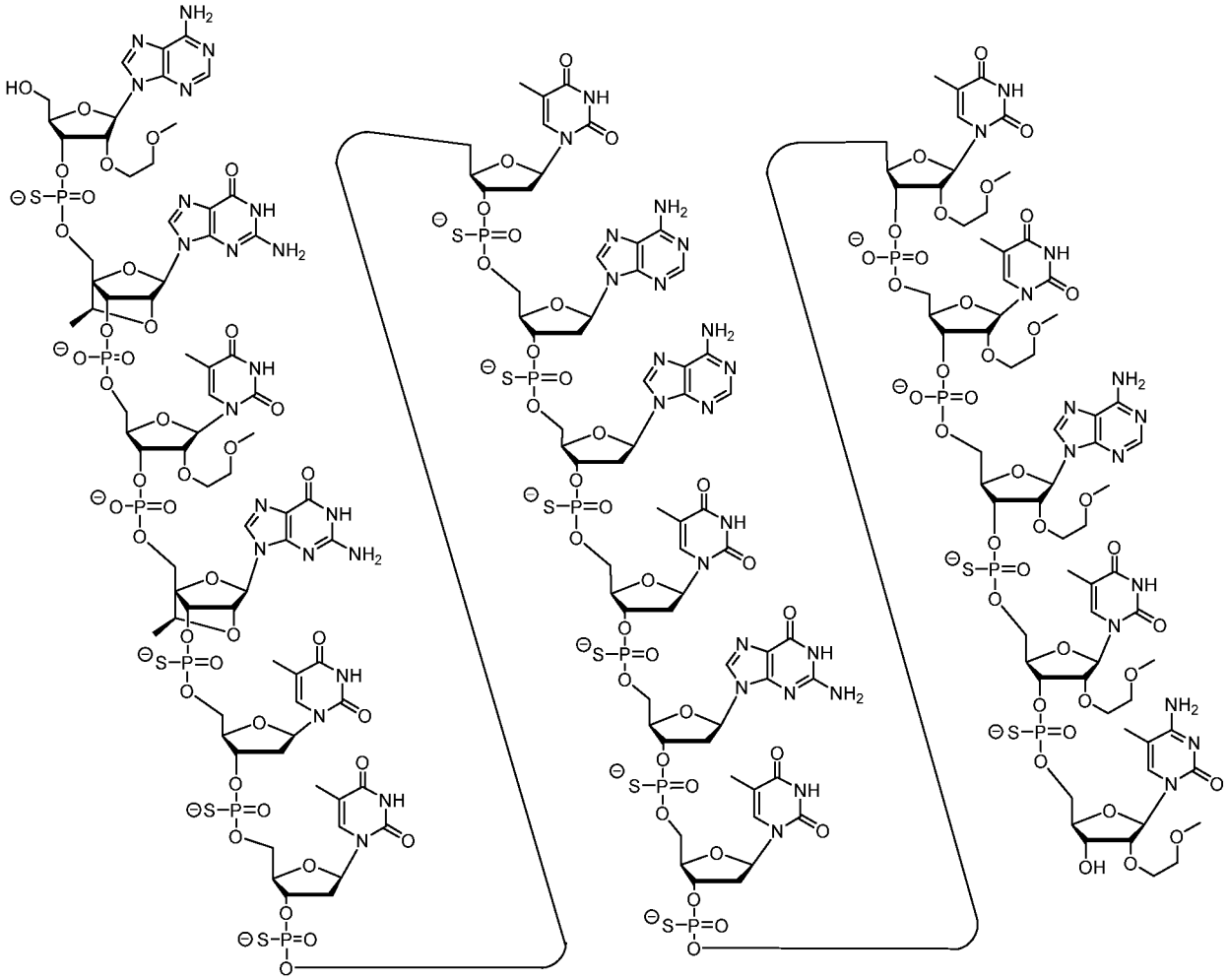
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666870 is described by the following chemical structure:



Structure 7. ISIS 666870

8. ISIS 666867

In certain embodiments, ISIS 666867 is characterized as a modified oligonucleotide having the nucleobase sequence (from 5' to 3') AGTGTTTAATGTTTATC (incorporated herein as SEQ ID NO: 1173), consisting of seventeen nucleosides, wherein each of nucleosides 1-2 and 13-17 are 2'-O-methoxyethylribose modified nucleosides, wherein each of nucleosides 3 and 4 are cEt modified nucleosides, wherein each of nucleosides 5-12 are 2'-deoxyribonucleosides, wherein the internucleoside linkages between nucleosides 2 to 3, 3 to 4, 13 to14, and 14 to 15 are phosphodiester linkages and the internucleoside linkages between nucleosides 1 to 2, 4 to 5, 5 to 6, 6 to 7, 7 to 8, 8 to 9, 9 to 10, 10 to 11, 11 to 12, 12 to 13, 15 to 16, and 16 to 17 are phosphorothioate linkages, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 666867 is described by the following chemical notation: Aes Geo Tko Gks Tds Tds Tds Ads Ads Tds Gds Tds Teo Teo Aes Tes mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

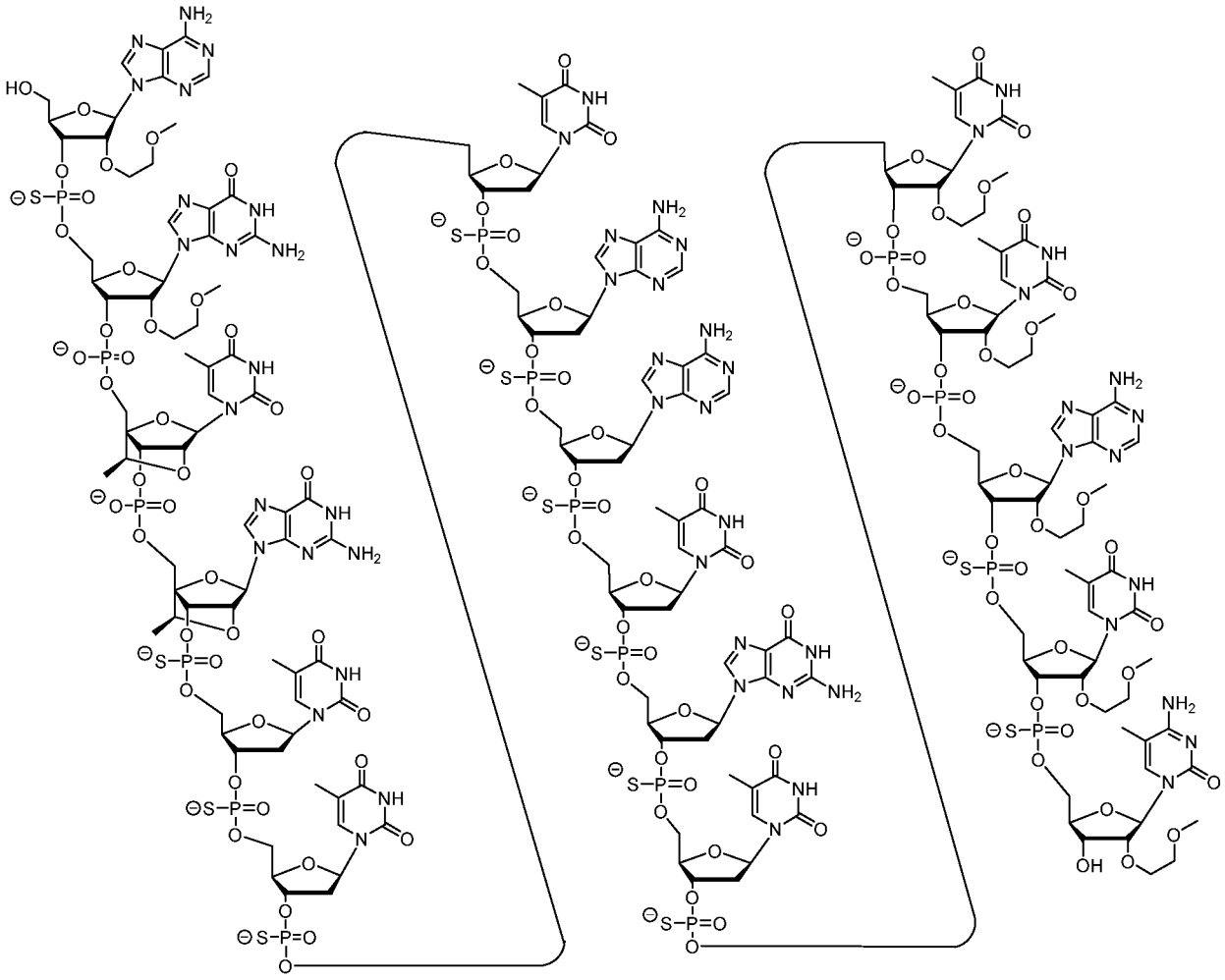
k = a cEt modified sugar,

d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage.

In certain embodiments, ISIS 666867 is described by the following chemical structure:



Structure 8. ISIS 666867

EXAMPLES

Non-limiting disclosure and incorporation by reference

While certain compounds, compositions, and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references recited in the present application is incorporated herein by reference in its entirety.

Example 1: Inhibition of human superoxide dismutase 1, soluble (SOD-1) in HepG2 cells by MOE gapmers

Modified oligonucleotides were designed targeting a superoxide dismutase 1, soluble (SOD-1) nucleic acid and were tested for their effects on SOD-1 mRNA in vitro. ISIS 146144, ISIS 146145, ISIS 150437, ISIS 150441, ISIS 150443, ISIS 150444, ISIS 150445, ISIS 150446, ISIS 150447, ISIS 150448, ISIS 150449, ISIS 150452, ISIS 150454, ISIS 150458, ISIS 150460, ISIS 150462-150467, ISIS 150470, ISIS 150472, ISIS 150474, ISIS 150475, ISIS 150476, ISIS 150479-150483, ISIS 150488, ISIS 150489, ISIS 150490, ISIS 150491-150493, ISIS 150495-150498, ISIS 150511, ISIS 333605, ISIS 333606, ISIS 333609-333617, ISIS 333619, ISIS 333620-333636, ISIS 333638, and ISIS 333640, previously disclosed in WO 2005/040180, were also included in this assay. ISIS 333611, previously disclosed in WO 2005/040180, was also designated as a benchmark or comparator oligonucleotide. ISIS 333611 was recently tested in human clinical trials. See, MILLER et al., "An antisense oligonucleotide against SOD1 delivered intrathecally for patients with SOD1 familial amyotrophic lateral sclerosis: a phase 1, randomised, first-in-man study" Lancet Neurol. (2013) 12(5): 435-442.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 7,000 nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR.

Human primer probe set RTS3898 (forward sequence CTCTCAGGAGACCATTGCATCA, designated herein as SEQ ID NO: 11; reverse sequence TCCTGTCTTTGTACTTTCTTCATTTCC; designated herein as SEQ ID NO: 12; probe sequence CCGCACACTGGTGGTCCATGAAAA, designated herein as SEQ ID NO: 13) was used to measure mRNA levels. In cases where the oligonucleotide overlapped the amplicon of the primer probe set, an alternative primer probe set, HTS90 (forward sequence CGTGGCCTAGCGAGTTATGG, designated herein as SEQ ID NO: 14; reverse sequence GAAATTGATGATGCCCTGCA; designated herein as SEQ ID NO: 15; probe sequence

ACGAAGGCCGTGTGCGTGCTGX, designated herein as SEQ ID NO: 16), was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells. 'n.d.' indicates that inhibition levels were not measured using the particular primer probe set.

The newly designed modified oligonucleotides in the Tables below were designed as 5-10-5 MOE gapmers. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of ten 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000). 'n/a' indicates that the modified oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 1

Percent Inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
590065	1	20	CGCCCACTCTGGCCCCAAAC	7	807	826	118
590066	35	54	CCGCGACTACTTTATAGGCC	5	841	860	119
333611	167	186	CCGTCGCCCTTCAGCACGCA	85	973	992	21
590067	202	221	CCTTCTGCTCGAAATTGATG	74	1008	1027	120
590068	203	222	TCCTTCTGCTCGAAATTGAT	58	n/a	n/a	121
590069	204	223	TTCCTTCTGCTCGAAATTGA	50	n/a	n/a	122
590070	205	224	TTTCCTTCTGCTCGAAATTG	47	n/a	n/a	123
590071	206	225	CTTTCCTTCTGCTCGAAATT	31	n/a	n/a	124
590072	207	226	ACTTTCCTTCTGCTCGAAAT	42	n/a	n/a	125
590073	208	227	TACTTTCCTTCTGCTCGAAA	38	n/a	n/a	126
590074	209	228	TTACTTTCCTTCTGCTCGAA	33	n/a	n/a	127
590075	210	229	ATTACTTTCCTTCTGCTCGA	39	n/a	n/a	128
590076	211	230	CATTACTTTCCTTCTGCTCG	28	n/a	n/a	129

590077	212	231	CCATTACTTTCCTTCTGCTC	58	n/a	n/a	130
590078	213	232	TCCATTACTTTCCTTCTGCT	58	n/a	n/a	131
590079	214	233	GTCCATTACTTTCCTTCTGC	69	n/a	n/a	132
590080	215	234	GGTCCATTACTTTCCTTCTG	68	n/a	n/a	133
590081	216	235	TGGTCCATTACTTTCCTTCT	61	n/a	n/a	134
590082	217	236	CTGGTCCATTACTTTCCTTC	69	n/a	n/a	135
590083	218	237	ACTGGTCCATTACTTTCCTT	54	4972	4991	136
150445	219	238	CACTGGTCCATTACTTTCCT	84	4973	4992	22
590084	220	239	TCACTGGTCCATTACTTTCC	65	4974	4993	137
590085	221	240	TTCACTGGTCCATTACTTTC	45	4975	4994	138
590086	222	241	CTTCACTGGTCCATTACTTT	43	4976	4995	139
590087	223	242	CCTTCACTGGTCCATTACTT	67	4977	4996	140
590088	224	243	ACCTTCACTGGTCCATTACT	59	4978	4997	141
436841	225	244	CACCTTCACTGGTCCATTAC	65	4979	4998	142
150446	226	245	ACACCTTCACTGGTCCATTA	83	4980	4999	23
393336	227	246	CACACCTTCACTGGTCCATT	81	4981	5000	143
150447	228	247	CCACACCTTCACTGGTCCAT	89	4982	5001	24
590089	229	248	CCCACACCTTCACTGGTCCA	82	4983	5002	144
590090	230	249	CCCCACACCTTCACTGGTCC	89	4984	5003	145
590091	231	250	TCCCCACACCTTCACTGGTC	84	4985	5004	146
590092	232	251	TTCCCCACACCTTCACTGGT	61	4986	5005	147
590093	233	252	CTTCCCCACACCTTCACTGG	60	4987	5006	148
590094	234	253	GCTTCCCCACACCTTCACTG	78	4988	5007	149
590095	235	254	TGCTTCCCCACACCTTCACT	72	4989	5008	150
590096	236	255	ATGCTTCCCCACACCTTCAC	76	4990	5009	151
393337	237	256	AATGCTTCCCCACACCTTCA	76	4991	5010	152
590097	238	257	TAATGCTTCCCCACACCTTC	68	4992	5011	153
590098	264	283	TCCATGCAGGCCTTCAGTCA	63	5018	5037	154
590099	265	284	ATCCATGCAGGCCTTCAGTC	64	5019	5038	155
590100	266	285	AATCCATGCAGGCCTTCAGT	52	5020	5039	156
590101	267	286	GAATCCATGCAGGCCTTCAG	53	5021	5040	157
590102	268	287	GGAATCCATGCAGGCCTTCA	65	5022	5041	158
393339	269	288	TGGAATCCATGCAGGCCTTC	43	5023	5042	159
590103	270	289	ATGGAATCCATGCAGGCCTT	56	5024	5043	160
590104	271	290	CATGGAATCCATGCAGGCCT	57	5025	5044	161
590105	272	291	ACATGGAATCCATGCAGGCC	52	5026	5045	162

590106	273	292	AACATGGAATCCATGCAGGC	54	5027	5046	163
590107	274	293	GAACATGGAATCCATGCAGG	51	5028	5047	164
590108	275	294	TGAACATGGAATCCATGCAG	58	5029	5048	165
393340	276	295	ATGAACATGGAATCCATGCA	62	5030	5049	166
590109	316	335	GACCTGCACTGGTACAGCCT	69	7632	7651	167
436847	317	336	GGACCTGCACTGGTACAGCC	74	7633	7652	168
590110	318	337	AGGACCTGCACTGGTACAGC	70	7634	7653	169
590111	319	338	GAGGACCTGCACTGGTACAG	74	7635	7654	170
590112	320	339	TGAGGACCTGCACTGGTACA	68	7636	7655	171
590113	321	340	GTGAGGACCTGCACTGGTAC	80	7637	7656	172
393343	322	341	AGTGAGGACCTGCACTGGTA	79	7638	7657	173
590114	323	342	AAGTGAGGACCTGCACTGGT	65	7639	7658	174
590115	324	343	AAAGTGAGGACCTGCACTGG	48	7640	7659	175
590116	325	344	TAAAGTGAGGACCTGCACTG	51	7641	7660	176
436848	326	345	TTAAAGTGAGGACCTGCACT	59	7642	7661	177
590117	327	346	ATTAAAGTGAGGACCTGCAC	43	7643	7662	178
590118	328	347	GATTAAAGTGAGGACCTGCA	43	7644	7663	179
590119	329	348	GGATTAAAGTGAGGACCTGC	67	7645	7664	180
590120	330	349	AGGATTAAAGTGAGGACCTG	63	7646	7665	181
436849	331	350	GAGGATTAAAGTGAGGACCT	64	7647	7666	182
393344	332	351	AGAGGATTAAAGTGAGGACC	59	7648	7667	183
590121	333	352	TAGAGGATTAAAGTGAGGAC	52	7649	7668	184
590122	334	353	ATAGAGGATTAAAGTGAGGA	36	7650	7669	185
590123	335	354	GATAGAGGATTAAAGTGAGG	25	7651	7670	186
590124	336	355	GGATAGAGGATTAAAGTGAG	34	7652	7671	187
590125	337	356	TGGATAGAGGATTAAAGTGA	49	7653	7672	188
590126	338	357	CTGGATAGAGGATTAAAGTG	34	7654	7673	189
590127	339	358	TCTGGATAGAGGATTAAAGT	39	7655	7674	190
590128	360	379	ATCCTTTGGCCCACCGTGTT	60	7676	7695	191

Table 2

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	% inhibition with HTS90	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	76	95	973	992	21

393347	361	380	CATCCTTTGGCCCACCGTGT	70	72	7677	7696	192
590129	362	381	TCATCCTTTGGCCCACCGTG	66	68	7678	7697	193
590130	363	382	TTCATCCTTTGGCCCACCGT	53	55	7679	7698	194
590131	364	383	CTTCATCCTTTGGCCCACCG	52	50	7680	7699	195
590132	365	384	TCTTCATCCTTTGGCCCACC	61	64	7681	7700	196
590133	366	385	CTCTTCATCCTTTGGCCCAC	45	54	7682	7701	197
590134	367	386	TCTCTTCATCCTTTGGCCCA	44	34	7683	7702	198
590135	368	387	CTCTCTTCATCCTTTGGCCC	52	49	7684	7703	199
590136	369	388	CCTCTCTTCATCCTTTGGCC	48	47	7685	7704	200
590137	370	389	GCCTCTCTTCATCCTTTGGC	35	44	n/a	n/a	201
590138	371	390	TGCCTCTCTTCATCCTTTGG	52	45	n/a	n/a	202
590139	372	391	ATGCCTCTCTTCATCCTTTG	50	45	n/a	n/a	203
590140	373	392	CATGCCTCTCTTCATCCTTT	49	27	n/a	n/a	204
590141	374	393	ACATGCCTCTCTTCATCCTT	34	18	n/a	n/a	205
590142	375	394	AACATGCCTCTCTTCATCCT	38	35	n/a	n/a	206
333612	376	395	CAACATGCCTCTCTTCATCC	34	33	n/a	n/a	25
333613	377	396	CCAACATGCCTCTCTTCATC	46	55	n/a	n/a	26
333614	378	397	TCCAACATGCCTCTCTTCAT	42	48	n/a	n/a	27
333615	379	398	CTCCAACATGCCTCTCTTCA	42	15	n/a	n/a	28
333616	380	399	TCTCCAACATGCCTCTCTTC	35	44	n/a	n/a	29
333617	381	400	GTCTCCAACATGCCTCTCTT	42	47	n/a	n/a	30
590143	501	520	TGCTTTTTCATGGACCACCA	n.d.	65	n/a	n/a	207
590144	502	521	CTGCTTTTTCATGGACCACC	n.d.	70	n/a	n/a	208
590145	503	522	TCTGCTTTTTCATGGACCAC	n.d.	64	n/a	n/a	209
436860	504	523	ATCTGCTTTTTCATGGACCA	n.d.	65	n/a	n/a	210
590146	505	524	CATCTGCTTTTTCATGGACC	n.d.	68	9655	9674	211
590147	506	525	TCATCTGCTTTTTCATGGAC	n.d.	59	9656	9675	212
393359	507	526	GTCATCTGCTTTTTCATGGA	n.d.	56	9657	9676	213
590148	508	527	AGTCATCTGCTTTTTCATGG	n.d.	45	9658	9677	214
590149	509	528	AAGTCATCTGCTTTTTCATG	n.d.	23	9659	9678	215
590150	510	529	CAAGTCATCTGCTTTTTCAT	n.d.	43	9660	9679	216
590151	511	530	CCAAGTCATCTGCTTTTTCA	n.d.	72	9661	9680	217
489513	512	531	CCCAAGTCATCTGCTTTTTC	n.d.	73	9662	9681	218
590152	513	532	GCCCAAGTCATCTGCTTTTT	n.d.	74	9663	9682	219
436861	514	533	TGCCCAAGTCATCTGCTTTT	n.d.	75	9664	9683	220
590153	515	534	TTGCCCAAGTCATCTGCTTT	n.d.	47	9665	9684	221

393360	516	535	TTTGCCCAAGTCATCTGCTT	n.d.	57	9666	9685	222
590154	517	536	CTTTGCCCAAGTCATCTGCT	n.d.	79	9667	9686	223
590155	518	537	CCTTTGCCCAAGTCATCTGC	n.d.	67	9668	9687	224
590156	519	538	ACCTTTGCCCAAGTCATCTG	n.d.	57	9669	9688	225
333620	520	539	CACCTTTGCCCAAGTCATCT	n.d.	68	9670	9689	31
333621	521	540	CCACCTTTGCCCAAGTCATC	n.d.	72	9671	9690	32
333622	522	541	TCCACCTTTGCCCAAGTCAT	n.d.	77	9672	9691	33
333623	523	542	TTCCACCTTTGCCCAAGTCA	n.d.	73	9673	9692	34
333624	524	543	TTTCCACCTTTGCCCAAGTC	n.d.	77	9674	9693	35
333625	525	544	ATTTCCACCTTTGCCCAAGT	n.d.	79	9675	9694	36
333626	526	545	CATTTCCACCTTTGCCCAAG	n.d.	72	9676	9695	37
333627	527	546	TCATTTCCACCTTTGCCCAA	n.d.	55	9677	9696	38
333628	528	547	TTCATTTCCACCTTTGCCCA	n.d.	59	9678	9697	39
333629	529	548	CTTCATTTCCACCTTTGCCC	n.d.	73	9679	9698	40
333630	530	549	TCTTCATTTCCACCTTTGCC	n.d.	76	9680	9699	41
333631	531	550	TTCTTCATTTCCACCTTTGC	n.d.	62	9681	9700	42
333632	532	551	TTTCTTCATTTCCACCTTTG	n.d.	64	9682	9701	43
333633	533	552	CTTTCTTCATTTCCACCTTT	n.d.	69	9683	9702	44
333634	534	553	ACTTTCTTCATTTCCACCTT	n.d.	55	9684	9703	45
333635	535	554	TACTTTCTTCATTTCCACCT	n.d.	72	9685	9704	46
489517	582	601	CCCAATTACACCACAAGCCA	68	72	9732	9751	226
436863	583	602	TCCCAATTACACCACAAGCC	83	86	9733	9752	227
590157	584	603	ATCCCAATTACACCACAAGC	64	62	9734	9753	228
590158	585	604	GATCCCAATTACACCACAAG	51	61	9735	9754	229
590159	586	605	CGATCCCAATTACACCACAA	60	55	9736	9755	230
590160	587	606	GCGATCCCAATTACACCACA	59	63	9737	9756	231
150463	588	607	GGCGATCCCAATTACACCAC	78	79	9738	9757	47
393363	589	608	GGGCGATCCCAATTACACCA	65	65	9739	9758	232
590161	590	609	TGGGCGATCCCAATTACACC	56	60	9740	9759	233
590162	591	610	TTGGGCGATCCCAATTACAC	48	51	9741	9760	234
489518	592	611	ATTGGGCGATCCCAATTACA	51	59	9742	9761	235
436864	593	612	TATTGGGCGATCCCAATTAC	39	41	9743	9762	236
590163	594	613	TTATTGGGCGATCCCAATTA	35	34	9744	9763	237
590164	595	614	TTTATTGGGCGATCCCAATT	42	44	9745	9764	238
590165	596	615	GTTTATTGGGCGATCCCAAT	58	61	9746	9765	239
393364	597	616	TGTTTATTGGGCGATCCCAA	60	69	9747	9766	240

590166	598	617	ATGTTTATTGGGCGATCCCA	51	54	9748	9767	241
590167	599	618	AATGTTTATTGGGCGATCCC	48	45	9749	9768	242
590168	600	619	GAATGTTTATTGGGCGATCC	60	65	9750	9769	243
150464	601	620	GGAATGTTTATTGGGCGATC	58	63	9751	9770	48
393365	607	626	TCCAAGGGAATGTTTATTGG	50	58	9757	9776	244

Table 3

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	80	973	992	21
590169	608	627	ATCCAAGGGAATGTTTATTG	63	9758	9777	245
590170	609	628	CATCCAAGGGAATGTTTATT	53	9759	9778	246
590171	610	629	ACATCCAAGGGAATGTTTAT	49	9760	9779	247
590172	611	630	TACATCCAAGGGAATGTTTA	56	9761	9780	248
489519	612	631	CTACATCCAAGGGAATGTTT	60	9762	9781	249
590173	613	632	ACTACATCCAAGGGAATGTT	61	9763	9782	250
590174	614	633	GACTACATCCAAGGGAATGT	65	9764	9783	251
393366	615	634	AGACTACATCCAAGGGAATG	58	9765	9784	252
590175	616	635	CAGACTACATCCAAGGGAAT	50	9766	9785	253
436865	617	636	TCAGACTACATCCAAGGGAA	69	9767	9786	254
590176	618	637	CTCAGACTACATCCAAGGGA	78	9768	9787	255
150465	619	638	CCTCAGACTACATCCAAGGG	91	9769	9788	49
590177	620	639	GCCTCAGACTACATCCAAGG	90	9770	9789	256
590178	621	640	GGCCTCAGACTACATCCAAG	92	9771	9790	257
489520	622	641	GGGCCTCAGACTACATCCAA	88	9772	9791	258
590179	643	662	CAGGATAACAGATGAGTTAA	79	9793	9812	259
590180	644	663	GCAGGATAACAGATGAGTTA	83	9794	9813	260
590181	645	664	AGCAGGATAACAGATGAGTT	81	9795	9814	261
590182	646	665	TAGCAGGATAACAGATGAGT	68	9796	9815	262
590183	647	666	CTAGCAGGATAACAGATGAG	74	9797	9816	263
590184	648	667	GCTAGCAGGATAACAGATGA	70	9798	9817	264
393370	649	668	AGCTAGCAGGATAACAGATG	61	9799	9818	265
590185	650	669	CAGCTAGCAGGATAACAGAT	78	9800	9819	266
590186	651	670	ACAGCTAGCAGGATAACAGA	72	9801	9820	267

489522	652	671	TACAGCTAGCAGGATAACAG	78	9802	9821	268
590187	653	672	CTACAGCTAGCAGGATAACA	88	9803	9822	269
378879	654	673	TCTACAGCTAGCAGGATAAC	86	9804	9823	270
590188	655	674	TTCTACAGCTAGCAGGATAA	85	9805	9824	271
393371	656	675	TTTCTACAGCTAGCAGGATA	84	9806	9825	272
436868	657	676	ATTTCTACAGCTAGCAGGAT	81	9807	9826	273
590189	658	677	CATTTCTACAGCTAGCAGGA	87	9808	9827	274
590190	659	678	ACATTTCTACAGCTAGCAGG	92	9809	9828	275
590191	660	679	TACATTTCTACAGCTAGCAG	88	9810	9829	276
590192	661	680	ATACATTTCTACAGCTAGCA	88	9811	9830	277
489523	662	681	GATACATTTCTACAGCTAGC	93	9812	9831	278
590193	683	702	ACAGTGTTTAATGTTTATCA	74	9833	9852	279
590194	684	703	TACAGTGTTTAATGTTTATC	64	9834	9853	280
590195	685	704	TTACAGTGTTTAATGTTTAT	56	9835	9854	281
590196	686	705	ATTACAGTGTTTAATGTTTA	50	9836	9855	282
590197	687	706	GATTACAGTGTTTAATGTTT	74	9837	9856	283
590198	688	707	AGATTACAGTGTTTAATGTT	37	9838	9857	284
590199	689	708	AAGATTACAGTGTTTAATGT	58	9839	9858	285
393375	690	709	TAAGATTACAGTGTTTAATG	58	9840	9859	286
590200	691	710	TTAAGATTACAGTGTTTAAT	46	9841	9860	287
436876	772	791	CAAATCTTCCAAGTGATCAT	36	9922	9941	288
590201	773	792	ACAAATCTTCCAAGTGATCA	33	9923	9942	289
590202	774	793	TACAAATCTTCCAAGTGATC	34	9924	9943	290
150474	775	794	ATACAAATCTTCCAAGTGAT	47	9925	9944	50
590203	776	795	TATACAAATCTTCCAAGTGA	29	9926	9945	291
393382	777	796	CTATACAAATCTTCCAAGTG	41	9927	9946	292
436877	778	797	ACTATACAAATCTTCCAAGT	45	9928	9947	293
590204	779	798	AACTATACAAATCTTCCAAG	27	9929	9948	294
590205	780	799	AAACTATACAAATCTTCCAA	33	9930	9949	295
590206	781	800	AAAACTATACAAATCTTCCA	35	9931	9950	296
489533	782	801	TAAAACTATACAAATCTTCC	26	9932	9951	297
590207	783	802	ATAAAACTATACAAATCTTC	19	9933	9952	298
590208	784	803	TATAAAACTATACAAATCTT	2	9934	9953	299
590209	785	804	TTATAAAACTATACAAATCT	7	9935	9954	300
590210	786	805	TTTATAAAACTATACAAATC	0	9936	9955	301
590211	787	806	TTTTATAAAACTATACAAAT	4	9937	9956	302

590212	788	807	GTTTTATAAAACTATACAAA	5	9938	9957	303
590213	789	808	AGTTTTATAAAACTATACAA	3	9939	9958	304
436878	790	809	GAGTTTTATAAAACTATACA	7	9940	9959	305
150475	791	810	TGAGTTTTATAAAACTATAC	28	9941	9960	51
489536	812	831	CATTGAAACAGACATTTTAA	28	9962	9981	306
150479	813	832	TCATTGAAACAGACATTTTA	36	9963	9982	52
393385	814	833	GTCATTGAAACAGACATTTT	50	9964	9983	307
590214	815	834	GGTCATTGAAACAGACATTT	45	9965	9984	308
590215	816	835	AGGTCATTGAAACAGACATT	47	9966	9985	309
590216	817	836	CAGGTCATTGAAACAGACAT	39	9967	9986	310
590217	818	837	ACAGGTCATTGAAACAGACA	44	9968	9987	311
590218	819	838	TACAGGTCATTGAAACAGAC	42	9969	9988	312
150480	820	839	ATACAGGTCATTGAAACAGA	46	9970	9989	53
393386	821	840	AATACAGGTCATTGAAACAG	36	9971	9990	313
489537	822	841	AAATACAGGTCATTGAAACA	12	9972	9991	314
590219	823	842	AAAATACAGGTCATTGAAAC	16	9973	9992	315
590220	824	843	CAAAATACAGGTCATTGAAA	21	9974	9993	316

Table 4

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
590251	n/a	n/a	CCTTGCCTTCTGCTCGAAAT	57	1013	1032	317
590252	n/a	n/a	AATAAAGTTGACCTCTTTTT	45	5479	5498	318
590253	n/a	n/a	CTCTGATATAAAAATCTTGT	54	8142	8161	319
590254	n/a	n/a	GCCCCGCGGCGGCCTCGGTC	38	1238	1257	320
590255	n/a	n/a	GCTATCGCCATTATTACAAG	38	7722	7741	321
590256	n/a	n/a	CTCAAATGTGAAAGTTGTCC	57	3414	3433	322
590257	n/a	n/a	GTTCTATATTCAATAAATGC	37	7925	7944	323
590258	n/a	n/a	AATTAAAGTTCCCAAATACA	0	7578	7597	324
590259	n/a	n/a	GATCATTACAAAAGTTAAGA	17	6150	6169	325
590260	n/a	n/a	CCTTCTCTGCCCTTGCAGCC	55	1685	1704	326
590261	n/a	n/a	ACCCAAATAACTATGTTGTA	n.d.	9394	9413	327
590262	n/a	n/a	CCAGGTTTTAAACTTAACAA	n.d.	8890	8909	328
590263	n/a	n/a	ATCTCAGGACTAAAATAAAC	44	3663	3682	329

590264	n/a	n/a	AAATAACTATGTTGTAGACC	n.d.	9390	9409	330
590265	n/a	n/a	AAGAACCTTTTCCAGAAAAT	37	2449	2468	331
590266	n/a	n/a	GGAACAGAAACAAGTCTATG	25	7458	7477	332
590267	n/a	n/a	AGAAAGCTATCGCCATTATT	27	7727	7746	333
590268	n/a	n/a	TTCCCAAATACATTCTAAAA	7	7570	7589	334
590269	n/a	n/a	AACTGCTCTAGGCCTGTGTC	53	4787	4806	335
590270	n/a	n/a	AAATGGATCAAATCTGATCA	31	6595	6614	336
590271	n/a	n/a	GTAGGTGCACATCAAAATCA	58	1928	1947	337
590272	n/a	n/a	TCTGATATAAAAATCTTGTC	28	8141	8160	338
590273	n/a	n/a	ACCATATGAACTCCAGAAAG	45	7741	7760	339
590274	n/a	n/a	AACATCAAGGTAGTTCATGA	10	8379	8398	340
590275	n/a	n/a	GCAATTACAGAAATGGATCA	42	6605	6624	341
590276	n/a	n/a	TTTTAAGCATATTCCAAAGT	45	6331	6350	342
590277	n/a	n/a	TCAACCCCCAGCTCAAACAC	26	6174	6193	343
590278	n/a	n/a	AGAAAAATAACATTAATCCT	n.d.	9541	9560	344
590279	n/a	n/a	AAGATTTTAAACACGGAATA	31	3085	3104	345
146145	165	184	GTCGCCCTTCAGCACGCACA	82	971	990	54
333611	167	186	CCGTCGCCCTTCAGCACGCA	81	973	992	21
590250	399	418	AGCAGTCACATTGCCCAAGT	75	8454	8473	346
489525	682	701	CAGTGTTTAATGTTTATCAG	69	9832	9851	347
436879	825	844	GCAAAATACAGGTCATTGAA	49	9975	9994	348
590221	826	845	GGCAAAATACAGGTCATTGA	54	9976	9995	349
590222	827	846	TGGCAAAATACAGGTCATTG	52	9977	9996	350
393387	828	847	CTGGCAAAATACAGGTCATT	51	9978	9997	351
590223	829	848	TCTGGCAAAATACAGGTCAT	47	9979	9998	352
590224	830	849	GTCTGGCAAAATACAGGTCA	44	9980	9999	353
590225	831	850	AGTCTGGCAAAATACAGGTC	50	9981	10000	354
489538	832	851	AAGTCTGGCAAAATACAGGT	38	9982	10001	355
590226	833	852	TAAGTCTGGCAAAATACAGG	33	9983	10002	356
590227	834	853	TTAAGTCTGGCAAAATACAG	20	9984	10003	357
150482	853	872	TTTAATACCCATCTGTGATT	29	10003	10022	55
590228	854	873	GTTTAATACCCATCTGTGAT	33	10004	10023	358
150483	855	874	AGTTTAATACCCATCTGTGA	44	10005	10024	56
590229	856	875	AAGTTTAATACCCATCTGTG	51	10006	10025	359
590230	857	876	CAAGTTTAATACCCATCTGT	42	10007	10026	360
590231	858	877	ACAAGTTTAATACCCATCTG	38	10008	10027	361

393389	859	878	GACAAGTTTAATACCCATCT	48	10009	10028	362
590232	860	879	TGACAAGTTTAATACCCATC	55	10010	10029	363
590233	861	880	CTGACAAGTTTAATACCCAT	49	10011	10030	364
489541	862	881	TCTGACAAGTTTAATACCCA	52	10012	10031	365
590234	863	882	TTCTGACAAGTTTAATACCC	39	10013	10032	366
590235	864	883	ATTCTGACAAGTTTAATACC	21	10014	10033	367
590236	865	884	AATTCTGACAAGTTTAATAC	4	10015	10034	368
393390	866	885	AAATTCTGACAAGTTTAATA	7	10016	10035	369
590237	867	886	GAAATTCTGACAAGTTTAAT	5	10017	10036	370
436881	868	887	AGAAATTCTGACAAGTTTAA	33	10018	10037	371
590238	869	888	AAGAAATTCTGACAAGTTTA	20	10019	10038	372
590239	891	910	TTATTCACAGGCTTGAATGA	23	10041	10060	373
489544	892	911	TTTATTCACAGGCTTGAATG	41	10042	10061	374
590240	893	912	TTTTATTCACAGGCTTGAAT	40	10043	10062	375
436884	894	913	TTTTTATTCACAGGCTTGAA	31	10044	10063	376
590241	895	914	GTTTTTATTCACAGGCTTGA	39	10045	10064	377
150488	896	915	GGTTTTTATTCACAGGCTTG	51	10046	10065	57
590242	897	916	GGGTTTTTATTCACAGGCTT	46	10047	10066	378
150489	898	917	AGGGTTTTTATTCACAGGCT	52	10048	10067	58
590243	899	918	CAGGGTTTTTATTCACAGGC	49	10049	10068	379
590244	900	919	ACAGGGTTTTTATTCACAGG	38	10050	10069	380
590245	901	920	TACAGGGTTTTTATTCACAG	34	10051	10070	381
150490	902	921	ATACAGGGTTTTTATTCACA	30	10052	10071	59
590246	903	922	CATACAGGGTTTTTATTCAC	34	10053	10072	382
150491	904	923	CCATACAGGGTTTTTATTCA	34	10054	10073	60
590247	905	924	GCCATACAGGGTTTTTATTC	34	10055	10074	383
590248	906	925	TGCCATACAGGGTTTTTATT	33	10056	10075	384
393393	907	926	GTGCCATACAGGGTTTTTAT	43	10057	10076	385
590249	908	927	AGTGCCATACAGGGTTTTTA	12	10058	10077	386

Table 5

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	86	973	992	21

590280	n/a	n/a	TGGAAAAACTCAAATGTGAA	51	3422	3441	387
590281	n/a	n/a	TTTCCCTTTCTTTTCCACAC	76	5738	5757	388
590282	n/a	n/a	TCTTTCCCTTTCTTTTCCAC	65	5740	5759	389
590283	n/a	n/a	TACCTTCTCTGCCCTTGCAG	74	1687	1706	390
590284	n/a	n/a	GCAAGGGCCAAGGCTGCTGC	75	6879	6898	391
590285	n/a	n/a	AAAGCTAAATTATGAATTAA	12	7592	7611	392
590286	n/a	n/a	CTAATGAAGGCTCAGTATGA	59	3193	3212	393
590287	n/a	n/a	GGAGTCAAATGCCAAAGAAC	60	2463	2482	394
590288	n/a	n/a	TGAATTAAAGTTCCCAAATA	5	7580	7599	395
590289	n/a	n/a	ACTTGGTGCAGGCAGAATAT	63	6916	6935	396
590290	n/a	n/a	CCTCTGATATAAAAATCTTG	67	8143	8162	397
590291	n/a	n/a	AAAGTTGGAGAGAGTTTCTG	8	4940	4959	398
590292	n/a	n/a	TCTCTGCCCTTGCAGCCCAA	80	1682	1701	399
590293	n/a	n/a	TTACTTGGTGCAGGCAGAAT	56	6918	6937	400
590294	n/a	n/a	AATGGAGTCAAATGCCAAAG	66	2466	2485	401
590295	n/a	n/a	TATGAATTAAAGTTCCCAAA	20	7582	7601	402
590296	n/a	n/a	AGTTCTATATTCAATAAATG	21	7926	7945	403
590297	n/a	n/a	TACAAGTAGTATACCATATG	33	7753	7772	404
590298	n/a	n/a	TAGCCTTAGAGCTGTACAAA	70	1553	1572	405
590299	n/a	n/a	GTCCCCATTTGTCAATTCCT	71	7882	7901	406
590300	n/a	n/a	AACCTGCCTACTGGCAGAGC	59	2095	2114	407
590301	n/a	n/a	CTTGTTCCCACACTCAATGC	56	4747	4766	408
590302	n/a	n/a	ACAAGTCATGATAACCTGCA	61	8952	8971	409
590303	n/a	n/a	TGTTTTCCAAACTCAGATCT	52	8796	8815	410
590304	n/a	n/a	AGAACCTCATAATATTAGAA	9	9557	9576	411
590305	n/a	n/a	GGTTTTAAACTTAACAAAAT	1	8887	8906	412
590306	n/a	n/a	CTCTGGTGTATTTTTAGTAA	65	1831	1850	413
590307	n/a	n/a	TATCTCTGCATATCTGGAAA	71	3034	3053	414
590308	n/a	n/a	CAGCCTTTTTAACCCAAAAG	68	4407	4426	415
590309	n/a	n/a	TGGAATGCTCCACTATCCAA	57	3012	3031	416
590310	n/a	n/a	CGTTCAGAAGTTTGTCTCTG	67	2126	2145	417
590311	n/a	n/a	CTGCTCAGGGAAGGTGGAAA	53	2922	2941	418
590312	n/a	n/a	TCAAGAGAAGCTAGGAAAAC	50	3154	3173	419
590313	n/a	n/a	TCCCTTTCTTTTCCACACCT	74	5736	5755	420
590314	n/a	n/a	TTGTTCCCACACTCAATGCA	56	4746	4765	421
590315	n/a	n/a	TCACCAGCACAGCACAACAC	58	5076	5095	422

590316	n/a	n/a	CCTGGGATCATTACAAAAGT	42	6155	6174	423
590317	n/a	n/a	AGTAGTATACCATATGAACT	35	7749	7768	424
590318	n/a	n/a	TCTAATATGGTCAAATGTAA	27	8779	8798	425
590319	n/a	n/a	GGTTGGGCTCTGGTGTATTT	64	1838	1857	426
590320	n/a	n/a	TGCCCTTTACTTGGTGCAGG	56	6924	6943	427
590321	n/a	n/a	AGAGAGTTTCTGAACAAAGA	24	4932	4951	428
590322	n/a	n/a	GAATTTCAGCAATTACAGAA	33	6613	6632	429
590323	n/a	n/a	ACAAGTTAAACAAGTCATGA	9	8961	8980	430
590324	n/a	n/a	TGTGCCCTTTACTTGGTGCA	47	6926	6945	431
590325	n/a	n/a	TTAGGAGGAGGAAAAGGACC	23	1719	1738	432
590326	n/a	n/a	ACTGGCAGAGCAATTTTAAA	25	2086	2105	433
590327	n/a	n/a	AGTCAAATGCCAAAGAACCT	58	2461	2480	434
590328	n/a	n/a	AAGCATCAGATGGATTAGGG	17	8411	8430	435
590329	n/a	n/a	GTCCGCGGGACCCTCAGGAA	54	1414	1433	436
590330	n/a	n/a	CAATTACAGAAATGGATCAA	42	6604	6623	437
590331	n/a	n/a	GCTGTCAAGTAATCACTACC	27	9606	9625	438
590332	n/a	n/a	AGTGCAAAGTTGGAGAGAGT	33	4945	4964	439
590333	n/a	n/a	ACTTGCTTCCAATCCCAAAT	78	6436	6455	440
590334	n/a	n/a	AACTCAAATGTGAAAGTTGT	51	3416	3435	441
590335	n/a	n/a	TTTTAGTAAGATCTTCAAAT	14	1820	1839	442
590336	n/a	n/a	ATTTCAGCAATTACAGAAAT	27	6611	6630	443
590337	n/a	n/a	TTAAGTGTCCCCATTTGTCA	56	7888	7907	444
590338	n/a	n/a	TTAGCAACCTGCCTACTGGC	57	2100	2119	445
590339	n/a	n/a	TATTACAAGAGTTAAGCATC	41	7711	7730	446
590340	n/a	n/a	ATGTTGAATATACATGTACA	36	4545	4564	447
590341	n/a	n/a	TTTGTCTCTGACCATCTTAG	74	2116	2135	448
590342	n/a	n/a	TTTTCCACCAGTTGGTAACT	59	2253	2272	449
590343	n/a	n/a	CAACAGCTTCCCACAAGTTA	28	8973	8992	450
590344	n/a	n/a	CAAATGTGAAAGTTGTCCCT	62	3412	3431	451
590345	n/a	n/a	GCTACCTTCTCTGCCCTTGC	73	1689	1708	452
590346	n/a	n/a	TCTTAGCAGAACAGTGTTCT	51	8743	8762	453
590347	n/a	n/a	ATACATTCTAAAAAGAAACA	41	7563	7582	454
590348	n/a	n/a	GCACATATTTACAAGTAGTA	58	7762	7781	455
590349	n/a	n/a	GGGTCACCAGCACAGCACAA	35	5079	5098	456
590350	n/a	n/a	GTGCAAGGGCCAAGGCTGCT	66	6881	6900	457
590351	n/a	n/a	ACCTGGGTTCATGCATGGAT	72	2902	2921	458

590352	n/a	n/a	ATCACTATTTGAAACTAAAT	0	6569	6588	459
590353	n/a	n/a	ATACAATAAAGTTGACCTCT	64	5483	5502	460
590354	n/a	n/a	TTTTAAACTTAACAAAATGT	10	8885	8904	461
590355	n/a	n/a	CTCCCCGCGCTCCCGCCACG	15	1268	1287	462
590356	n/a	n/a	GAAGGCTCAGTATGAAGAGA	65	3188	3207	463

Table 6

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	87	973	992	21
590357	n/a	n/a	AGAAAACAGCTGATTTACCT	40	4915	4934	464
590358	n/a	n/a	CCACAAGTTAAACAAGTCAT	n.d.	8963	8982	465
590359	n/a	n/a	CAAATTTGCAAACAAGTAGC	61	8331	8350	466
590360	n/a	n/a	CCTAATTTGAACTGCAAGTA	n.d.	8665	8684	467
590361	n/a	n/a	AAAAAACTCATCTCCCCAGC	70	6969	6988	468
590362	n/a	n/a	AGGCTCAGTATGAAGAGATC	67	3186	3205	469
590363	n/a	n/a	TGTTATCAAGAGCACAGGGC	58	3383	3402	470
590364	n/a	n/a	CCTCAAAAGGGAGATGGTAA	41	4768	4787	471
590365	n/a	n/a	AGTATGGGTCACCAGCACAG	71	5084	5103	472
590366	n/a	n/a	TCACAATCTAGTGCAGTTAC	70	5584	5603	473
590367	n/a	n/a	CAAGTGAGAAACCCAATCCT	n.d.	8856	8875	474
590368	n/a	n/a	AGAAAATCTGGCCATTTTAA	n.d.	8832	8851	475
590369	n/a	n/a	ACAGGTAATGGTGCTCCGTG	71	3716	3735	476
590370	n/a	n/a	TGAAAGGCTTTCAGAAAACA	44	8102	8121	477
590371	n/a	n/a	CAGGCAAGTTACAGGAAGCA	64	6687	6706	478
590372	n/a	n/a	CAGCAAGCTGCTTAACTGCT	65	4800	4819	479
590373	n/a	n/a	TGTTGCAAAGACATTACCTT	n.d.	9455	9474	480
590374	n/a	n/a	GAAACTAAATTAGCAAGATG	43	6559	6578	481
590375	n/a	n/a	TCAAGAGCACAGGGCCAAAA	60	3378	3397	482
590376	n/a	n/a	AGGAGGAGGAAAAGGACCTC	53	1717	1736	483
590377	n/a	n/a	CCTCAGCCTTTTTAACCCAA	73	4410	4429	484
590378	n/a	n/a	CTATGTTGTAGACCACCACA	n.d.	9384	9403	485
590379	n/a	n/a	CTCCGTGGCTACATACAGAA	66	3703	3722	486
590380	n/a	n/a	TTTATCTGGATCTTTAGAAA	n.d.	8642	8661	487

590381	n/a	n/a	AAAAAAAGGAAAGTGAAAGT	n.d.	9279	9298	488
590382	n/a	n/a	GGTTCATGCATGGATTCTCA	76	2897	2916	489
590383	n/a	n/a	CTGCAAAGTGTCACACAAAC	76	1630	1649	490
590384	n/a	n/a	TTCAGAAGTACCAAAGGGTA	53	8227	8246	491
590385	n/a	n/a	TAAAAGCATTCCAGCATTTG	44	7848	7867	492
590386	n/a	n/a	TAGTATACCATATGAACTCC	73	7747	7766	493
590387	n/a	n/a	TGCATATCTGGAAAGCTGGA	59	3028	3047	494
590388	n/a	n/a	CTTAACTGCTCTAGGCCTGT	54	4790	4809	495
590389	n/a	n/a	AGGCACCGACCGGGCGGCAC	21	1155	1174	496
590390	n/a	n/a	TGCAAAGTTGGAGAGAGTTT	32	4943	4962	497
590391	n/a	n/a	TCCTCAAAAGGGAGATGGTA	37	4769	4788	498
590392	n/a	n/a	AGTATACCATATGAACTCCA	76	7746	7765	499
590393	n/a	n/a	TATTTGTACATGTTGAATAT	2	4554	4573	500
590394	n/a	n/a	ACCCAAAAGGTGTATGTCTC	71	4396	4415	501
590395	n/a	n/a	CTTTGGAAAAAAAGGAAAGT	n.d.	9285	9304	502
590396	n/a	n/a	GGGAGAAAGGCAGGCAAGTT	20	6697	6716	503
590397	n/a	n/a	TTAAGCCCAGGAAGTAAAAG	9	7862	7881	504
590398	n/a	n/a	AGACATTACCTTTAAACATT	n.d.	9447	9466	505
590399	n/a	n/a	GTGGCTTAAGAAATGCTCCG	26	2050	2069	506
590400	n/a	n/a	GTGAGAAGGGAACAGAAACA	48	7466	7485	507
590401	n/a	n/a	AAAAGCATCAGATGGATTAG	21	8413	8432	508
590402	n/a	n/a	TTCCACCAGTTGGTAACTTC	78	2251	2270	509
590403	n/a	n/a	TTTTTAGTAAGATCTTCAAA	15	1821	1840	510
590404	n/a	n/a	ATCTGTGTCCAAATCCCAGG	59	4847	4866	511
590405	n/a	n/a	TAAGATCTTCAAATAAGCTA	33	1814	1833	512
590406	n/a	n/a	ATCAACTCTTTCCCTTTCTT	63	5746	5765	513
590407	n/a	n/a	TGTGTCCTCAAAAGGGAGAT	37	4773	4792	514
590408	n/a	n/a	TACCTCCTCCCAACAATACC	n.d.	9590	9609	515
590409	n/a	n/a	TTCTGCTTTACAACTATGGC	n.d.	9133	9152	516
590410	n/a	n/a	GTACATGTTGAATATACATG	35	4549	4568	517
590411	n/a	n/a	TTTGTGGCTAATCTTAAGGT	47	5699	5718	518
590412	n/a	n/a	TCCTGCCTCAGCCTTTTTAA	34	4415	4434	519
590413	n/a	n/a	CGGTGTCCGCGGGACCCTCA	59	1418	1437	520
590414	n/a	n/a	GAAATGGATCAAATCTGATC	50	6596	6615	521
590415	n/a	n/a	GGTAGTTCATGAGCTAAATT	31	8371	8390	522
590416	n/a	n/a	AATGGAGTCTCGACTAGTTT	62	8072	8091	523

590417	n/a	n/a	CAAGTATGGGTCACCAGCAC	57	5086	5105	524
590418	n/a	n/a	GGTGTCCGCGGGACCCTCAG	40	1417	1436	525
590419	n/a	n/a	CGCCACGCGCAGGCCCAGCC	37	1255	1274	526
590420	n/a	n/a	TCTAGGCCTGTGTCCTCAAA	75	4781	4800	527
590421	n/a	n/a	ACTGTCCTGGGCTAATGAAG	36	3204	3223	528
590422	n/a	n/a	AAGCATCTTGTTACCTCTCT	52	7698	7717	529
590423	n/a	n/a	GCCCAGGAAGTAAAAGCATT	38	7858	7877	530
590424	n/a	n/a	GTAAGATCTTCAAATAAGCT	46	1815	1834	531
590425	n/a	n/a	AAAGGGAGATGGTAATCTTG	48	4763	4782	532
590426	n/a	n/a	GCCAAGGCTGCTGCCTTACA	66	6873	6892	533
590427	n/a	n/a	CAGACTAACTGTTCCTGTCC	43	2363	2382	534
590428	n/a	n/a	TTTGTCAATTCCTTTAAGCC	39	7875	7894	535
590429	n/a	n/a	ACTACCTCCTCCCAACAATA	n.d.	9592	9611	536
590430	n/a	n/a	TACCTCTCTTCATCCTTTGG	50	7687	7706	537
590431	n/a	n/a	ACTGCTCTAGGCCTGTGTCC	59	4786	4805	538
590432	n/a	n/a	CCTCCTCCCAACAATACCCA	n.d.	9588	9607	539
590433	n/a	n/a	GGCAGGCAAGTTACAGGAAG	42	6689	6708	540

Table 7

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
592596	2	21	TCGCCCACTCTGGCCCCAAA	86	808	827	541
592597	4	23	CCTCGCCCACTCTGGCCCCA	89	810	829	542
592598	6	25	CGCCTCGCCCACTCTGGCCC	56	812	831	543
592599	8	27	CGCGCCTCGCCCACTCTGGC	68	814	833	544
592600	10	29	TCCGCGCCTCGCCCACTCTG	64	816	835	545
592601	12	31	CCTCCGCGCCTCGCCCACTC	83	818	837	546
592602	14	33	GACCTCCGCGCCTCGCCCAC	89	820	839	547
592603	16	35	CAGACCTCCGCGCCTCGCCC	88	822	841	548
592604	18	37	GCCAGACCTCCGCGCCTCGC	79	824	843	549
592605	20	39	AGGCCAGACCTCCGCGCCTC	89	826	845	550
592606	22	41	ATAGGCCAGACCTCCGCGCC	88	828	847	551
592607	24	43	TTATAGGCCAGACCTCCGCG	75	830	849	552
592608	26	45	CTTTATAGGCCAGACCTCCG	21	832	851	553

592609	28	47	TACTTTATAGGCCAGACCTC	76	834	853	554
592610	30	49	ACTACTTTATAGGCCAGACC	60	836	855	555
592611	32	51	CGACTACTTTATAGGCCAGA	0	838	857	556
592612	34	53	CGCGACTACTTTATAGGCCA	0	840	859	557
592613	36	55	TCCGCGACTACTTTATAGGC	0	842	861	558
592614	38	57	TCTCCGCGACTACTTTATAG	7	844	863	559
592615	40	59	CGTCTCCGCGACTACTTTAT	0	846	865	560
592616	42	61	CCCGTCTCCGCGACTACTTT	0	848	867	561
592617	44	63	ACCCCGTCTCCGCGACTACT	0	850	869	562
592618	46	65	GCACCCCGTCTCCGCGACTA	0	852	871	563
592619	48	67	CAGCACCCCGTCTCCGCGAC	0	854	873	564
592620	50	69	ACCAGCACCCCGTCTCCGCG	0	856	875	565
592621	52	71	AAACCAGCACCCCGTCTCCG	2	858	877	566
592622	54	73	GCAAACCAGCACCCCGTCTC	4	860	879	567
592623	56	75	ACGCAAACCAGCACCCCGTC	0	862	881	568
592624	58	77	CGACGCAAACCAGCACCCCG	0	864	883	569
592625	60	79	TACGACGCAAACCAGCACCC	0	866	885	570
592626	62	81	ACTACGACGCAAACCAGCAC	0	868	887	571
592627	64	83	AGACTACGACGCAAACCAGC	1	870	889	572
592628	66	85	GGAGACTACGACGCAAACCA	0	872	891	573
592629	68	87	CAGGAGACTACGACGCAAAC	0	874	893	574
592630	70	89	TGCAGGAGACTACGACGCAA	0	876	895	575
592631	72	91	GCTGCAGGAGACTACGACGC	1	878	897	576
150511	74	93	ACGCTGCAGGAGACTACGAC	0	880	899	61
592632	90	109	GCAACGGAAACCCCAGACGC	2	896	915	577
592633	92	111	CTGCAACGGAAACCCCAGAC	0	898	917	578
592634	94	113	GACTGCAACGGAAACCCCAG	0	900	919	579
345715	95	114	GGACTGCAACGGAAACCCCA	0	901	920	580
592635	96	115	AGGACTGCAACGGAAACCCC	1	902	921	581
150437	98	117	CGAGGACTGCAACGGAAACC	6	904	923	62
592636	100	119	TCCGAGGACTGCAACGGAAA	6	906	925	582
592637	102	121	GTTCCGAGGACTGCAACGGA	12	908	927	583
592638	104	123	TGGTTCCGAGGACTGCAACG	0	910	929	584
592639	106	125	CCTGGTTCCGAGGACTGCAA	32	912	931	585
592640	108	127	GTCCTGGTTCCGAGGACTGC	68	914	933	586
345717	110	129	AGGTCCTGGTTCCGAGGACT	65	916	935	587

592641	112	131	CGAGGTCCTGGTTCCGAGGA	84	918	937	588
592642	114	133	GCCGAGGTCCTGGTTCCGAG	86	920	939	589
592643	116	135	ACGCCGAGGTCCTGGTTCCG	78	922	941	590
592644	118	137	CCACGCCGAGGTCCTGGTTC	79	924	943	591
345719	120	139	GGCCACGCCGAGGTCCTGGT	63	926	945	592
150441	122	141	TAGGCCACGCCGAGGTCCTG	81	928	947	63
592645	124	143	GCTAGGCCACGCCGAGGTCC	63	930	949	593
592646	126	145	TCGCTAGGCCACGCCGAGGT	56	932	951	594
592647	128	147	ACTCGCTAGGCCACGCCGAG	48	934	953	595
345721	130	149	TAACTCGCTAGGCCACGCCG	63	936	955	596
592648	132	151	CATAACTCGCTAGGCCACGC	38	938	957	597
592649	134	153	GCCATAACTCGCTAGGCCAC	52	940	959	598
592650	136	155	TCGCCATAACTCGCTAGGCC	59	942	961	599
592651	138	157	CGTCGCCATAACTCGCTAGG	55	944	963	600
592652	156	175	CAGCACGCACACGGCCTTCG	56	962	981	601
333605	158	177	TTCAGCACGCACACGGCCTT	85	964	983	64
333606	160	179	CCTTCAGCACGCACACGGCC	82	966	985	65
146144	162	181	GCCCTTCAGCACGCACACGG	58	968	987	66
333609	164	183	TCGCCCTTCAGCACGCACAC	79	970	989	67
146145	165	184	GTCGCCCTTCAGCACGCACA	86	971	990	54
333610	166	185	CGTCGCCCTTCAGCACGCAC	79	972	991	68
333611	167	186	CCGTCGCCCTTCAGCACGCA	83	973	992	21
592653	168	187	GCCGTCGCCCTTCAGCACGC	79	974	993	602
592654	169	188	GGCCGTCGCCCTTCAGCACG	72	975	994	603
592655	170	189	GGGCCGTCGCCCTTCAGCAC	51	976	995	604
592656	172	191	CTGGGCCGTCGCCCTTCAGC	45	978	997	605
592657	174	193	CACTGGGCCGTCGCCCTTCA	33	980	999	606
592658	176	195	TGCACTGGGCCGTCGCCCTT	72	982	1001	607
592659	178	197	CCTGCACTGGGCCGTCGCCC	76	984	1003	608

Table 8

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	87	973	992	21

150443	180	199	GCCCTGCACTGGGCCGTCGC	65	986	1005	69
592660	182	201	ATGCCCTGCACTGGGCCGTC	52	988	1007	609
592661	184	203	TGATGCCCTGCACTGGGCCG	30	990	1009	610
592662	186	205	GATGATGCCCTGCACTGGGC	38	992	1011	611
592663	188	207	TTGATGATGCCCTGCACTGG	36	994	1013	612
150444	190	209	AATTGATGATGCCCTGCACT	48	996	1015	70
592664	192	211	GAAATTGATGATGCCCTGCA	35	998	1017	15
592665	194	213	TCGAAATTGATGATGCCCTG	40	1000	1019	614
592666	196	215	GCTCGAAATTGATGATGCCC	68	1002	1021	615
592667	198	217	CTGCTCGAAATTGATGATGC	63	1004	1023	616
592668	200	219	TTCTGCTCGAAATTGATGAT	47	1006	1025	617
592669	239	258	TTAATGCTTCCCCACACCTT	68	4993	5012	618
592670	241	260	CTTTAATGCTTCCCCACACC	71	4995	5014	619
592671	243	262	TCCTTTAATGCTTCCCCACA	69	4997	5016	620
150448	245	264	AGTCCTTTAATGCTTCCCCA	76	4999	5018	71
592672	247	266	TCAGTCCTTTAATGCTTCCC	75	5001	5020	621
592673	249	268	AGTCAGTCCTTTAATGCTTC	58	5003	5022	622
592674	251	270	TCAGTCAGTCCTTTAATGCT	46	5005	5024	623
592675	253	272	CTTCAGTCAGTCCTTTAATG	41	5007	5026	624
592676	255	274	GCCTTCAGTCAGTCCTTTAA	62	5009	5028	625
150449	257	276	AGGCCTTCAGTCAGTCCTTT	65	5011	5030	72
592677	259	278	GCAGGCCTTCAGTCAGTCCT	69	5013	5032	626
592678	261	280	ATGCAGGCCTTCAGTCAGTC	65	5015	5034	627
592679	263	282	CCATGCAGGCCTTCAGTCAG	53	5017	5036	628
592680	277	296	CATGAACATGGAATCCATGC	63	5031	5050	629
592681	279	298	CTCATGAACATGGAATCCAT	60	5033	5052	630
592682	281	300	AACTCATGAACATGGAATCC	56	5035	5054	631
592683	284	303	CCAAACTCATGAACATGGAA	60	5038	5057	632
592684	286	305	CTCCAAACTCATGAACATGG	69	5040	5059	633
592685	288	307	ATCTCCAAACTCATGAACAT	40	5042	5061	634
592686	290	309	TTATCTCCAAACTCATGAAC	35	5044	5063	635
592687	292	311	TATTATCTCCAAACTCATGA	26	5046	5065	636
592688	294	313	TGTATTATCTCCAAACTCAT	41	5048	5067	637
150452	296	315	GCTGTATTATCTCCAAACTC	51	5050	5069	73
592689	298	317	CTGCTGTATTATCTCCAAAC	43	5052	5071	638
592690	300	319	GCCTGCTGTATTATCTCCAA	37	n/a	n/a	639

592691	302	321	CAGCCTGCTGTATTATCTCC	33	n/a	n/a	640
592692	304	323	TACAGCCTGCTGTATTATCT	27	n/a	n/a	641
592693	306	325	GGTACAGCCTGCTGTATTAT	21	n/a	n/a	642
592694	308	327	CTGGTACAGCCTGCTGTATT	23	n/a	n/a	643
592695	310	329	CACTGGTACAGCCTGCTGTA	46	n/a	n/a	644
592696	312	331	TGCACTGGTACAGCCTGCTG	40	n/a	n/a	645
592697	314	333	CCTGCACTGGTACAGCCTGC	62	n/a	n/a	646
592698	340	359	TTCTGGATAGAGGATTAAAG	41	7656	7675	647
592699	342	361	TTTTCTGGATAGAGGATTAA	29	7658	7677	648
592700	344	363	TGTTTTCTGGATAGAGGATT	51	7660	7679	649
592701	346	365	CGTGTTTTCTGGATAGAGGA	64	7662	7681	650
592702	348	367	ACCGTGTTTTCTGGATAGAG	44	7664	7683	651
592703	350	369	CCACCGTGTTTTCTGGATAG	62	7666	7685	652
592704	352	371	GCCCACCGTGTTTTCTGGAT	60	7668	7687	653
592705	354	373	TGGCCCACCGTGTTTTCTGG	62	7670	7689	654
592706	356	375	TTTGGCCCACCGTGTTTTCT	49	7672	7691	655
592707	358	377	CCTTTGGCCCACCGTGTTTT	52	7674	7693	656
592708	382	401	AGTCTCCAACATGCCTCTCT	53	n/a	n/a	657
592709	384	403	CAAGTCTCCAACATGCCTCT	39	n/a	n/a	658
489501	386	405	CCCAAGTCTCCAACATGCCT	75	8441	8460	659
150454	388	407	TGCCCAAGTCTCCAACATGC	86	8443	8462	74
592710	390	409	ATTGCCCAAGTCTCCAACAT	71	8445	8464	660
592711	392	411	ACATTGCCCAAGTCTCCAAC	64	8447	8466	661
592712	394	413	TCACATTGCCCAAGTCTCCA	59	8449	8468	662
489502	396	415	AGTCACATTGCCCAAGTCTC	70	8451	8470	663
592713	398	417	GCAGTCACATTGCCCAAGTC	70	8453	8472	664
592714	400	419	CAGCAGTCACATTGCCCAAG	84	8455	8474	665
592715	402	421	GTCAGCAGTCACATTGCCCA	83	8457	8476	666
592716	404	423	TTGTCAGCAGTCACATTGCC	59	8459	8478	667
489503	406	425	CTTTGTCAGCAGTCACATTG	47	8461	8480	668
592717	408	427	ATCTTTGTCAGCAGTCACAT	54	8463	8482	669
592718	410	429	CCATCTTTGTCAGCAGTCAC	76	8465	8484	670
592719	412	431	CACCATCTTTGTCAGCAGTC	75	8467	8486	671
592720	414	433	CACACCATCTTTGTCAGCAG	66	8469	8488	672
489504	416	435	GCCACACCATCTTTGTCAGC	60	8471	8490	673
592721	418	437	CGGCCACACCATCTTTGTCA	62	8473	8492	674

592722	420	439	ATCGGCCACACCATCTTTGT	57	8475	8494	675
592723	422	441	ACATCGGCCACACCATCTTT	54	8477	8496	676
150458	424	443	ACACATCGGCCACACCATCT	77	8479	8498	75
489505	426	445	AGACACATCGGCCACACCAT	84	8481	8500	677
592724	428	447	ATAGACACATCGGCCACACC	66	8483	8502	678

Table 9

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	% inhibition with HTS90	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	87	n.d.	973	992	21
592725	430	449	CAATAGACACATCGGCCACA	67	65	8485	8504	679
592726	432	451	TTCAATAGACACATCGGCCA	62	66	8487	8506	680
592727	434	453	TCTTCAATAGACACATCGGC	56	49	8489	8508	681
489506	436	455	AATCTTCAATAGACACATCG	25	28	8491	8510	682
592728	438	457	AGAATCTTCAATAGACACAT	12	0	8493	8512	683
592729	440	459	ACAGAATCTTCAATAGACAC	24	16	8495	8514	684
592730	442	461	TCACAGAATCTTCAATAGAC	34	24	8497	8516	685
592731	444	463	GATCACAGAATCTTCAATAG	15	14	8499	8518	686
489507	446	465	GAGATCACAGAATCTTCAAT	42	46	8501	8520	687
592732	448	467	GTGAGATCACAGAATCTTCA	n.d.	58	8503	8522	688
592733	450	469	GAGTGAGATCACAGAATCTT	n.d.	45	8505	8524	689
592734	452	471	GAGAGTGAGATCACAGAATC	n.d.	48	8507	8526	690
592735	454	473	CTGAGAGTGAGATCACAGAA	n.d.	66	8509	8528	691
489508	456	475	TCCTGAGAGTGAGATCACAG	n.d.	60	8511	8530	692
333619	458	477	TCTCCTGAGAGTGAGATCAC	n.d.	65	8513	8532	76
592736	460	479	GGTCTCCTGAGAGTGAGATC	n.d.	40	8515	8534	693
592737	462	481	ATGGTCTCCTGAGAGTGAGA	n.d.	37	8517	8536	694
592738	464	483	CAATGGTCTCCTGAGAGTGA	n.d.	41	8519	8538	695
489509	466	485	TGCAATGGTCTCCTGAGAGT	n.d.	43	8521	8540	696
592739	468	487	GATGCAATGGTCTCCTGAGA	n.d.	16	8523	8542	697
592740	470	489	ATGATGCAATGGTCTCCTGA	n.d.	6	8525	8544	698
592741	472	491	CAATGATGCAATGGTCTCCT	n.d.	0	8527	8546	699
592742	474	493	GCCAATGATGCAATGGTCTC	n.d.	25	8529	8548	700
489510	476	495	CGGCCAATGATGCAATGGTC	n.d.	32	8531	8550	701

592743	478	497	TGCGGCCAATGATGCAATGG	n.d.	14	8533	8552	702
592744	480	499	TGTGCGGCCAATGATGCAAT	n.d.	0	8535	8554	703
592745	482	501	AGTGTGCGGCCAATGATGCA	n.d.	7	8537	8556	704
592746	484	503	CCAGTGTGCGGCCAATGATG	n.d.	25	8539	8558	705
489511	486	505	CACCAGTGTGCGGCCAATGA	n.d.	28	8541	8560	706
150460	488	507	ACCACCAGTGTGCGGCCAAT	n.d.	52	8543	8562	77
592747	490	509	GGACCACCAGTGTGCGGCCA	n.d.	44	n/a	n/a	707
592748	492	511	ATGGACCACCAGTGTGCGGC	n.d.	40	n/a	n/a	708
150462	494	513	TCATGGACCACCAGTGTGCG	n.d.	39	n/a	n/a	78
592749	496	515	TTTCATGGACCACCAGTGTG	n.d.	35	n/a	n/a	709
592750	498	517	TTTTTCATGGACCACCAGTG	n.d.	23	n/a	n/a	710
592751	500	519	GCTTTTTCATGGACCACCAG	n.d.	63	n/a	n/a	711
333636	536	555	GTACTTTCTTCATTTCCACC	n.d.	65	9686	9705	79
333638	538	557	TTGTACTTTCTTCATTTCCA	n.d.	66	9688	9707	80
333640	540	559	CTTTGTACTTTCTTCATTTC	n.d.	37	9690	9709	81
592752	543	562	TGTCTTTGTACTTTCTTCAT	n.d.	63	9693	9712	712
592753	545	564	CCTGTCTTTGTACTTTCTTC	n.d.	74	9695	9714	713
592754	547	566	TTCCTGTCTTTGTACTTTCT	n.d.	72	9697	9716	714
592755	549	568	GTTTCCTGTCTTTGTACTTT	n.d.	57	9699	9718	715
592756	568	587	AAGCCAAACGACTTCCAGCG	72	66	9718	9737	716
592757	570	589	ACAAGCCAAACGACTTCCAG	72	74	9720	9739	717
489516	572	591	CCACAAGCCAAACGACTTCC	85	82	9722	9741	718
592758	574	593	CACCACAAGCCAAACGACTT	72	73	9724	9743	719
592759	576	595	TACACCACAAGCCAAACGAC	74	68	9726	9745	720
592760	578	597	ATTACACCACAAGCCAAACG	67	61	9728	9747	721
592761	580	599	CAATTACACCACAAGCCAAA	64	56	9730	9749	722
150466	640	659	GATAACAGATGAGTTAAGGG	66	65	9790	9809	82
489521	642	661	AGGATAACAGATGAGTTAAG	79	78	9792	9811	723
592762	663	682	GGATACATTTCTACAGCTAG	91	87	9813	9832	724
592763	665	684	CAGGATACATTTCTACAGCT	92	89	9815	9834	725
592764	667	686	ATCAGGATACATTTCTACAG	88	83	9817	9836	726
592765	669	688	TTATCAGGATACATTTCTAC	77	72	9819	9838	727
592766	671	690	GTTTATCAGGATACATTTCT	90	89	9821	9840	728
592767	673	692	ATGTTTATCAGGATACATTT	82	76	9823	9842	729
592768	675	694	TAATGTTTATCAGGATACAT	80	79	9825	9844	730
592769	677	696	TTTAATGTTTATCAGGATAC	82	78	9827	9846	731

592770	679	698	TGTTTAATGTTTATCAGGAT	79	75	9829	9848	732
592771	681	700	AGTGTTTAATGTTTATCAGG	84	81	9831	9850	733
489526	692	711	TTTAAGATTACAGTGTTTAA	36	38	9842	9861	734
592772	694	713	CTTTTAAGATTACAGTGTTT	46	47	9844	9863	735
592773	696	715	CACTTTTAAGATTACAGTGT	39	42	9846	9865	736
592774	698	717	TACACTTTTAAGATTACAGT	21	24	9848	9867	737
592775	700	719	ATTACACTTTTAAGATTACA	3	0	9850	9869	738
489527	702	721	CAATTACACTTTTAAGATTA	0	0	9852	9871	739
150467	704	723	CACAATTACACTTTTAAGAT	58	73	9854	9873	83
592776	706	725	CACACAATTACACTTTTAAG	29	5	9856	9875	740
592777	708	727	GTCACACAATTACACTTTTA	59	49	9858	9877	741
592778	710	729	AAGTCACACAATTACACTTT	40	34	9860	9879	742
489528	712	731	AAAAGTCACACAATTACACT	31	27	9862	9881	743
592779	714	733	GAAAAAGTCACACAATTACA	21	7	9864	9883	744
592780	716	735	CTGAAAAAGTCACACAATTA	18	13	9866	9885	745
592781	718	737	CTCTGAAAAAGTCACACAAT	32	26	9868	9887	746
592782	720	739	AACTCTGAAAAAGTCACACA	35	20	9870	9889	747

Table 10

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	74	973	992	21
489529	722	741	GCAACTCTGAAAAAGTCACA	41	9872	9891	748
592783	724	743	AAGCAACTCTGAAAAAGTCA	34	9874	9893	749
592784	727	746	TTAAAGCAACTCTGAAAAAG	4	9877	9896	750
592785	729	748	CTTTAAAGCAACTCTGAAAA	36	9879	9898	751
592786	731	750	TACTTTAAAGCAACTCTGAA	28	9881	9900	752
592787	733	752	GGTACTTTAAAGCAACTCTG	48	9883	9902	753
592788	735	754	CAGGTACTTTAAAGCAACTC	38	9885	9904	754
592789	737	756	TACAGGTACTTTAAAGCAAC	20	9887	9906	755
592790	739	758	ACTACAGGTACTTTAAAGCA	26	9889	9908	756
592791	741	760	TCACTACAGGTACTTTAAAG	34	9891	9910	757
592792	743	762	TCTCACTACAGGTACTTTAA	50	9893	9912	758

592793	745	764	TTTCTCACTACAGGTACTTT	36	9895	9914	759
592794	747	766	AGTTTCTCACTACAGGTACT	53	9897	9916	760
592795	749	768	TCAGTTTCTCACTACAGGTA	37	9899	9918	761
150470	751	770	AATCAGTTTCTCACTACAGG	30	9901	9920	84
592796	753	772	TAAATCAGTTTCTCACTACA	21	9903	9922	762
150472	755	774	CATAAATCAGTTTCTCACTA	37	9905	9924	85
592797	757	776	ATCATAAATCAGTTTCTCAC	35	9907	9926	763
592798	759	778	TGATCATAAATCAGTTTCTC	35	9909	9928	764
592799	761	780	AGTGATCATAAATCAGTTTC	5	9911	9930	765
592800	763	782	CAAGTGATCATAAATCAGTT	21	9913	9932	766
592801	765	784	TCCAAGTGATCATAAATCAG	41	9915	9934	767
592802	767	786	CTTCCAAGTGATCATAAATC	44	9917	9936	768
592803	769	788	ATCTTCCAAGTGATCATAAA	30	9919	9938	769
592804	771	790	AAATCTTCCAAGTGATCATA	32	9921	9940	770
489534	792	811	CTGAGTTTTATAAAACTATA	4	9942	9961	771
150476	794	813	AACTGAGTTTTATAAAACTA	9	9944	9963	86
592805	796	815	TTAACTGAGTTTTATAAAAC	14	9946	9965	772
592806	798	817	TTTTAACTGAGTTTTATAAA	3	9948	9967	773
592807	800	819	CATTTTAACTGAGTTTTATA	13	9950	9969	774
489535	802	821	GACATTTTAACTGAGTTTTA	34	9952	9971	775
592808	804	823	CAGACATTTTAACTGAGTTT	40	9954	9973	776
592809	806	825	AACAGACATTTTAACTGAGT	36	9956	9975	777
592810	808	827	GAAACAGACATTTTAACTGA	25	9958	9977	778
592811	810	829	TTGAAACAGACATTTTAACT	24	9960	9979	779
592812	835	854	TTTAAGTCTGGCAAAATACA	23	9985	10004	780
592813	837	856	GATTTAAGTCTGGCAAAATA	31	9987	10006	781
592814	839	858	GTGATTTAAGTCTGGCAAAA	41	9989	10008	782
592815	841	860	CTGTGATTTAAGTCTGGCAA	49	9991	10010	783
592816	843	862	ATCTGTGATTTAAGTCTGGC	53	9993	10012	784
150481	845	864	CCATCTGTGATTTAAGTCTG	51	9995	10014	87
592817	847	866	ACCCATCTGTGATTTAAGTC	51	9997	10016	785
592818	849	868	ATACCCATCTGTGATTTAAG	43	9999	10018	786
592819	851	870	TAATACCCATCTGTGATTTA	42	10001	10020	787
592820	870	889	AAAGAAATTCTGACAAGTTT	22	10020	10039	788
489542	872	891	ACAAAGAAATTCTGACAAGT	13	10022	10041	789
592821	874	893	TGACAAAGAAATTCTGACAA	24	10024	10043	790

592822	876	895	AATGACAAAGAAATTCTGAC	25	10026	10045	791
592823	878	897	TGAATGACAAAGAAATTCTG	6	10028	10047	792
592824	880	899	CTTGAATGACAAAGAAATTC	24	10030	10049	793
489543	882	901	GGCTTGAATGACAAAGAAAT	29	10032	10051	794
592825	884	903	CAGGCTTGAATGACAAAGAA	35	10034	10053	795
592826	886	905	CACAGGCTTGAATGACAAAG	32	10036	10055	796
592827	888	907	TTCACAGGCTTGAATGACAA	41	10038	10057	797
592828	890	909	TATTCACAGGCTTGAATGAC	30	10040	10059	798
150492	909	928	AAGTGCCATACAGGGTTTTT	32	10059	10078	88
592829	911	930	ATAAGTGCCATACAGGGTTT	0	10061	10080	799
150493	913	932	TAATAAGTGCCATACAGGGT	24	10063	10082	89
592830	915	934	CATAATAAGTGCCATACAGG	26	10065	10084	800
150495	917	936	CTCATAATAAGTGCCATACA	35	10067	10086	90
150496	919	938	GCCTCATAATAAGTGCCATA	37	10069	10088	91
592831	921	940	TAGCCTCATAATAAGTGCCA	19	10071	10090	801
592832	923	942	AATAGCCTCATAATAAGTGC	0	10073	10092	802
592833	925	944	TTAATAGCCTCATAATAAGT	19	10075	10094	803
150497	927	946	TTTTAATAGCCTCATAATAA	17	10077	10096	92
592834	929	948	TCTTTTAATAGCCTCATAAT	27	10079	10098	804
592835	931	950	ATTCTTTTAATAGCCTCATA	27	10081	10100	805
150498	933	952	GGATTCTTTTAATAGCCTCA	39	10083	10102	93
592836	935	954	TTGGATTCTTTTAATAGCCT	24	10085	10104	806
592837	937	956	ATTTGGATTCTTTTAATAGC	0	10087	10106	807
592838	939	958	GAATTTGGATTCTTTTAATA	10	10089	10108	808
592839	941	960	TTGAATTTGGATTCTTTTAA	13	10091	10110	809
592840	943	962	GTTTGAATTTGGATTCTTTT	29	10093	10112	810
592841	945	964	TAGTTTGAATTTGGATTCTT	31	10095	10114	811
592842	947	966	TTTAGTTTGAATTTGGATTC	8	10097	10116	812
592843	949	968	TTTTTAGTTTGAATTTGGAT	10	n/a	n/a	813
592844	951	970	TTTTTTTAGTTTGAATTTGG	7	n/a	n/a	814

Example 2: Inhibition of human SOD-1 in HepG2 cells by MOE gapmers

Modified oligonucleotides were designed targeting a superoxide dismutase 1, soluble (SOD-1) nucleic acid and were tested for their effects on SOD-1 mRNA in vitro. ISIS 146143, ISIS 150438-150440, ISIS 150442, ISIS 150450, ISIS 150455-150457, ISIS 150459, ISIS 150461, ISIS 150469, ISIS 150473, ISIS 150478, ISIS 150484, ISIS 150486, ISIS 150494, ISIS 150508-150510, ISIS 333607, ISIS 333608, ISIS

333611, ISIS 333618, previously disclosed in WO 2005/040180, were also included in this assay. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 5,000 nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR.

Human primer probe set RTS3898 was used to measure mRNA levels. In cases where the oligonucleotide overlapped the amplicon of the primer probe set, an alternative primer probe set, HTS90, was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells. 'n.d.' indicates that inhibition levels were not measured using the particular primer probe set.

The newly designed modified oligonucleotides in the Tables below were designed as 5-10-5 MOE gapmers. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of ten 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000). 'n/a' indicates that the modified oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 11

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	64	973	992	21
596301	550	569	CGTTTCCTGTCTTTGTACTT	n.d.	9700	9719	815
596302	569	588	CAAGCCAAACGACTTCCAGC	54	9719	9738	816
596303	571	590	CACAAGCCAAACGACTTCCA	47	9721	9740	817
596304	573	592	ACCACAAGCCAAACGACTTC	28	9723	9742	818

596305	575	594	ACACCACAAGCCAAACGACT	49	9725	9744	819
596306	577	596	TTACACCACAAGCCAAACGA	24	9727	9746	820
596307	641	660	GGATAACAGATGAGTTAAGG	48	9791	9810	821
596308	664	683	AGGATACATTTCTACAGCTA	79	9814	9833	822
596309	666	685	TCAGGATACATTTCTACAGC	70	9816	9835	823
596310	668	687	TATCAGGATACATTTCTACA	58	9818	9837	824
489524	672	691	TGTTTATCAGGATACATTTC	52	9822	9841	825
596311	674	693	AATGTTTATCAGGATACATT	54	9824	9843	826
596312	676	695	TTAATGTTTATCAGGATACA	34	9826	9845	827
596313	678	697	GTTTAATGTTTATCAGGATA	71	9828	9847	828
596314	680	699	GTGTTTAATGTTTATCAGGA	73	9830	9849	829
596315	693	712	TTTTAAGATTACAGTGTTTA	13	9843	9862	830
596316	695	714	ACTTTTAAGATTACAGTGTT	24	9845	9864	831
596317	697	716	ACACTTTTAAGATTACAGTG	15	9847	9866	832
596318	699	718	TTACACTTTTAAGATTACAG	0	9849	9868	833
596319	701	720	AATTACACTTTTAAGATTAC	1	9851	9870	834
596320	705	724	ACACAATTACACTTTTAAGA	0	9855	9874	835
596321	707	726	TCACACAATTACACTTTTAA	15	9857	9876	836
596322	711	730	AAAGTCACACAATTACACTT	15	9861	9880	837
596323	715	734	TGAAAAAGTCACACAATTAC	0	9865	9884	838
596324	717	736	TCTGAAAAAGTCACACAATT	5	9867	9886	839
596325	719	738	ACTCTGAAAAAGTCACACAA	21	9869	9888	840
596326	723	742	AGCAACTCTGAAAAAGTCAC	14	9873	9892	841
596327	730	749	ACTTTAAAGCAACTCTGAAA	0	9880	9899	842
489530	732	751	GTACTTTAAAGCAACTCTGA	22	9882	9901	843
596328	734	753	AGGTACTTTAAAGCAACTCT	36	9884	9903	844
596329	740	759	CACTACAGGTACTTTAAAGC	18	9890	9909	845
150469	742	761	CTCACTACAGGTACTTTAAA	25	9892	9911	94
596330	744	763	TTCTCACTACAGGTACTTTA	28	9894	9913	846
596331	746	765	GTTTCTCACTACAGGTACTT	30	9896	9915	847
596332	748	767	CAGTTTCTCACTACAGGTAC	25	9898	9917	848
596333	750	769	ATCAGTTTCTCACTACAGGT	22	9900	9919	849
489531	752	771	AAATCAGTTTCTCACTACAG	0	9902	9921	850
596334	756	775	TCATAAATCAGTTTCTCACT	21	9906	9925	851
596335	760	779	GTGATCATAAATCAGTTTCT	37	9910	9929	852
489532	762	781	AAGTGATCATAAATCAGTTT	8	9912	9931	853

596336	764	783	CCAAGTGATCATAAATCAGT	39	9914	9933	854
436935	766	785	TTCCAAGTGATCATAAATCA	18	9916	9935	855
596337	768	787	TCTTCCAAGTGATCATAAAT	12	9918	9937	856
150473	770	789	AATCTTCCAAGTGATCATAA	4	9920	9939	95
596338	795	814	TAACTGAGTTTTATAAAACT	0	9945	9964	857
596339	807	826	AAACAGACATTTTAACTGAG	4	9957	9976	858
596340	809	828	TGAAACAGACATTTTAACTG	0	9959	9978	859
150478	811	830	ATTGAAACAGACATTTTAAC	0	9961	9980	96
596341	836	855	ATTTAAGTCTGGCAAAATAC	16	9986	10005	860
596342	840	859	TGTGATTTAAGTCTGGCAAA	34	9990	10009	861
489539	842	861	TCTGTGATTTAAGTCTGGCA	44	9992	10011	862
596343	844	863	CATCTGTGATTTAAGTCTGG	29	9994	10013	863
596344	846	865	CCCATCTGTGATTTAAGTCT	41	9996	10015	864
596345	848	867	TACCCATCTGTGATTTAAGT	50	9998	10017	865
596346	850	869	AATACCCATCTGTGATTTAA	0	10000	10019	866
489540	852	871	TTAATACCCATCTGTGATTT	11	10002	10021	867
150484	871	890	CAAAGAAATTCTGACAAGTT	7	10021	10040	97
596347	873	892	GACAAAGAAATTCTGACAAG	8	10023	10042	868
596348	877	896	GAATGACAAAGAAATTCTGA	0	10027	10046	869
596349	883	902	AGGCTTGAATGACAAAGAAA	27	10033	10052	870
150486	885	904	ACAGGCTTGAATGACAAAGA	19	10035	10054	98
596350	910	929	TAAGTGCCATACAGGGTTTT	13	10060	10079	871
596351	914	933	ATAATAAGTGCCATACAGGG	18	10064	10083	872
150494	916	935	TCATAATAAGTGCCATACAG	0	10066	10085	99
596352	918	937	CCTCATAATAAGTGCCATAC	23	10068	10087	873
596353	920	939	AGCCTCATAATAAGTGCCAT	6	10070	10089	874
596354	922	941	ATAGCCTCATAATAAGTGCC	19	10072	10091	875
596355	928	947	CTTTTAATAGCCTCATAATA	0	10078	10097	876
596356	930	949	TTCTTTTAATAGCCTCATAA	5	10080	10099	877
596357	932	951	GATTCTTTTAATAGCCTCAT	4	10082	10101	878
596358	934	953	TGGATTCTTTTAATAGCCTC	13	10084	10103	879
596359	936	955	TTTGGATTCTTTTAATAGCC	14	10086	10105	880
596360	938	957	AATTTGGATTCTTTTAATAG	14	10088	10107	881
596361	940	959	TGAATTTGGATTCTTTTAAT	0	10090	10109	882
596362	946	965	TTAGTTTGAATTTGGATTCT	0	10096	10115	883
596363	948	967	TTTTAGTTTGAATTTGGATT	0	n/a	n/a	884

596364	950	969	TTTTTTAGTTTGAATTTGGA	0	n/a	n/a	885

Table 12

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition with RTS3898	% inhibition with HTS90	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	66	n.d.	973	992	21
596230	246	265	CAGTCCTTTAATGCTTCCCC	51	40	5000	5019	886
596231	248	267	GTCAGTCCTTTAATGCTTCC	34	34	5002	5021	887
596232	250	269	CAGTCAGTCCTTTAATGCTT	35	29	5004	5023	888
596233	252	271	TTCAGTCAGTCCTTTAATGC	24	21	5006	5025	889
596234	256	275	GGCCTTCAGTCAGTCCTTTA	41	39	5010	5029	890
150450	258	277	CAGGCCTTCAGTCAGTCCTT	56	51	5012	5031	100
596235	260	279	TGCAGGCCTTCAGTCAGTCC	42	46	5014	5033	891
596236	262	281	CATGCAGGCCTTCAGTCAGT	37	33	5016	5035	892
596237	278	297	TCATGAACATGGAATCCATG	24	19	5032	5051	893
596238	280	299	ACTCATGAACATGGAATCCA	27	20	5034	5053	894
596239	295	314	CTGTATTATCTCCAAACTCA	32	28	5049	5068	895
596240	309	328	ACTGGTACAGCCTGCTGTAT	22	28	n/a	n/a	896
596241	311	330	GCACTGGTACAGCCTGCTGT	31	24	n/a	n/a	897
596242	313	332	CTGCACTGGTACAGCCTGCT	38	29	n/a	n/a	898
596243	315	334	ACCTGCACTGGTACAGCCTG	46	48	n/a	n/a	899
596244	341	360	TTTCTGGATAGAGGATTAAA	6	14	7657	7676	900
596245	343	362	GTTTTCTGGATAGAGGATTA	28	39	7659	7678	901
596246	347	366	CCGTGTTTTCTGGATAGAGG	44	37	7663	7682	902
596247	349	368	CACCGTGTTTTCTGGATAGA	24	11	7665	7684	903
596248	351	370	CCCACCGTGTTTTCTGGATA	46	40	7667	7686	904
596249	353	372	GGCCCACCGTGTTTTCTGGA	46	41	7669	7688	905
596250	355	374	TTGGCCCACCGTGTTTTCTG	35	26	7671	7690	906
596251	357	376	CTTTGGCCCACCGTGTTTTC	31	15	7673	7692	907
596252	359	378	TCCTTTGGCCCACCGTGTTT	30	23	7675	7694	908
596253	383	402	AAGTCTCCAACATGCCTCTC	20	6	n/a	n/a	909
596254	387	406	GCCCAAGTCTCCAACATGCC	61	53	8442	8461	910
596255	389	408	TTGCCCAAGTCTCCAACATG	41	33	8444	8463	911
596256	391	410	CATTGCCCAAGTCTCCAACA	39	25	8446	8465	912

150455	393	412	CACATTGCCCAAGTCTCCAA	36	19	8448	8467	101
596257	397	416	CAGTCACATTGCCCAAGTCT	40	27	8452	8471	913
596258	401	420	TCAGCAGTCACATTGCCCAA	52	42	8456	8475	914
596259	403	422	TGTCAGCAGTCACATTGCCC	55	49	8458	8477	915
596260	405	424	TTTGTCAGCAGTCACATTGC	26	16	8460	8479	916
596261	407	426	TCTTTGTCAGCAGTCACATT	20	11	8462	8481	917
596262	409	428	CATCTTTGTCAGCAGTCACA	34	13	8464	8483	918
596263	411	430	ACCATCTTTGTCAGCAGTCA	41	30	8466	8485	919
596264	415	434	CCACACCATCTTTGTCAGCA	39	20	8470	8489	920
596265	417	436	GGCCACACCATCTTTGTCAG	23	5	8472	8491	921
150456	419	438	TCGGCCACACCATCTTTGTC	32	28	8474	8493	102
150457	421	440	CATCGGCCACACCATCTTTG	34	38	8476	8495	103
596266	423	442	CACATCGGCCACACCATCTT	27	13	8478	8497	922
596267	425	444	GACACATCGGCCACACCATC	45	30	8480	8499	923
150459	427	446	TAGACACATCGGCCACACCA	46	36	8482	8501	104
596268	429	448	AATAGACACATCGGCCACAC	30	25	8484	8503	924
596269	431	450	TCAATAGACACATCGGCCAC	35	0	8486	8505	925
596270	433	452	CTTCAATAGACACATCGGCC	39	16	8488	8507	926
596271	435	454	ATCTTCAATAGACACATCGG	16	0	8490	8509	927
596272	437	456	GAATCTTCAATAGACACATC	22	11	8492	8511	928
596273	439	458	CAGAATCTTCAATAGACACA	17	0	8494	8513	929
596274	441	460	CACAGAATCTTCAATAGACA	10	14	8496	8515	930
596275	443	462	ATCACAGAATCTTCAATAGA	11	10	8498	8517	931
596276	445	464	AGATCACAGAATCTTCAATA	14	29	8500	8519	932
596277	447	466	TGAGATCACAGAATCTTCAA	n.d.	30	8502	8521	933
596278	449	468	AGTGAGATCACAGAATCTTC	n.d.	30	8504	8523	934
596279	453	472	TGAGAGTGAGATCACAGAAT	n.d.	18	8508	8527	935
333618	457	476	CTCCTGAGAGTGAGATCACA	n.d.	27	8512	8531	105
596281	459	478	GTCTCCTGAGAGTGAGATCA	n.d.	23	8514	8533	936
596282	461	480	TGGTCTCCTGAGAGTGAGAT	n.d.	24	8516	8535	937
596283	463	482	AATGGTCTCCTGAGAGTGAG	n.d.	22	8518	8537	938
596284	465	484	GCAATGGTCTCCTGAGAGTG	n.d.	57	8520	8539	939
596285	467	486	ATGCAATGGTCTCCTGAGAG	n.d.	0	8522	8541	940
596286	469	488	TGATGCAATGGTCTCCTGAG	n.d.	1	8524	8543	941
596287	471	490	AATGATGCAATGGTCTCCTG	n.d.	0	8526	8545	942
596288	473	492	CCAATGATGCAATGGTCTCC	n.d.	8	8528	8547	943

596289	475	494	GGCCAATGATGCAATGGTCT	n.d.	9	8530	8549	944
596290	477	496	GCGGCCAATGATGCAATGGT	n.d.	13	8532	8551	945
596291	479	498	GTGCGGCCAATGATGCAATG	n.d.	12	8534	8553	946
596292	481	500	GTGTGCGGCCAATGATGCAA	n.d.	15	8536	8555	947
596293	483	502	CAGTGTGCGGCCAATGATGC	n.d.	0	8538	8557	948
596294	485	504	ACCAGTGTGCGGCCAATGAT	n.d.	0	8540	8559	949
596295	487	506	CCACCAGTGTGCGGCCAATG	n.d.	22	8542	8561	950
596296	489	508	GACCACCAGTGTGCGGCCAA	n.d.	16	n/a	n/a	951
596297	491	510	TGGACCACCAGTGTGCGGCC	n.d.	28	n/a	n/a	952
150461	493	512	CATGGACCACCAGTGTGCGG	n.d.	25	n/a	n/a	106
596298	495	514	TTCATGGACCACCAGTGTGC	n.d.	21	n/a	n/a	953
596299	497	516	TTTTCATGGACCACCAGTGT	n.d.	17	n/a	n/a	954
596300	499	518	CTTTTTCATGGACCACCAGT	n.d.	9	n/a	n/a	955

Example 3: Inhibition of human SOD-1 in HepG2 cells by deoxy, MOE and cEt gapmers

Modified oligonucleotides were designed targeting a superoxide dismutase 1, soluble (SOD-1) nucleic acid and were tested for their effects on SOD-1 mRNA in vitro. ISIS 333611, which was previously described in WO 2005/040180, was included as a benchmark. ISIS 590067, ISIS 590074, ISIS 590082, ISIS 590130, ISIS 590138, and ISIS 590146, which are 5-10-5 MOE gapmers as described above in Example 1, were also included in this assay. ISIS 590512, which has a similar sequence as ISIS 333611 but with deoxy, MOE, and cEt sugar modifications, was also included in this study.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 3,000 nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR.

Human primer probe set RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells. 'n.d.' indicates that inhibition levels were not measured.

The newly designed modified oligonucleotides in the Tables below were designed as deoxy, MOE, and cEt gapmers. The gapmers are 17 nucleosides in length wherein each nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety. The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose;

and 'e' indicates a 2'-MOE modified sugar. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000). 'n/a' indicates that the modified oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 13

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
590434	1	17	CCACTCTGGCCC CAAAC	eeekkddddddddkkeee	17	807	823	956
590435	2	18	CCCACTCTGGCC CCAAA	eeekkddddddddkkeee	15	808	824	957
590436	3	19	GCCCACTCTGGC CCCAA	eeekkddddddddkkeee	22	809	825	958
590437	4	20	CGCCCACTCTGG CCCCA	eeekkddddddddkkeee	14	810	826	959
590438	35	51	CGACTACTTTAT AGGCC	eeekkddddddddkkeee	12	841	857	960
590439	36	52	GCGACTACTTTA TAGGC	eeekkddddddddkkeee	12	842	858	961
590440	37	53	CGCGACTACTTT ATAGG	eeekkddddddddkkeee	11	843	859	962
590441	38	54	CCGCGACTACTT TATAG	eeekkddddddddkkeee	5	844	860	963
590442	76	92	CGCTGCAGGAGA CTACG	eeekkddddddddkkeee	0	882	898	964
590443	77	93	ACGCTGCAGGAG ACTAC	eeekkddddddddkkeee	25	883	899	965
590444	167	183	TCGCCCTTCAGC ACGCA	eeekkddddddddkkeee	31	973	989	966
590445	168	184	GTCGCCCTTCAG CACGC	eeekkddddddddkkeee	28	974	990	967
590512	169	185	CGTCGCCCTTCA GCACG	eeekkddddddddkkeee	8	975	991	968
590446	170	186	CCGTCGCCCTTC AGCAC	eeekkddddddddkkeee	27	976	992	969

590447	171	187	GCCGTCGCCCTTCAGCA	eeekkddddddddkkeee	33	977	993	970
590448	202	218	TCTGCTCGAAATTGATG	eeekkddddddddkkeee	34	1008	1024	971
590449	203	219	TTCTGCTCGAAATTGAT	eeekkddddddddkkeee	18	1009	1025	972
590450	204	220	CTTCTGCTCGAAATTGA	eeekkddddddddkkeee	13	1010	1026	973
590451	205	221	CCTTCTGCTCGAAATTG	eeekkddddddddkkeee	16	1011	1027	974
590452	206	222	TCCTTCTGCTCGAAATT	eeekkddddddddkkeee	14	n/a	n/a	975
590453	207	223	TTCCTTCTGCTCGAAAT	eeekkddddddddkkeee	13	n/a	n/a	976
590454	208	224	TTTCCTTCTGCTCGAAA	eeekkddddddddkkeee	6	n/a	n/a	977
590455	209	225	CTTTCCTTCTGCTCGAA	eeekkddddddddkkeee	0	n/a	n/a	978
590456	210	226	ACTTTCCTTCTGCTCGA	eeekkddddddddkkeee	0	n/a	n/a	979
590457	211	227	TACTTTCCTTCTGCTCG	eeekkddddddddkkeee	n.d.	n/a	n/a	980
590458	212	228	TTACTTTCCTTCTGCTC	eeekkddddddddkkeee	n.d.	n/a	n/a	981
590459	213	229	ATTACTTTCCTTCTGCT	eeekkddddddddkkeee	n.d.	n/a	n/a	982
590461	214	230	CATTACTTTCCTTCTGC	eeekkddddddddkkeee	n.d.	n/a	n/a	983
590462	215	231	CCATTACTTTCCTTCTG	eeekkddddddddkkeee	n.d.	n/a	n/a	984
590463	216	232	TCCATTACTTTCCTTCT	eeekkddddddddkkeee	n.d.	n/a	n/a	985
590464	217	233	GTCCATTACTTTCCTTC	eeekkddddddddkkeee	n.d.	n/a	n/a	986
590465	218	234	GGTCCATTACTTTCCTT	eeekkddddddddkkeee	n.d.	4972	4988	987
590466	219	235	TGGTCCATTACTTTCCT	eeekkddddddddkkeee	5	4973	4989	988
590467	220	236	CTGGTCCATTACTTTCC	eeekkddddddddkkeee	11	4974	4990	989
590468	221	237	ACTGGTCCATTACTTTC	eeekkddddddddkkeee	14	4975	4991	990
590469	222	238	CACTGGTCCATTACTTT	eeekkddddddddkkeee	12	4976	4992	991
590470	223	239	TCACTGGTCCATTACTT	eeekkddddddddkkeee	15	4977	4993	992
590471	224	240	TTCACTGGTCCATTACT	eeekkddddddddkkeee	14	4978	4994	993
590472	225	241	CTTCACTGGTCCATTAC	eeekkddddddddkkeee	11	4979	4995	994
590473	226	242	CCTTCACTGGTCCATTA	eeekkddddddddkkeee	8	4980	4996	995

590474	227	243	ACCTTCACTGGT CCATT	eeekkddddddddkkeee	44	4981	4997	996
590475	228	244	CACCTTCACTGG TCCAT	eeekkddddddddkkeee	53	4982	4998	997
590476	229	245	ACACCTTCACTG GTCCA	eeekkddddddddkkeee	20	4983	4999	998
590477	230	246	CACACCTTCACT GGTCC	eeekkddddddddkkeee	12	4984	5000	999
590478	231	247	CCACACCTTCAC TGGTC	eeekkddddddddkkeee	36	4985	5001	1000
590479	232	248	CCCACACCTTCA CTGGT	eeekkddddddddkkeee	18	4986	5002	1001
590480	233	249	CCCCACACCTTC ACTGG	eeekkddddddddkkeee	14	4987	5003	1002
590481	235	251	TTCCCCACACCT TCACT	eeekkddddddddkkeee	8	4989	5005	1003
590482	236	252	CTTCCCCACACC TTCAC	eeekkddddddddkkeee	29	4990	5006	1004
590483	237	253	GCTTCCCCACAC CTTCA	eeekkddddddddkkeee	36	4991	5007	1005
590484	238	254	TGCTTCCCCACA CCTTC	eeekkddddddddkkeee	43	4992	5008	1006
590485	239	255	ATGCTTCCCCAC ACCTT	eeekkddddddddkkeee	41	4993	5009	1007
590486	240	256	AATGCTTCCCCA CACCT	eeekkddddddddkkeee	35	4994	5010	1008
590487	241	257	TAATGCTTCCCC ACACC	eeekkddddddddkkeee	52	4995	5011	1009
590488	264	280	ATGCAGGCCTTC AGTCA	eeekkddddddddkkeee	37	5018	5034	1010
590489	265	281	CATGCAGGCCTT CAGTC	eeekkddddddddkkeee	41	5019	5035	1011
590490	266	282	CCATGCAGGCCT TCAGT	eeekkddddddddkkeee	21	5020	5036	1012
590491	267	283	TCCATGCAGGCC TTCAG	eeekkddddddddkkeee	18	5021	5037	1013
590492	268	284	ATCCATGCAGGC CTTCA	eeekkddddddddkkeee	27	5022	5038	1014
590493	269	285	AATCCATGCAGG CCTTC	eeekkddddddddkkeee	13	5023	5039	1015
590494	270	286	GAATCCATGCAG GCCTT	eeekkddddddddkkeee	9	5024	5040	1016
590495	271	287	GGAATCCATGCA GGCCT	eeekkddddddddkkeee	7	5025	5041	1017
590496	272	288	TGGAATCCATGC AGGCC	eeekkddddddddkkeee	12	5026	5042	1018
590497	273	289	ATGGAATCCATG CAGGC	eeekkddddddddkkeee	9	5027	5043	1019
590498	274	290	CATGGAATCCAT GCAGG	eeekkddddddddkkeee	14	5028	5044	1020
590499	275	291	ACATGGAATCCA TGCAG	eeekkddddddddkkeee	0	5029	5045	1021

590500	276	292	AACATGGAATCCATGCA	eeekkddddddddkkeee	10	5030	5046	1022
590501	277	293	GAACATGGAATCCATGC	eeekkddddddddkkeee	9	5031	5047	1023
590502	278	294	TGAACATGGAATCCATG	eeekkddddddddkkeee	2	5032	5048	1024
590503	279	295	ATGAACATGGAATCCAT	eeekkddddddddkkeee	8	5033	5049	1025
590504	316	332	CTGCACTGGTACAGCCT	eeekkddddddddkkeee	3	7632	7648	1026
590505	317	333	CCTGCACTGGTACAGCC	eeekkddddddddkkeee	17	7633	7649	1027
590506	318	334	ACCTGCACTGGTACAGC	eeekkddddddddkkeee	12	7634	7650	1028
590507	319	335	GACCTGCACTGGTACAG	eeekkddddddddkkeee	7	7635	7651	1029
590508	320	336	GGACCTGCACTGGTACA	eeekkddddddddkkeee	7	7636	7652	1030
590509	321	337	AGGACCTGCACTGGTAC	eeekkddddddddkkeee	4	7637	7653	1031
590510	322	338	GAGGACCTGCACTGGTA	eeekkddddddddkkeee	17	7638	7654	1032
590511	323	339	TGAGGACCTGCACTGGT	eeekkddddddddkkeee	8	7639	7655	1033

Table 14

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
590512	169	185	CGTCGCCCTTCAGCACG	eeekkddddddddkkeee	45	975	991	968
590513	324	340	GTGAGGACCTGCACTGG	eeekkddddddddkkeee	21	7640	7656	1034
590514	325	341	AGTGAGGACCTGCACTG	eeekkddddddddkkeee	21	7641	7657	1035
590515	326	342	AAGTGAGGACCTGCACT	eeekkddddddddkkeee	16	7642	7658	1036
590516	327	343	AAAGTGAGGACCTGCAC	eeekkddddddddkkeee	20	7643	7659	1037
590517	328	344	TAAAGTGAGGACCTGCA	eeekkddddddddkkeee	19	7644	7660	1038
590518	329	345	TTAAAGTGAGGACCTGC	eeekkddddddddkkeee	14	7645	7661	1039
590519	330	346	ATTAAAGTGAGGACCTG	eeekkddddddddkkeee	51	7646	7662	1040
590520	331	347	GATTAAAGTGAGGACCT	eeekkddddddddkkeee	8	7647	7663	1041

590521	332	348	GGATTAAAGTG AGGACC	eeekkddddddkkeee	30	7648	7664	1042
590522	333	349	AGGATTAAAGT GAGGAC	eeekkddddddkkeee	23	7649	7665	1043
590523	334	350	GAGGATTAAAG TGAGGA	eeekkddddddkkeee	40	7650	7666	1044
590524	335	351	AGAGGATTAAA GTGAGG	eeekkddddddkkeee	16	7651	7667	1045
590525	336	352	TAGAGGATTAA AGTGAG	eeekkddddddkkeee	21	7652	7668	1046
590526	337	353	ATAGAGGATTA AAGTGA	eeekkddddddkkeee	9	7653	7669	1047
590527	338	354	GATAGAGGATT AAAGTG	eeekkddddddkkeee	8	7654	7670	1048
590528	339	355	GGATAGAGGAT TAAAGT	eeekkddddddkkeee	14	7655	7671	1049
590530	340	356	TGGATAGAGGA TTAAAG	eeekkddddddkkeee	23	7656	7672	1050
590531	341	357	CTGGATAGAGG ATTAAA	eeekkddddddkkeee	26	7657	7673	1051
590532	342	358	TCTGGATAGAG GATTAA	eeekkddddddkkeee	25	7658	7674	1052
590533	360	376	CTTTGGCCCACC GTGTT	eeekkddddddkkeee	41	7676	7692	1053
590534	361	377	CCTTTGGCCCAC CGTGT	eeekkddddddkkeee	46	7677	7693	1054
590535	362	378	TCCTTTGGCCCA CCGTG	eeekkddddddkkeee	39	7678	7694	1055
590536	363	379	ATCCTTTGGCCC ACCGT	eeekkddddddkkeee	n.d.	7679	7695	1056
590537	364	380	CATCCTTTGGCC CACCG	eeekkddddddkkeee	n.d.	7680	7696	1057
590538	365	381	TCATCCTTTGGC CCACC	eeekkddddddkkeee	n.d.	7681	7697	1058
590539	366	382	TTCATCCTTTGG CCCAC	eeekkddddddkkeee	n.d.	7682	7698	1059
590540	367	383	CTTCATCCTTTG GCCCA	eeekkddddddkkeee	n.d.	7683	7699	1060
590541	368	384	TCTTCATCCTTT GGCCC	eeekkddddddkkeee	n.d.	7684	7700	1061
590542	369	385	CTCTTCATCCTT TGGCC	eeekkddddddkkeee	n.d.	7685	7701	1062
590543	370	386	TCTCTTCATCCT TTGGC	eeekkddddddkkeee	n.d.	7686	7702	1063
590544	371	387	CTCTCTTCATCC TTTGG	eeekkddddddkkeee	2	7687	7703	1064
590545	374	390	TGCCTCTCTTCA TCCTT	eeekkddddddkkeee	6	n/a	n/a	1065
590546	375	391	ATGCCTCTCTTC ATCCT	eeekkddddddkkeee	0	n/a	n/a	1066
590547	376	392	CATGCCTCTCTT CATCC	eeekkddddddkkeee	14	n/a	n/a	1067

590548	377	393	ACATGCCTCTCT TCATC	eeekkddddddkkeee	0	n/a	n/a	1068
590549	378	394	AACATGCCTCTC TTCAT	eeekkddddddkkeee	13	n/a	n/a	1069
590550	379	395	CAACATGCCTCT CTTCA	eeekkddddddkkeee	3	n/a	n/a	1070
590551	380	396	CCAACATGCCTC TCTTC	eeekkddddddkkeee	0	n/a	n/a	1071
590552	381	397	TCCAACATGCCT CTCTT	eeekkddddddkkeee	0	n/a	n/a	1072
590553	382	398	CTCCAACATGCC TCTCT	eeekkddddddkkeee	5	n/a	n/a	1073
590554	383	399	TCTCCAACATGC CTCTC	eeekkddddddkkeee	10	n/a	n/a	1074
590555	384	400	GTCTCCAACATG CCTCT	eeekkddddddkkeee	8	n/a	n/a	1075
590556	402	418	AGCAGTCACATT GCCCA	eeekkddddddkkeee	18	8457	8473	1076
590557	403	419	CAGCAGTCACA TTGCCC	eeekkddddddkkeee	7	8458	8474	1077
590558	429	445	AGACACATCGG CCACAC	eeekkddddddkkeee	21	8484	8500	1078
590559	436	452	CTTCAATAGACA CATCG	eeekkddddddkkeee	9	8491	8507	1079
590560	449	465	GAGATCACAGA ATCTTC	eeekkddddddkkeee	13	8504	8520	1080
590561	501	517	TTTTTCATGGAC CACCA	eeekkddddddkkeee	76	n/a	n/a	1081
590562	502	518	CTTTTTCATGGA CCACC	eeekkddddddkkeee	87	n/a	n/a	1082
590563	503	519	GCTTTTTCATGG ACCAC	eeekkddddddkkeee	71	n/a	n/a	1083
590564	504	520	TGCTTTTTCATG GACCA	eeekkddddddkkeee	51	n/a	n/a	1084
590565	505	521	CTGCTTTTTCAT GGACC	eeekkddddddkkeee	65	9655	9671	1085
590566	506	522	TCTGCTTTTTCA TGGAC	eeekkddddddkkeee	55	9656	9672	1086
590567	507	523	ATCTGCTTTTTC ATGGA	eeekkddddddkkeee	42	9657	9673	1087
590568	508	524	CATCTGCTTTTT CATGG	eeekkddddddkkeee	70	9658	9674	1088
590569	509	525	TCATCTGCTTTT TCATG	eeekkddddddkkeee	71	9659	9675	1089
590570	510	526	GTCATCTGCTTT TTCAT	eeekkddddddkkeee	74	9660	9676	1090
590571	511	527	AGTCATCTGCTT TTTCA	eeekkddddddkkeee	76	9661	9677	1091
590572	512	528	AAGTCATCTGCT TTTTC	eeekkddddddkkeee	83	9662	9678	1092
590573	513	529	CAAGTCATCTGC TTTTT	eeekkddddddkkeee	42	9663	9679	1093

590574	514	530	CCAAGTCATCTG CTTTT	eeekkddddddkkeee	50	9664	9680	1094
590575	515	531	CCCAAGTCATCT GCTTT	eeekkddddddkkeee	72	9665	9681	1095
590576	516	532	GCCCAAGTCATC TGCTT	eeekkddddddkkeee	93	9666	9682	1096
590577	517	533	TGCCCAAGTCAT CTGCT	eeekkddddddkkeee	90	9667	9683	1097
590578	518	534	TTGCCCAAGTCA TCTGC	eeekkddddddkkeee	92	9668	9684	1098
590579	524	540	CCACCTTTGCCC AAGTC	eeekkddddddkkeee	91	9674	9690	1099
590580	525	541	TCCACCTTTGCC CAAGT	eeekkddddddkkeee	88	9675	9691	1100
590581	526	542	TTCCACCTTTGC CCAAG	eeekkddddddkkeee	87	9676	9692	1101
590582	527	543	TTTCCACCTTTG CCCAA	eeekkddddddkkeee	78	9677	9693	1102
590583	528	544	ATTTCCACCTTT GCCCA	eeekkddddddkkeee	63	9678	9694	1103
590584	529	545	CATTTCCACCTT TGCCC	eeekkddddddkkeee	73	9679	9695	1104
590585	530	546	TCATTTCCACCT TTGCC	eeekkddddddkkeee	57	9680	9696	1105
590586	531	547	TTCATTTCCACC TTTGC	eeekkddddddkkeee	33	9681	9697	1106
590587	533	549	TCTTCATTTCCA CCTTT	eeekkddddddkkeee	31	9683	9699	1107
590588	536	552	CTTTCTTCATTT CCACC	eeekkddddddkkeee	11	9686	9702	1108
590589	537	553	ACTTTCTTCATT TCCAC	eeekkddddddkkeee	15	9687	9703	1109
590590	538	554	TACTTTCTTCAT TTCCA	eeekkddddddkkeee	18	9688	9704	1110

Table 15

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
590512	169	185	CGTCGCCCTTCAG CACG	eeekkddddddkkeee	21	975	991	968
590591	582	598	AATTACACCACA AGCCA	eeekkddddddkkeee	21	9732	9748	1111
590592	583	599	CAATTACACCAC AAGCC	eeekkddddddkkeee	33	9733	9749	1112
590593	584	600	CCAATTACACCA CAAGC	eeekkddddddkkeee	29	9734	9750	1113

590594	585	601	CCCAATTACACC ACAAG	eeekkddddddkkeee	29	9735	9751	1114
590595	588	604	GATCCCAATTAC ACCAC	eeekkddddddkkeee	3	9738	9754	1115
590596	589	605	CGATCCCAATTAC ACCA	eeekkddddddkkeee	12	9739	9755	1116
590597	590	606	GCGATCCCAATT ACACC	eeekkddddddkkeee	19	9740	9756	1117
590598	591	607	GGCGATCCCAAT TACAC	eeekkddddddkkeee	9	9741	9757	1118
590599	592	608	GGGCGATCCCAA TTACA	eeekkddddddkkeee	18	9742	9758	1119
590600	593	609	TGGGCGATCCCA ATTAC	eeekkddddddkkeee	20	9743	9759	1120
590601	594	610	TTGGGCGATCCC AATTA	eeekkddddddkkeee	26	9744	9760	1121
590602	595	611	ATTGGGCGATCC CAATT	eeekkddddddkkeee	19	9745	9761	1122
590603	596	612	TATTGGGCGATCC CAAT	eeekkddddddkkeee	3	9746	9762	1123
590604	597	613	TTATTGGGCGATC CCAA	eeekkddddddkkeee	15	9747	9763	1124
590605	598	614	TTTATTGGGCGAT CCCA	eeekkddddddkkeee	20	9748	9764	1125
590606	599	615	GTTTATTGGGCGA TCCC	eeekkddddddkkeee	18	9749	9765	1126
590607	600	616	TGTTTATTGGGCG ATCC	eeekkddddddkkeee	21	9750	9766	1127
590608	601	617	ATGTTTATTGGGC GATC	eeekkddddddkkeee	28	9751	9767	1128
590609	602	618	AATGTTTATTGGG CGAT	eeekkddddddkkeee	30	9752	9768	1129
590610	603	619	GAATGTTTATTGG GCGA	eeekkddddddkkeee	14	9753	9769	1130
590611	604	620	GGAATGTTTATTG GGCG	eeekkddddddkkeee	15	9754	9770	1131
590612	607	623	AAGGGAATGTTT ATTGG	eeekkddddddkkeee	2	9757	9773	1132
590613	608	624	CAAGGGAATGTT TATTG	eeekkddddddkkeee	n.d.	9758	9774	1133
590614	609	625	CCAAGGGAATGT TTATT	eeekkddddddkkeee	n.d.	9759	9775	1134
590615	610	626	TCCAAGGGAATG TTTAT	eeekkddddddkkeee	n.d.	9760	9776	1135
590616	611	627	ATCCAAGGGAAT GTTTA	eeekkddddddkkeee	n.d.	9761	9777	1136
590617	612	628	CATCCAAGGGAA TGTTT	eeekkddddddkkeee	n.d.	9762	9778	1137
590618	613	629	ACATCCAAGGGA ATGTT	eeekkddddddkkeee	n.d.	9763	9779	1138
590619	614	630	TACATCCAAGGG AATGT	eeekkddddddkkeee	n.d.	9764	9780	1139

590620	615	631	CTACATCCAAGG GAATG	eeekkddddddkkeee	n.d.	9765	9781	1140
590621	616	632	ACTACATCCAAG GGAAT	eeekkddddddkkeee	7	9766	9782	1141
590622	617	633	GACTACATCCAA GGGAA	eeekkddddddkkeee	19	9767	9783	1142
590623	618	634	AGACTACATCCA AGGGA	eeekkddddddkkeee	39	9768	9784	1143
590624	619	635	CAGACTACATCC AAGGG	eeekkddddddkkeee	53	9769	9785	1144
590625	620	636	TCAGACTACATCC AAGG	eeekkddddddkkeee	57	9770	9786	1145
590626	621	637	CTCAGACTACATC CAAG	eeekkddddddkkeee	76	9771	9787	1146
590627	622	638	CCTCAGACTACAT CCAA	eeekkddddddkkeee	58	9772	9788	1147
590628	623	639	GCCTCAGACTAC ATCCA	eeekkddddddkkeee	43	9773	9789	1148
590629	624	640	GGCCTCAGACTA CATCC	eeekkddddddkkeee	24	9774	9790	1149
590630	625	641	GGGCCTCAGACT ACATC	eeekkddddddkkeee	24	9775	9791	1150
590631	643	659	GATAACAGATGA GTTAA	eeekkddddddkkeee	11	9793	9809	1151
590632	644	660	GGATAACAGATG AGTTA	eeekkddddddkkeee	32	9794	9810	1152
590633	645	661	AGGATAACAGAT GAGTT	eeekkddddddkkeee	45	9795	9811	1153
590634	646	662	CAGGATAACAGA TGAGT	eeekkddddddkkeee	65	9796	9812	1154
590635	647	663	GCAGGATAACAG ATGAG	eeekkddddddkkeee	58	9797	9813	1155
590636	648	664	AGCAGGATAACA GATGA	eeekkddddddkkeee	45	9798	9814	1156
590637	649	665	TAGCAGGATAAC AGATG	eeekkddddddkkeee	34	9799	9815	1157
590638	650	666	CTAGCAGGATAA CAGAT	eeekkddddddkkeee	39	9800	9816	1158
590639	651	667	GCTAGCAGGATA ACAGA	eeekkddddddkkeee	10	9801	9817	1159
590640	652	668	AGCTAGCAGGAT AACAG	eeekkddddddkkeee	15	9802	9818	1160
590641	653	669	CAGCTAGCAGGA TAACA	eeekkddddddkkeee	21	9803	9819	1161
590642	654	670	ACAGCTAGCAGG ATAAC	eeekkddddddkkeee	20	9804	9820	1162
590643	655	671	TACAGCTAGCAG GATAA	eeekkddddddkkeee	40	9805	9821	1163
590644	656	672	CTACAGCTAGCA GGATA	eeekkddddddkkeee	55	9806	9822	1164
590645	657	673	TCTACAGCTAGC AGGAT	eeekkddddddkkeee	51	9807	9823	1165

590646	658	674	TTCTACAGCTAGCAGGA	eeekkddddddkkeee	31	9808	9824	1166
590647	659	675	TTTCTACAGCTAGCAGG	eeekkddddddkkeee	38	9809	9825	1167
590648	660	676	ATTTCTACAGCTAGCAG	eeekkddddddkkeee	45	9810	9826	1168
590649	661	677	CATTTCTACAGCTAGCA	eeekkddddddkkeee	34	9811	9827	1169
590650	664	680	ATACATTTCTACAGCTA	eeekkddddddkkeee	57	9814	9830	1170
590651	665	681	GATACATTTCTACAGCT	eeekkddddddkkeee	40	9815	9831	1171
590652	683	699	GTGTTTAATGTTTATCA	eeekkddddddkkeee	37	9833	9849	1172
590653	684	700	AGTGTTTAATGTTTATC	eeekkddddddkkeee	67	9834	9850	1173
590654	685	701	CAGTGTTTAATGTTTAT	eeekkddddddkkeee	54	9835	9851	1174
590655	686	702	ACAGTGTTTAATGTTTA	eeekkddddddkkeee	56	9836	9852	1175
590656	687	703	TACAGTGTTTAATGTTT	eeekkddddddkkeee	30	9837	9853	1176
590657	688	704	TTACAGTGTTTAATGTT	eeekkddddddkkeee	18	9838	9854	1177
590658	689	705	ATTACAGTGTTTAATGT	eeekkddddddkkeee	24	9839	9855	1178
590659	690	706	GATTACAGTGTTTAATG	eeekkddddddkkeee	10	9840	9856	1179
590660	691	707	AGATTACAGTGTTTAAT	eeekkddddddkkeee	45	9841	9857	1180
590661	692	708	AAGATTACAGTGTTTAA	eeekkddddddkkeee	34	9842	9858	1181
590662	693	709	TAAGATTACAGTGTTTA	eeekkddddddkkeee	54	9843	9859	1182
590663	694	710	TTAAGATTACAGTGTTT	eeekkddddddkkeee	54	9844	9860	1183
590664	772	788	ATCTTCCAAGTGATCAT	eeekkddddddkkeee	7	9922	9938	1184
590665	773	789	AATCTTCCAAGTGATCA	eeekkddddddkkeee	23	9923	9939	1185
590666	774	790	AAATCTTCCAAGTGATC	eeekkddddddkkeee	4	9924	9940	1186
590667	775	791	CAAATCTTCCAAGTGAT	eeekkddddddkkeee	18	9925	9941	1187

Table 16

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
590512	169	185	CGTCGCCCTTCAGCACG	eeekkddddddkkeee	16	975	991	968
590668	777	793	TACAAATCTTCCAAGTG	eeekkddddddkkeee	17	9927	9943	1188
590669	778	794	ATACAAATCTTCCAAGT	eeekkddddddkkeee	15	9928	9944	1189
590670	779	795	TATACAAATCTTCCAAG	eeekkddddddkkeee	11	9929	9945	1190
590671	780	796	CTATACAAATCTTCCAA	eeekkddddddkkeee	13	9930	9946	1191
590672	781	797	ACTATACAAATCTTCCA	eeekkddddddkkeee	10	9931	9947	1192
590673	782	798	AACTATACAAATCTTCC	eeekkddddddkkeee	28	9932	9948	1193
590674	783	799	AAACTATACAAATCTTC	eeekkddddddkkeee	26	9933	9949	1194
590675	786	802	ATAAAACTATACAAATC	eeekkddddddkkeee	14	9936	9952	1195
590676	791	807	GTTTTATAAAACTATAC	eeekkddddddkkeee	22	9941	9957	1196
590677	793	809	GAGTTTTATAAAACTAT	eeekkddddddkkeee	6	9943	9959	1197
590678	814	830	ATTGAAACAGACATTTT	eeekkddddddkkeee	22	9964	9980	1198
590679	815	831	CATTGAAACAGACATTT	eeekkddddddkkeee	11	9965	9981	1199
590680	816	832	TCATTGAAACAGACATT	eeekkddddddkkeee	10	9966	9982	1200
590681	817	833	GTCATTGAAACAGACAT	eeekkddddddkkeee	23	9967	9983	1201
590682	818	834	GGTCATTGAAACAGACA	eeekkddddddkkeee	11	9968	9984	1202
590683	819	835	AGGTCATTGAAACAGAC	eeekkddddddkkeee	21	9969	9985	1203
590684	820	836	CAGGTCATTGAAACAGA	eeekkddddddkkeee	14	9970	9986	1204
590685	821	837	ACAGGTCATTGAAACAG	eeekkddddddkkeee	14	9971	9987	1205

590686	822	838	TACAGGTCA TTGAAACA	eeekkddddddkkeee	9	9972	9988	1206
590687	823	839	ATACAGGTC ATTGAAAC	eeekkddddddkkeee	14	9973	9989	1207
590688	824	840	AATACAGGT CATTGAAA	eeekkddddddkkeee	6	9974	9990	1208
590689	825	841	AAATACAGG TCATTGAA	eeekkddddddkkeee	2	9975	9991	1209
590690	826	842	AAAATACAG GTCATTGA	eeekkddddddkkeee	n.d.	9976	9992	1210
590691	827	843	CAAAATACA GGTCATTG	eeekkddddddkkeee	n.d.	9977	9993	1211
590692	828	844	GCAAAATAC AGGTCATT	eeekkddddddkkeee	n.d.	9978	9994	1212
590693	829	845	GGCAAAATA CAGGTCAT	eeekkddddddkkeee	n.d.	9979	9995	1213
590694	830	846	TGGCAAAAT ACAGGTCA	eeekkddddddkkeee	n.d.	9980	9996	1214
590695	831	847	CTGGCAAAA TACAGGTC	eeekkddddddkkeee	n.d.	9981	9997	1215
590696	832	848	TCTGGCAAA ATACAGGT	eeekkddddddkkeee	n.d.	9982	9998	1216
590697	833	849	GTCTGGCAA AATACAGG	eeekkddddddkkeee	n.d.	9983	9999	1217
590698	834	850	AGTCTGGCA AAATACAG	eeekkddddddkkeee	1	9984	10000	1218
590699	835	851	AAGTCTGGC AAAATACA	eeekkddddddkkeee	10	9985	10001	1219
590700	836	852	TAAGTCTGG CAAAATAC	eeekkddddddkkeee	4	9986	10002	1220
590701	837	853	TTAAGTCTGG CAAAATA	eeekkddddddkkeee	2	9987	10003	1221
590702	853	869	AATACCCAT CTGTGATT	eeekkddddddkkeee	7	10003	10019	1222
590703	854	870	TAATACCCAT CTGTGAT	eeekkddddddkkeee	4	10004	10020	1223
590704	855	871	TTAATACCCA TCTGTGA	eeekkddddddkkeee	2	10005	10021	1224
590705	856	872	TTTAATACCC ATCTGTG	eeekkddddddkkeee	0	10006	10022	1225
590706	857	873	GTTTAATACC CATCTGT	eeekkddddddkkeee	17	10007	10023	1226
590707	858	874	AGTTTAATAC CCATCTG	eeekkddddddkkeee	10	10008	10024	1227
590708	859	875	AAGTTTAAT ACCCATCT	eeekkddddddkkeee	12	10009	10025	1228

590709	860	876	CAAGTTTAAT ACCCATC	eeekkddddddkkeee	37	10010	10026	1229
590710	861	877	ACAAGTTTA ATACCCAT	eeekkddddddkkeee	23	10011	10027	1230
590711	862	878	GACAAGTTT AATACCCA	eeekkddddddkkeee	24	10012	10028	1231
590712	863	879	TGACAAGTTT AATACCC	eeekkddddddkkeee	27	10013	10029	1232
590713	864	880	CTGACAAGT TTAATACC	eeekkddddddkkeee	10	10014	10030	1233
590714	865	881	TCTGACAAG TTTAATAC	eeekkddddddkkeee	0	10015	10031	1234
590715	866	882	TTCTGACAA GTTTAATA	eeekkddddddkkeee	6	10016	10032	1235
590716	867	883	ATTCTGACA AGTTTAAT	eeekkddddddkkeee	9	10017	10033	1236
590717	868	884	AATTCTGAC AAGTTTAA	eeekkddddddkkeee	15	10018	10034	1237
590718	869	885	AAATTCTGA CAAGTTTA	eeekkddddddkkeee	21	10019	10035	1238
590719	870	886	GAAATTCTG ACAAGTTT	eeekkddddddkkeee	14	10020	10036	1239
590720	871	887	AGAAATTCT GACAAGTT	eeekkddddddkkeee	8	10021	10037	1240
590721	872	888	AAGAAATTC TGACAAGT	eeekkddddddkkeee	18	10022	10038	1241
590722	891	907	TTCACAGGCT TGAATGA	eeekkddddddkkeee	9	10041	10057	1242
590723	892	908	ATTCACAGG CTTGAATG	eeekkddddddkkeee	11	10042	10058	1243
590724	893	909	TATTCACAG GCTTGAAT	eeekkddddddkkeee	0	10043	10059	1244
590725	894	910	TTATTCACAG GCTTGAA	eeekkddddddkkeee	10	10044	10060	1245
590726	895	911	TTTATTCACA GGCTTGA	eeekkddddddkkeee	29	10045	10061	1246
590727	896	912	TTTTATTCAC AGGCTTG	eeekkddddddkkeee	28	10046	10062	1247
590728	897	913	TTTTTATTCA CAGGCTT	eeekkddddddkkeee	31	10047	10063	1248
590729	898	914	GTTTTTATTC ACAGGCT	eeekkddddddkkeee	10	10048	10064	1249
590731	899	915	GGTTTTTATT CACAGGC	eeekkddddddkkeee	22	10049	10065	1250
590732	900	916	GGGTTTTTAT TCACAGG	eeekkddddddkkeee	17	10050	10066	1251

590733	901	917	AGGGTTTTTA TTCACAG	eeekkddddddkkeee	24	10051	10067	1252
590734	902	918	CAGGGTTTTT ATTCACA	eeekkddddddkkeee	17	10052	10068	1253
590735	903	919	ACAGGGTTTT TATTCAC	eeekkddddddkkeee	10	10053	10069	1254
590736	904	920	TACAGGGTTT TTATTCA	eeekkddddddkkeee	11	10054	10070	1255
590737	905	921	ATACAGGGT TTTTATTC	eeekkddddddkkeee	3	10055	10071	1256
590738	906	922	CATACAGGG TTTTTATT	eeekkddddddkkeee	0	10056	10072	1257
590739	907	923	CCATACAGG GTTTTTAT	eeekkddddddkkeee	1	10057	10073	1258
590740	908	924	GCCATACAG GGTTTTTA	eeekkddddddkkeee	11	10058	10074	1259
590741	909	925	TGCCATACA GGGTTTTT	eeekkddddddkkeee	9	10059	10075	1260
590742	910	926	GTGCCATAC AGGGTTTT	eeekkddddddkkeee	7	10060	10076	1261
590743	911	927	AGTGCCATA CAGGGTTT	eeekkddddddkkeee	9	10061	10077	1262
590744	938	954	TTGGATTCTT TTAATAG	eeekkddddddkkeee	8	10088	10104	1263
590745	951	967	TTTTAGTTTG AATTTGG	eeekkddddddkkeee	12	n/a	n/a	1264

Table 17

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCT TCAGCACGCA	eeeeeddddddddddeeeee	66	973	992	21
590067	202	221	CCTTCTGCTCG AAATTGATG	eeeeeddddddddddeeeee	53	1008	1027	120
590074	209	228	TTACTTTCCTT CTGCTCGAA	eeeeeddddddddddeeeee	30	n/a	n/a	127
590457	211	227	TACTTTCCTTC TGCTCG	eeekkddddddkkeee	14	n/a	n/a	980
590458	212	228	TTACTTTCCTT CTGCTC	eeekkddddddkkeee	22	n/a	n/a	981
590459	213	229	ATTACTTTCCT TCTGCT	eeekkddddddkkeee	15	n/a	n/a	982

590461	214	230	CATTACTTTCC TTCTGC	eeekkddddddkkeee	28	n/a	n/a	983
590462	215	231	CCATTACTTTC CTTCTG	eeekkddddddkkeee	37	n/a	n/a	984
590463	216	232	TCCATTACTTT CCTTCT	eeekkddddddkkeee	18	n/a	n/a	985
590082	217	236	CTGGTCCATT ACTTTCCTTC	eeeeedddddddddeeeee	50	n/a	n/a	135
590464	217	233	GTCCATTACTT TCCTTC	eeekkddddddkkeee	33	n/a	n/a	986
590465	218	234	GGTCCATTAC TTTCCTT	eeekkddddddkkeee	18	4972	4988	987
590130	363	382	TTCATCCTTTG GCCCACCGT	eeeeedddddddddeeeee	30	7679	7698	194
590536	363	379	ATCCTTTGGC CCACCGT	eeekkddddddkkeee	51	7679	7695	1056
590537	364	380	CATCCTTTGG CCCACCG	eeekkddddddkkeee	38	7680	7696	1057
590538	365	381	TCATCCTTTGG CCCACC	eeekkddddddkkeee	27	7681	7697	1058
590539	366	382	TTCATCCTTTG GCCCAC	eeekkddddddkkeee	26	7682	7698	1059
590540	367	383	CTTCATCCTTT GGCCCA	eeekkddddddkkeee	35	7683	7699	1060
590541	368	384	TCTTCATCCTT TGGCCC	eeekkddddddkkeee	15	7684	7700	1061
590542	369	385	CTCTTCATCCT TTGGCC	eeekkddddddkkeee	26	7685	7701	1062
590543	370	386	TCTCTTCATCC TTTGGC	eeekkddddddkkeee	14	7686	7702	1063
590138	371	390	TGCCTCTCTTC ATCCTTTGG	eeeeedddddddddeeeee	32	n/a	n/a	202
590146	505	524	CATCTGCTTTT TCATGGACC	eeeeedddddddddeeeee	46	9655	9674	211
590613	608	624	CAAGGGAATG TTTATTG	eeekkddddddkkeee	19	9758	9774	1133
590614	609	625	CCAAGGGAAT GTTTATT	eeekkddddddkkeee	36	9759	9775	1134
590615	610	626	TCCAAGGGAA TGTTTAT	eeekkddddddkkeee	32	9760	9776	1135
590616	611	627	ATCCAAGGGA ATGTTTA	eeekkddddddkkeee	42	9761	9777	1136
590617	612	628	CATCCAAGGG AATGTTT	eeekkddddddkkeee	16	9762	9778	1137
590618	613	629	ACATCCAAGG GAATGTT	eeekkddddddkkeee	30	9763	9779	1138

590619	614	630	TACATCCAAG GGAATGT	eeekkddddddkkeee	30	9764	9780	1139
590620	615	631	CTACATCCAA GGGAATG	eeekkddddddkkeee	40	9765	9781	1140
590690	826	842	AAAATACAGG TCATTGA	eeekkddddddkkeee	28	9976	9992	1210
590691	827	843	CAAAATACAG GTCATTG	eeekkddddddkkeee	23	9977	9993	1211
590692	828	844	GCAAAATACA GGTCATT	eeekkddddddkkeee	43	9978	9994	1212
590693	829	845	GGCAAAATAC AGGTCAT	eeekkddddddkkeee	39	9979	9995	1213
590694	830	846	TGGCAAAATA CAGGTCA	eeekkddddddkkeee	26	9980	9996	1214
590695	831	847	CTGGCAAAAT ACAGGTC	eeekkddddddkkeee	18	9981	9997	1215
590696	832	848	TCTGGCAAAA TACAGGT	eeekkddddddkkeee	0	9982	9998	1216
590697	833	849	GTCTGGCAAA ATACAGG	eeekkddddddkkeee	24	9983	9999	1217

Example 4: Inhibition of human SOD-1 in HepG2 cells by deoxy, MOE and cEt gapmers

Modified oligonucleotides were designed targeting a superoxide dismutase 1, soluble (SOD-1) nucleic acid and were tested for their effects on SOD-1 mRNA in vitro. ISIS 333611, a 5-10-5 MOE gapmer which was previously described in WO 2005/040180, was included as a benchmark.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 4,000 nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR.

Human primer probe set RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells. 'n.d.' indicates that inhibition levels were not measured.

The newly designed modified oligonucleotides in the Tables below were designed as deoxy, MOE, and cEt gapmers or 5-10-5 gapmers. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of ten 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The deoxy, MOE and cEt

oligonucleotides are 17 nucleosides in length wherein the nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety. The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose; and 'e' indicates a 2'-MOE modified sugar. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000). 'n/a' indicates that the modified oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 18

Percent inhibition of SOD-1 mRNA by 5-10-5 MOE gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
596168	3	22	CTCGCCCACTCTGGCCCCAA	45	809	828	1265
596169	5	24	GCCTCGCCCACTCTGGCCCC	37	811	830	1266
596170	7	26	GCGCCTCGCCCACTCTGGCC	33	813	832	1267
596171	9	28	CCGCGCCTCGCCCACTCTGG	27	815	834	1268
596172	11	30	CTCCGCGCCTCGCCCACTCT	40	817	836	1269
596173	13	32	ACCTCCGCGCCTCGCCCACT	77	819	838	1270
596174	15	34	AGACCTCCGCGCCTCGCCCA	72	821	840	1271
596175	17	36	CCAGACCTCCGCGCCTCGCC	46	823	842	1272
596176	19	38	GGCCAGACCTCCGCGCCTCG	49	825	844	1273
150508	21	40	TAGGCCAGACCTCCGCGCCT	33	827	846	107
596177	23	42	TATAGGCCAGACCTCCGCGC	40	829	848	1274
596178	25	44	TTTATAGGCCAGACCTCCGC	69	831	850	1275
150509	27	46	ACTTTATAGGCCAGACCTCC	64	833	852	108
596179	31	50	GACTACTTTATAGGCCAGAC	74	837	856	1276
596180	33	52	GCGACTACTTTATAGGCCAG	19	839	858	1277
596181	37	56	CTCCGCGACTACTTTATAGG	27	843	862	1278
596182	39	58	GTCTCCGCGACTACTTTATA	22	845	864	1279
596183	41	60	CCGTCTCCGCGACTACTTTA	20	847	866	1280
596184	43	62	CCCCGTCTCCGCGACTACTT	16	849	868	1281

596185	45	64	CACCCCGTCTCCGCGACTAC	13	851	870	1282
596186	47	66	AGCACCCCGTCTCCGCGACT	24	853	872	1283
596187	49	68	CCAGCACCCCGTCTCCGCGA	38	855	874	1284
596188	51	70	AACCAGCACCCCGTCTCCGC	11	857	876	1285
596189	53	72	CAAACCAGCACCCCGTCTCC	13	859	878	1286
596190	55	74	CGCAAACCAGCACCCCGTCT	21	861	880	1287
150510	57	76	GACGCAAACCAGCACCCCGT	45	863	882	109
596191	59	78	ACGACGCAAACCAGCACCCC	30	865	884	1288
596192	61	80	CTACGACGCAAACCAGCACC	19	867	886	1289
596193	63	82	GACTACGACGCAAACCAGCA	40	869	888	1290
596194	65	84	GAGACTACGACGCAAACCAG	23	871	890	1291
596195	67	86	AGGAGACTACGACGCAAACC	35	873	892	1292
596196	69	88	GCAGGAGACTACGACGCAAA	33	875	894	1293
596197	71	90	CTGCAGGAGACTACGACGCA	36	877	896	1294
596198	73	92	CGCTGCAGGAGACTACGACG	23	879	898	1295
596199	91	110	TGCAACGGAAACCCCAGACG	21	897	916	1296
596200	93	112	ACTGCAACGGAAACCCCAGA	43	899	918	1297
596201	97	116	GAGGACTGCAACGGAAACCC	24	903	922	1298
596202	99	118	CCGAGGACTGCAACGGAAAC	29	905	924	1299
596203	101	120	TTCCGAGGACTGCAACGGAA	5	907	926	1300
150438	103	122	GGTTCCGAGGACTGCAACGG	35	909	928	110
345716	105	124	CTGGTTCCGAGGACTGCAAC	51	911	930	1301
150439	107	126	TCCTGGTTCCGAGGACTGCA	24	913	932	111
596204	109	128	GGTCCTGGTTCCGAGGACTG	14	915	934	1302
150440	111	130	GAGGTCCTGGTTCCGAGGAC	31	917	936	112
596205	113	132	CCGAGGTCCTGGTTCCGAGG	18	919	938	1303
345718	115	134	CGCCGAGGTCCTGGTTCCGA	24	921	940	1304
596206	117	136	CACGCCGAGGTCCTGGTTCC	23	923	942	1305
596207	119	138	GCCACGCCGAGGTCCTGGTT	38	925	944	1306
596208	123	142	CTAGGCCACGCCGAGGTCCT	39	929	948	1307
345720	125	144	CGCTAGGCCACGCCGAGGTC	52	931	950	1308
596209	127	146	CTCGCTAGGCCACGCCGAGG	46	933	952	1309
596210	129	148	AACTCGCTAGGCCACGCCGA	44	935	954	1310
596211	131	150	ATAACTCGCTAGGCCACGCC	12	937	956	1311
596212	133	152	CCATAACTCGCTAGGCCACG	22	939	958	1312
345722	135	154	CGCCATAACTCGCTAGGCCA	59	941	960	1313

150442	137	156	GTCGCCATAACTCGCTAGGC	40	943	962	113
146143	157	176	TCAGCACGCACACGGCCTTC	52	963	982	114
195753	159	178	CTTCAGCACGCACACGGCCT	57	965	984	115
333607	161	180	CCCTTCAGCACGCACACGGC	37	967	986	116
333608	163	182	CGCCCTTCAGCACGCACACG	23	969	988	117
333611	167	186	CCGTCGCCCTTCAGCACGCA	67	973	992	21
596213	171	190	TGGGCCGTCGCCCTTCAGCA	12	977	996	1314
596214	173	192	ACTGGGCCGTCGCCCTTCAG	26	979	998	1315
596215	175	194	GCACTGGGCCGTCGCCCTTC	14	981	1000	1316
596216	177	196	CTGCACTGGGCCGTCGCCCT	24	983	1002	1317
596217	181	200	TGCCCTGCACTGGGCCGTCG	38	987	1006	1318
596218	183	202	GATGCCCTGCACTGGGCCGT	15	989	1008	1319
596219	185	204	ATGATGCCCTGCACTGGGCC	20	991	1010	1320
596220	189	208	ATTGATGATGCCCTGCACTG	8	995	1014	1321
596221	191	210	AAATTGATGATGCCCTGCAC	14	997	1016	1322
596222	193	212	CGAAATTGATGATGCCCTGC	32	999	1018	1323
596223	195	214	CTCGAAATTGATGATGCCCT	31	1001	1020	1324
596224	197	216	TGCTCGAAATTGATGATGCC	20	1003	1022	1325
596225	199	218	TCTGCTCGAAATTGATGATG	14	1005	1024	1326
596226	201	220	CTTCTGCTCGAAATTGATGA	11	1007	1026	1327
596227	240	259	TTTAATGCTTCCCCACACCT	15	4994	5013	1328
596228	242	261	CCTTTAATGCTTCCCCACAC	1	4996	5015	1329
596229	244	263	GTCCTTTAATGCTTCCCCAC	9	4998	5017	1330

Table 19

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
596530	164	180	CCCTTCAGCACGCACAC	eekkddddddddkkeee	74	970	986	1331
596721	164	180	CCCTTCAGCACGCACAC	eekkddddddddkkee	81	970	986	1331
596531	165	181	GCCCTTCAGCACGCACA	eekkddddddddkkeee	75	971	987	1332

596722	165	181	GCCCTTCAGC ACGCACA	eekkddddddddkkee	60	971	987	1332
596532	166	182	CGCCCTTCAG CACGCAC	eekkddddddddkkeee	67	972	988	1333
596723	166	182	CGCCCTTCAG CACGCAC	eekkddddddddkkee	73	972	988	1333
333611	167	186	CCGTCGCCCT TCAGCACGCA	eeeeeddddddddddeeeee	73	973	992	21
596720	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkeee	56	973	989	966
596911	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkee	63	973	989	966
596533	168	184	GTCGCCCTTC AGCACGC	eekkddddddddkkeee	60	974	990	967
596724	168	184	GTCGCCCTTC AGCACGC	eekkddddddddkkee	72	974	990	967
596534	169	185	CGTCGCCCTT CAGCACG	eekkddddddddkkeee	52	975	991	968
596725	169	185	CGTCGCCCTT CAGCACG	eekkddddddddkkee	43	975	991	968
596535	170	186	CCGTCGCCCT TCAGCAC	eekkddddddddkkeee	71	976	992	969
596726	170	186	CCGTCGCCCT TCAGCAC	eekkddddddddkkee	75	976	992	969
596536	171	187	GCCGTCGCCC TTCAGCA	eekkddddddddkkeee	64	977	993	970
596727	171	187	GCCGTCGCCC TTCAGCA	eekkddddddddkkee	57	977	993	970
596537	577	593	CACCACAAGC CAAACGA	eekkddddddddkkeee	48	9727	9743	1334
596728	577	593	CACCACAAGC CAAACGA	eekkddddddddkkee	46	9727	9743	1334
596538	578	594	ACACCACAAG CCAAACG	eekkddddddddkkeee	27	9728	9744	1335
596729	578	594	ACACCACAAG CCAAACG	eekkddddddddkkee	45	9728	9744	1335
596539	579	595	TACACCACAA GCCAAAC	eekkddddddddkkeee	56	9729	9745	1336
596730	579	595	TACACCACAA GCCAAAC	eekkddddddddkkee	63	9729	9745	1336
596540	580	596	TTACACCACA AGCCAAA	eekkddddddddkkeee	60	9730	9746	1337

596731	580	596	TTACACCACA AGCCAAA	eekkddddddddkkee	63	9730	9746	1337
596541	581	597	ATTACACCAC AAGCCAA	eekkddddddddkkeee	46	9731	9747	1338
596732	581	597	ATTACACCAC AAGCCAA	eekkddddddddkkee	63	9731	9747	1338
596542	582	598	AATTACACCA CAAGCCA	eekkddddddddkkeee	62	9732	9748	1111
596733	582	598	AATTACACCA CAAGCCA	eekkddddddddkkee	56	9732	9748	1111
596543	583	599	CAATTACACC ACAAGCC	eekkddddddddkkeee	58	9733	9749	1112
596734	583	599	CAATTACACC ACAAGCC	eekkddddddddkkee	61	9733	9749	1112
596544	584	600	CCAATTACAC CACAAGC	eekkddddddddkkeee	66	9734	9750	1113
596735	584	600	CCAATTACAC CACAAGC	eekkddddddddkkee	73	9734	9750	1113
596545	585	601	CCCAATTACA CCACAAG	eekkddddddddkkeee	63	9735	9751	1114
596736	585	601	CCCAATTACA CCACAAG	eekkddddddddkkee	74	9735	9751	1114
596546	588	604	GATCCCAATT ACACCAC	eekkddddddddkkeee	41	9738	9754	1115
596737	588	604	GATCCCAATT ACACCAC	eekkddddddddkkee	58	9738	9754	1115
596547	589	605	CGATCCCAAT TACACCA	eekkddddddddkkeee	57	9739	9755	1116
596738	589	605	CGATCCCAAT TACACCA	eekkddddddddkkee	59	9739	9755	1116
596548	590	606	GCGATCCCAA TTACACC	eekkddddddddkkeee	31	9740	9756	1117
596739	590	606	GCGATCCCAA TTACACC	eekkddddddddkkee	58	9740	9756	1117
596549	591	607	GGCGATCCCA ATTACAC	eekkddddddddkkeee	33	9741	9757	1118
596740	591	607	GGCGATCCCA ATTACAC	eekkddddddddkkee	66	9741	9757	1118
596550	592	608	GGGCGATCCC AATTACA	eekkddddddddkkeee	30	9742	9758	1119
596741	592	608	GGGCGATCCC AATTACA	eekkddddddddkkee	30	9742	9758	1119

596551	593	609	TGGGCGATCC CAATTAC	eekkddddddddkkeee	19	9743	9759	1120
596742	593	609	TGGGCGATCC CAATTAC	eekkddddddddkkee	46	9743	9759	1120
596552	594	610	TTGGGCGATC CCAATTA	eekkddddddddkkeee	14	9744	9760	1121
596743	594	610	TTGGGCGATC CCAATTA	eekkddddddddkkee	5	9744	9760	1121
596553	595	611	ATTGGGCGAT CCCAATT	eekkddddddddkkeee	2	9745	9761	1122
596744	595	611	ATTGGGCGAT CCCAATT	eekkddddddddkkee	23	9745	9761	1122
596554	596	612	TATTGGGCGA TCCCAAT	eekkddddddddkkeee	19	9746	9762	1123
596745	596	612	TATTGGGCGA TCCCAAT	eekkddddddddkkee	6	9746	9762	1123
596555	597	613	TTATTGGGCG ATCCCAA	eekkddddddddkkeee	41	9747	9763	1124
596746	597	613	TTATTGGGCG ATCCCAA	eekkddddddddkkee	41	9747	9763	1124
596556	598	614	TTTATTGGGC GATCCCA	eekkddddddddkkeee	34	9748	9764	1125
596747	598	614	TTTATTGGGC GATCCCA	eekkddddddddkkee	46	9748	9764	1125
596557	599	615	GTTTATTGGG CGATCCC	eekkddddddddkkeee	54	9749	9765	1126
596748	599	615	GTTTATTGGG CGATCCC	eekkddddddddkkee	68	9749	9765	1126
596558	600	616	TGTTTATTGG GCGATCC	eekkddddddddkkeee	50	9750	9766	1127
596749	600	616	TGTTTATTGG GCGATCC	eekkddddddddkkee	47	9750	9766	1127
596559	601	617	ATGTTTATTG GGCGATC	eekkddddddddkkeee	76	9751	9767	1128
596750	601	617	ATGTTTATTG GGCGATC	eekkddddddddkkee	64	9751	9767	1128
596560	602	618	AATGTTTATT GGGCGAT	eekkddddddddkkeee	61	9752	9768	1129
596751	602	618	AATGTTTATT GGGCGAT	eekkddddddddkkee	64	9752	9768	1129
596561	603	619	GAATGTTTAT TGGGCGA	eekkddddddddkkeee	47	9753	9769	1130

596752	603	619	GAATGTTTAT TGGGCGA	eekkddddddddkkee	65	9753	9769	1130
596562	604	620	GGAATGTTTA TTGGGCG	eekkddddddddkkeee	37	9754	9770	1131
596753	604	620	GGAATGTTTA TTGGGCG	eekkddddddddkkee	58	9754	9770	1131
596563	608	624	CAAGGGAATG TTTATTG	eekkddddddddkkeee	43	9758	9774	1133
596754	608	624	CAAGGGAATG TTTATTG	eekkddddddddkkee	38	9758	9774	1133
596564	609	625	CCAAGGGAAT GTTTATT	eekkddddddddkkeee	57	9759	9775	1134
596755	609	625	CCAAGGGAAT GTTTATT	eekkddddddddkkee	52	9759	9775	1134
596565	610	626	TCCAAGGGAA TGTTTAT	eekkddddddddkkeee	27	9760	9776	1135
596756	610	626	TCCAAGGGAA TGTTTAT	eekkddddddddkkee	57	9760	9776	1135
596566	611	627	ATCCAAGGGA ATGTTTA	eekkddddddddkkeee	35	9761	9777	1136
596757	611	627	ATCCAAGGGA ATGTTTA	eekkddddddddkkee	39	9761	9777	1136
596567	616	632	ACTACATCCA AGGGAAT	eekkddddddddkkeee	42	9766	9782	1141
596758	616	632	ACTACATCCA AGGGAAT	eekkddddddddkkee	48	9766	9782	1141

Table 20

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCT TCAGCACGCA	eeeeddddddddddeeeee	64	973	992	21
596720	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkeee	56	973	989	966
596911	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkee	60	973	989	966
596568	617	633	GACTACATCC AAGGGAA	eekkddddddddkkeee	50	9767	9783	1142

596759	617	633	GACTACATCC AAGGGAA	eekkddddddddkkee	57	9767	9783	1142
596569	618	634	AGACTACATC CAAGGGA	eekkddddddddkkeee	53	9768	9784	1143
596760	618	634	AGACTACATC CAAGGGA	eekkddddddddkkee	55	9768	9784	1143
596570	619	635	CAGACTACAT CCAAGGG	eekkddddddddkkeee	81	9769	9785	1144
596761	619	635	CAGACTACAT CCAAGGG	eekkddddddddkkee	78	9769	9785	1144
596571	620	636	TCAGACTACA TCCAAGG	eekkddddddddkkeee	79	9770	9786	1145
596762	620	636	TCAGACTACA TCCAAGG	eekkddddddddkkee	78	9770	9786	1145
596572	621	637	CTCAGACTAC ATCCAAG	eekkddddddddkkeee	85	9771	9787	1146
596763	621	637	CTCAGACTAC ATCCAAG	eekkddddddddkkee	76	9771	9787	1146
596573	622	638	CCTCAGACTA CATCCAA	eekkddddddddkkeee	73	9772	9788	1147
596764	622	638	CCTCAGACTA CATCCAA	eekkddddddddkkee	87	9772	9788	1147
596574	623	639	GCCTCAGACT ACATCCA	eekkddddddddkkeee	69	9773	9789	1148
596765	623	639	GCCTCAGACT ACATCCA	eekkddddddddkkee	82	9773	9789	1148
596575	624	640	GGCCTCAGAC TACATCC	eekkddddddddkkeee	70	9774	9790	1149
596766	624	640	GGCCTCAGAC TACATCC	eekkddddddddkkee	76	9774	9790	1149
596576	625	641	GGGCCTCAGA CTACATC	eekkddddddddkkeee	55	9775	9791	1150
596767	625	641	GGGCCTCAGA CTACATC	eekkddddddddkkee	58	9775	9791	1150
596577	640	656	AACAGATGA GTTAAGGG	eekkddddddddkkeee	73	9790	9806	1339
596768	640	656	AACAGATGA GTTAAGGG	eekkddddddddkkee	86	9790	9806	1339
596578	641	657	TAACAGATGA GTTAAGG	eekkddddddddkkeee	68	9791	9807	1340
596769	641	657	TAACAGATGA GTTAAGG	eekkddddddddkkee	80	9791	9807	1340

596579	642	658	ATAACAGATG AGTTAAG	eekkddddddddkkeee	27	9792	9808	1341
596770	642	658	ATAACAGATG AGTTAAG	eekkddddddddkkee	42	9792	9808	1341
596580	643	659	GATAACAGAT GAGTTAA	eekkddddddddkkeee	41	9793	9809	1151
596771	643	659	GATAACAGAT GAGTTAA	eekkddddddddkkee	28	9793	9809	1151
596581	644	660	GGATAACAG ATGAGTTA	eekkddddddddkkeee	63	9794	9810	1152
596772	644	660	GGATAACAG ATGAGTTA	eekkddddddddkkee	63	9794	9810	1152
596582	645	661	AGGATAACA GATGAGTT	eekkddddddddkkeee	84	9795	9811	1153
596773	645	661	AGGATAACA GATGAGTT	eekkddddddddkkee	86	9795	9811	1153
596583	646	662	CAGGATAAC AGATGAGT	eekkddddddddkkeee	95	9796	9812	1154
596774	646	662	CAGGATAAC AGATGAGT	eekkddddddddkkee	96	9796	9812	1154
596584	647	663	GCAGGATAA CAGATGAG	eekkddddddddkkeee	79	9797	9813	1155
596775	647	663	GCAGGATAA CAGATGAG	eekkddddddddkkee	86	9797	9813	1155
596585	651	667	GCTAGCAGG ATAACAGA	eekkddddddddkkeee	19	9801	9817	1159
596776	651	667	GCTAGCAGG ATAACAGA	eekkddddddddkkee	43	9801	9817	1159
596586	652	668	AGCTAGCAG GATAACAG	eekkddddddddkkeee	57	9802	9818	1160
596777	652	668	AGCTAGCAG GATAACAG	eekkddddddddkkee	54	9802	9818	1160
596587	653	669	CAGCTAGCAG GATAACA	eekkddddddddkkeee	71	9803	9819	1161
596778	653	669	CAGCTAGCAG GATAACA	eekkddddddddkkee	61	9803	9819	1161
596588	654	670	ACAGCTAGCA GGATAAC	eekkddddddddkkeee	79	9804	9820	1162
596779	654	670	ACAGCTAGCA GGATAAC	eekkddddddddkkee	83	9804	9820	1162
596589	655	671	TACAGCTAGC AGGATAA	eekkddddddddkkeee	85	9805	9821	1163

596780	655	671	TACAGCTAGC AGGATAA	eekkddddddddkkee	86	9805	9821	1163
596590	656	672	CTACAGCTAG CAGGATA	eekkddddddddkkeee	87	9806	9822	1164
596781	656	672	CTACAGCTAG CAGGATA	eekkddddddddkkee	91	9806	9822	1164
596591	657	673	TCTACAGCTA GCAGGAT	eekkddddddddkkeee	75	9807	9823	1165
596782	657	673	TCTACAGCTA GCAGGAT	eekkddddddddkkee	83	9807	9823	1165
596592	658	674	TTCTACAGCT AGCAGGA	eekkddddddddkkeee	74	9808	9824	1166
596783	658	674	TTCTACAGCT AGCAGGA	eekkddddddddkkee	79	9808	9824	1166
596593	659	675	TTTCTACAGC TAGCAGG	eekkddddddddkkeee	76	9809	9825	1167
596784	659	675	TTTCTACAGC TAGCAGG	eekkddddddddkkee	84	9809	9825	1167
596594	660	676	ATTTCTACAG CTAGCAG	eekkddddddddkkeee	66	9810	9826	1168
596785	660	676	ATTTCTACAG CTAGCAG	eekkddddddddkkee	75	9810	9826	1168
596595	665	681	GATACATTTC TACAGCT	eekkddddddddkkeee	64	9815	9831	1171
596786	665	681	GATACATTTC TACAGCT	eekkddddddddkkee	77	9815	9831	1171
596596	666	682	GGATACATTT CTACAGC	eekkddddddddkkeee	75	9816	9832	1342
596787	666	682	GGATACATTT CTACAGC	eekkddddddddkkee	84	9816	9832	1342
596597	667	683	AGGATACATT TCTACAG	eekkddddddddkkeee	60	9817	9833	1343
596788	667	683	AGGATACATT TCTACAG	eekkddddddddkkee	77	9817	9833	1343
596598	668	684	CAGGATACAT TTCTACA	eekkddddddddkkeee	79	9818	9834	1344
596789	668	684	CAGGATACAT TTCTACA	eekkddddddddkkee	85	9818	9834	1344
596599	672	688	TTATCAGGAT ACATTTC	eekkddddddddkkeee	57	9822	9838	1345
596790	672	688	TTATCAGGAT ACATTTC	eekkddddddddkkee	67	9822	9838	1345

596600	674	690	GTTTATCAGG ATACATT	eekkddddddddkkeee	85	9824	9840	1346
596791	674	690	GTTTATCAGG ATACATT	eekkddddddddkkee	88	9824	9840	1346
596601	675	691	TGTTTATCAG GATACAT	eekkddddddddkkeee	70	9825	9841	1347
596792	675	691	TGTTTATCAG GATACAT	eekkddddddddkkee	83	9825	9841	1347
596602	676	692	ATGTTTATCA GGATACA	eekkddddddddkkeee	85	9826	9842	1348
596793	676	692	ATGTTTATCA GGATACA	eekkddddddddkkee	81	9826	9842	1348
596603	677	693	AATGTTTATC AGGATAC	eekkddddddddkkeee	89	9827	9843	1349
596794	677	693	AATGTTTATC AGGATAC	eekkddddddddkkee	90	9827	9843	1349
596604	678	694	TAATGTTTAT CAGGATA	eekkddddddddkkeee	90	9828	9844	1350
596795	678	694	TAATGTTTAT CAGGATA	eekkddddddddkkee	85	9828	9844	1350
596605	679	695	TTAATGTTTA TCAGGAT	eekkddddddddkkeee	90	9829	9845	1351
596796	679	695	TTAATGTTTA TCAGGAT	eekkddddddddkkee	92	9829	9845	1351

Example 5: Inhibition of human SOD-1 in HepG2 cells by deoxy, MOE and cEt gapmers

Modified oligonucleotides were designed targeting an SOD-1 nucleic acid and were tested for their effects on SOD-1 mRNA in vitro. ISIS 333611, a 5-10-5 MOE gapmer, which was previously described in WO 2005/040180, was included as a benchmark.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cultured HepG2 cells at a density of 20,000 cells per well were transfected using electroporation with 5,000 nM modified oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR.

Human primer probe set RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells. 'n.d.' indicates that inhibition levels were not measured.

The newly designed modified oligonucleotides in the Tables below were designed as deoxy, MOE, and cEt gapmers. The gapmers are 17 nucleosides in length wherein each nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety. The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose; and 'e' indicates a 2'-MOE modified sugar. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000). 'n/a' indicates that the modified oligonucleotide does not target that particular gene sequence with 100% complementarity.

Table 21

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCTTCAGCACGCA	eeeeeddddddddddeeeee	71	973	992	21
596720	167	183	TCGCCCTTCAGCACGCA	eekkddddddddkkeee	53	973	989	966
596911	167	183	TCGCCCTTCAGCACGCA	eekkddddddddkkee	61	973	989	966
596606	681	697	GTTTAATGTTTATCAGG	eekkddddddddkkeee	87	9831	9847	1352
596797	681	697	GTTTAATGTTTATCAGG	eekkddddddddkkee	92	9831	9847	1352
596607	683	699	GTGTTTAATGTTTATCA	eekkddddddddkkeee	86	9833	9849	1172
596798	683	699	GTGTTTAATGTTTATCA	eekkddddddddkkee	86	9833	9849	1172
596608	684	700	AGTGTTTAATGTTTATC	eekkddddddddkkeee	88	9834	9850	1173
596799	684	700	AGTGTTTAATGTTTATC	eekkddddddddkkee	80	9834	9850	1173
596609	685	701	CAGTGTTTAATGTTTAT	eekkddddddddkkeee	77	9835	9851	1174

596800	685	701	CAGTGTTTAAT GTTTAT	eekkddddddddkkee	85	9835	9851	1174
596610	686	702	ACAGTGTTTA ATGTTTA	eekkddddddddkkeee	83	9836	9852	1175
596801	686	702	ACAGTGTTTA ATGTTTA	eekkddddddddkkee	84	9836	9852	1175
596611	690	706	GATTACAGTG TTTAATG	eekkddddddddkkeee	54	9840	9856	1179
596802	690	706	GATTACAGTG TTTAATG	eekkddddddddkkee	61	9840	9856	1179
596612	691	707	AGATTACAGT GTTTAAT	eekkddddddddkkeee	68	9841	9857	1180
596803	691	707	AGATTACAGT GTTTAAT	eekkddddddddkkee	63	9841	9857	1180
596613	697	713	CTTTTAAGATT ACAGTG	eekkddddddddkkeee	62	9847	9863	1353
596804	697	713	CTTTTAAGATT ACAGTG	eekkddddddddkkee	53	9847	9863	1353
596614	699	715	CACTTTTAAG ATTACAG	eekkddddddddkkeee	37	9849	9865	1354
596805	699	715	CACTTTTAAG ATTACAG	eekkddddddddkkee	49	9849	9865	1354
596615	710	726	TCACACAATT ACACTTT	eekkddddddddkkeee	28	9860	9876	1355
596806	710	726	TCACACAATT ACACTTT	eekkddddddddkkee	39	9860	9876	1355
596616	711	727	GTCACACAAT TACACTT	eekkddddddddkkeee	28	9861	9877	1356
596807	711	727	GTCACACAAT TACACTT	eekkddddddddkkee	35	9861	9877	1356
596617	713	729	AAGTCACACA ATTACAC	eekkddddddddkkeee	41	9863	9879	1357
596808	713	729	AAGTCACACA ATTACAC	eekkddddddddkkee	37	9863	9879	1357
596618	737	753	AGGTACTTTA AAGCAAC	eekkddddddddkkeee	35	9887	9903	1358
596809	737	753	AGGTACTTTA AAGCAAC	eekkddddddddkkee	42	9887	9903	1358
596619	739	755	ACAGGTACTT TAAAGCA	eekkddddddddkkeee	14	9889	9905	1359
596810	739	755	ACAGGTACTT TAAAGCA	eekkddddddddkkee	20	9889	9905	1359

596620	740	756	TACAGGTACT TTAAAGC	eekkddddddddkkeee	23	9890	9906	1360
596811	740	756	TACAGGTACT TTAAAGC	eekkddddddddkkee	26	9890	9906	1360
596621	741	757	CTACAGGTAC TTTAAAG	eekkddddddddkkeee	2	9891	9907	1361
596812	741	757	CTACAGGTAC TTTAAAG	eekkddddddddkkee	16	9891	9907	1361
596622	743	759	CACTACAGGT ACTTTAA	eekkddddddddkkeee	27	9893	9909	1362
596813	743	759	CACTACAGGT ACTTTAA	eekkddddddddkkee	38	9893	9909	1362
596623	744	760	TCACTACAGG TACTTTA	eekkddddddddkkeee	27	9894	9910	1363
596814	744	760	TCACTACAGG TACTTTA	eekkddddddddkkee	35	9894	9910	1363
596624	745	761	CTCACTACAG GTACTTT	eekkddddddddkkeee	40	9895	9911	1364
596815	745	761	CTCACTACAG GTACTTT	eekkddddddddkkee	54	9895	9911	1364
596625	746	762	TCTCACTACA GGTACTT	eekkddddddddkkeee	42	9896	9912	1365
596816	746	762	TCTCACTACA GGTACTT	eekkddddddddkkee	46	9896	9912	1365
596626	747	763	TTCTCACTACA GGTACT	eekkddddddddkkeee	26	9897	9913	1366
596817	747	763	TTCTCACTACA GGTACT	eekkddddddddkkee	37	9897	9913	1366
596627	748	764	TTTCTCACTAC AGGTAC	eekkddddddddkkeee	35	9898	9914	1367
596818	748	764	TTTCTCACTAC AGGTAC	eekkddddddddkkee	45	9898	9914	1367
596628	749	765	GTTTCTCACTA CAGGTA	eekkddddddddkkeee	25	9899	9915	1368
596819	749	765	GTTTCTCACTA CAGGTA	eekkddddddddkkee	38	9899	9915	1368
596629	750	766	AGTTTCTCACT ACAGGT	eekkddddddddkkeee	33	9900	9916	1369
596820	750	766	AGTTTCTCACT ACAGGT	eekkddddddddkkee	50	9900	9916	1369
596630	751	767	CAGTTTCTCAC TACAGG	eekkddddddddkkeee	38	9901	9917	1370

596821	751	767	CAGTTTCTCAC TACAGG	eekkddddddddkkee	38	9901	9917	1370
596631	752	768	TCAGTTTCTCA CTACAG	eekkddddddddkkeee	25	9902	9918	1371
596822	752	768	TCAGTTTCTCA CTACAG	eekkddddddddkkee	43	9902	9918	1371
596632	753	769	ATCAGTTTCTC ACTACA	eekkddddddddkkeee	31	9903	9919	1372
596823	753	769	ATCAGTTTCTC ACTACA	eekkddddddddkkee	44	9903	9919	1372
596633	754	770	AATCAGTTTCT CACTAC	eekkddddddddkkeee	34	9904	9920	1373
596824	754	770	AATCAGTTTCT CACTAC	eekkddddddddkkee	53	9904	9920	1373
596634	761	777	GATCATAAAT CAGTTTC	eekkddddddddkkeee	34	9911	9927	1374
596825	761	777	GATCATAAAT CAGTTTC	eekkddddddddkkee	38	9911	9927	1374
596635	762	778	TGATCATAAA TCAGTTT	eekkddddddddkkeee	49	9912	9928	1375
596826	762	778	TGATCATAAA TCAGTTT	eekkddddddddkkee	38	9912	9928	1375
596636	763	779	GTGATCATAA ATCAGTT	eekkddddddddkkeee	33	9913	9929	1376
596827	763	779	GTGATCATAA ATCAGTT	eekkddddddddkkee	48	9913	9929	1376
596637	764	780	AGTGATCATA AATCAGT	eekkddddddddkkeee	23	9914	9930	1377
596828	764	780	AGTGATCATA AATCAGT	eekkddddddddkkee	32	9914	9930	1377
596638	766	782	CAAGTGATCA TAAATCA	eekkddddddddkkeee	47	9916	9932	1378
596829	766	782	CAAGTGATCA TAAATCA	eekkddddddddkkee	29	9916	9932	1378
596639	767	783	CCAAGTGATC ATAAATC	eekkddddddddkkeee	40	9917	9933	1379
596830	767	783	CCAAGTGATC ATAAATC	eekkddddddddkkee	48	9917	9933	1379
596640	768	784	TCCAAGTGAT CATAAAT	eekkddddddddkkeee	42	9918	9934	1380
596831	768	784	TCCAAGTGAT CATAAAT	eekkddddddddkkee	39	9918	9934	1380

596641	770	786	CTTCCAAGTG ATCATAA	eekkddddddddkkeee	40	9920	9936	1381
596832	770	786	CTTCCAAGTG ATCATAA	eekkddddddddkkee	54	9920	9936	1381
596642	771	787	TCTTCCAAGTG ATCATA	eekkddddddddkkeee	33	9921	9937	1382
596833	771	787	TCTTCCAAGTG ATCATA	eekkddddddddkkee	43	9921	9937	1382
596643	772	788	ATCTTCCAAGT GATCAT	eekkddddddddkkeee	38	9922	9938	1184
596834	772	788	ATCTTCCAAGT GATCAT	eekkddddddddkkee	38	9922	9938	1184

Table 22

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCT TCAGCACGCA	eeeeeddddddddddeeeee	62	973	992	21
596720	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkeee	53	973	989	966
596911	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkee	58	973	989	966
596644	773	789	AATCTTCCAA GTGATCA	eekkddddddddkkeee	19	9923	9939	1185
596835	773	789	AATCTTCCAA GTGATCA	eekkddddddddkkee	38	9923	9939	1185
596645	774	790	AAATCTTCCA AGTGATC	eekkddddddddkkeee	46	9924	9940	1186
596836	774	790	AAATCTTCCA AGTGATC	eekkddddddddkkee	48	9924	9940	1186
596646	782	798	AACTATACAA ATCTTCC	eekkddddddddkkeee	60	9932	9948	1193
596837	782	798	AACTATACAA ATCTTCC	eekkddddddddkkee	63	9932	9948	1193
596647	783	799	AAACTATACA AATCTTC	eekkddddddddkkeee	55	9933	9949	1194
596838	783	799	AAACTATACA AATCTTC	eekkddddddddkkee	55	9933	9949	1194

596648	806	822	AGACATTTTA ACTGAGT	eekkddddddddkkeee	46	9956	9972	1383
596839	806	822	AGACATTTTA ACTGAGT	eekkddddddddkkee	53	9956	9972	1383
596649	817	833	GTCATTGAAA CAGACAT	eekkddddddddkkeee	2	9967	9983	1201
596840	817	833	GTCATTGAAA CAGACAT	eekkddddddddkkee	15	9967	9983	1201
596650	819	835	AGGTCATTGA AACAGAC	eekkddddddddkkeee	40	9969	9985	1203
596841	819	835	AGGTCATTGA AACAGAC	eekkddddddddkkee	44	9969	9985	1203
596651	822	838	TACAGGTCAT TGAAACA	eekkddddddddkkeee	26	9972	9988	1206
596842	822	838	TACAGGTCAT TGAAACA	eekkddddddddkkee	38	9972	9988	1206
596652	823	839	ATACAGGTCA TTGAAAC	eekkddddddddkkeee	33	9973	9989	1207
596843	823	839	ATACAGGTCA TTGAAAC	eekkddddddddkkee	22	9973	9989	1207
596653	825	841	AAATACAGGT CATTGAA	eekkddddddddkkeee	28	9975	9991	1209
596844	825	841	AAATACAGGT CATTGAA	eekkddddddddkkee	47	9975	9991	1209
596654	827	843	CAAAATACAG GTCATTG	eekkddddddddkkeee	44	9977	9993	1211
596845	827	843	CAAAATACAG GTCATTG	eekkddddddddkkee	56	9977	9993	1211
596655	830	846	TGGCAAAATA CAGGTCA	eekkddddddddkkeee	33	9980	9996	1214
596846	830	846	TGGCAAAATA CAGGTCA	eekkddddddddkkee	43	9980	9996	1214
596656	831	847	CTGGCAAAAT ACAGGTC	eekkddddddddkkeee	25	9981	9997	1215
596847	831	847	CTGGCAAAAT ACAGGTC	eekkddddddddkkee	53	9981	9997	1215
596657	833	849	GTCTGGCAAA ATACAGG	eekkddddddddkkeee	30	9983	9999	1217
596848	833	849	GTCTGGCAAA ATACAGG	eekkddddddddkkee	38	9983	9999	1217
596658	836	852	TAAGTCTGGC AAAATAC	eekkddddddddkkeee	24	9986	10002	1220

596849	836	852	TAAGTCTGGC AAAATAC	eekkddddddddkkee	46	9986	10002	1220
596659	837	853	TTAAGTCTGG CAAAATA	eekkddddddddkkeee	27	9987	10003	1221
596850	837	853	TTAAGTCTGG CAAAATA	eekkddddddddkkee	42	9987	10003	1221
596660	840	856	GATTTAAGTC TGGCAAA	eekkddddddddkkeee	19	9990	10006	1384
596851	840	856	GATTTAAGTC TGGCAAA	eekkddddddddkkee	35	9990	10006	1384
596661	841	857	TGATTTAAGT CTGGCAA	eekkddddddddkkeee	52	9991	10007	1385
596852	841	857	TGATTTAAGT CTGGCAA	eekkddddddddkkee	52	9991	10007	1385
596662	842	858	GTGATTTAAG TCTGGCA	eekkddddddddkkeee	54	9992	10008	1386
596853	842	858	GTGATTTAAG TCTGGCA	eekkddddddddkkee	69	9992	10008	1386
596663	843	859	TGTGATTTAA GTCTGGC	eekkddddddddkkeee	45	9993	10009	1387
596854	843	859	TGTGATTTAA GTCTGGC	eekkddddddddkkee	58	9993	10009	1387
596664	844	860	CTGTGATTTA AGTCTGG	eekkddddddddkkeee	n.d.	9994	10010	1388
596855	844	860	CTGTGATTTA AGTCTGG	eekkddddddddkkee	61	9994	10010	1388
596665	845	861	TCTGTGATTT AAGTCTG	eekkddddddddkkeee	49	9995	10011	1389
596856	845	861	TCTGTGATTT AAGTCTG	eekkddddddddkkee	49	9995	10011	1389
596666	846	862	ATCTGTGATT TAAGTCT	eekkddddddddkkeee	35	9996	10012	1390
596857	846	862	ATCTGTGATT TAAGTCT	eekkddddddddkkee	37	9996	10012	1390
596667	847	863	CATCTGTGAT TTAAGTC	eekkddddddddkkeee	42	9997	10013	1391
596858	847	863	CATCTGTGAT TTAAGTC	eekkddddddddkkee	48	9997	10013	1391
596668	848	864	CCATCTGTGA TTTAAGT	eekkddddddddkkeee	46	9998	10014	1392
596859	848	864	CCATCTGTGA TTTAAGT	eekkddddddddkkee	47	9998	10014	1392

596669	849	865	CCCATCTGTG ATTTAAG	eekkddddddddkkeee	49	9999	10015	1393
596860	849	865	CCCATCTGTG ATTTAAG	eekkddddddddkkee	49	9999	10015	1393
596670	850	866	ACCCATCTGT GATTTAA	eekkddddddddkkeee	33	10000	10016	1394
596861	850	866	ACCCATCTGT GATTTAA	eekkddddddddkkee	44	10000	10016	1394
596671	851	867	TACCCATCTG TGATTTA	eekkddddddddkkeee	29	10001	10017	1395
596862	851	867	TACCCATCTG TGATTTA	eekkddddddddkkee	45	10001	10017	1395
596672	854	870	TAATACCCAT CTGTGAT	eekkddddddddkkeee	25	10004	10020	1223
596863	854	870	TAATACCCAT CTGTGAT	eekkddddddddkkee	28	10004	10020	1223
596673	855	871	TTAATACCCA TCTGTGA	eekkddddddddkkeee	28	10005	10021	1224
596864	855	871	TTAATACCCA TCTGTGA	eekkddddddddkkee	26	10005	10021	1224
596674	858	874	AGTTTAATAC CCATCTG	eekkddddddddkkeee	29	10008	10024	1227
596865	858	874	AGTTTAATAC CCATCTG	eekkddddddddkkee	43	10008	10024	1227
596675	859	875	AAGTTTAATA CCCATCT	eekkddddddddkkeee	54	10009	10025	1228
596866	859	875	AAGTTTAATA CCCATCT	eekkddddddddkkee	59	10009	10025	1228
596676	860	876	CAAGTTTAAT ACCCATC	eekkddddddddkkeee	52	10010	10026	1229
596867	860	876	CAAGTTTAAT ACCCATC	eekkddddddddkkee	62	10010	10026	1229
596677	861	877	ACAAGTTTAA TACCCAT	eekkddddddddkkeee	58	10011	10027	1230
596868	861	877	ACAAGTTTAA TACCCAT	eekkddddddddkkee	61	10011	10027	1230
596678	862	878	GACAAGTTTA ATACCCA	eekkddddddddkkeee	54	10012	10028	1231
596869	862	878	GACAAGTTTA ATACCCA	eekkddddddddkkee	59	10012	10028	1231
596679	863	879	TGACAAGTTT AATACCC	eekkddddddddkkeee	43	10013	10029	1232

596870	863	879	TGACAAGTTT AATACCC	eekkddddddddkkee	52	10013	10029	1232
596680	864	880	CTGACAAGTT TAATACC	eekkddddddddkkeee	30	10014	10030	1233
596871	864	880	CTGACAAGTT TAATACC	eekkddddddddkkee	36	10014	10030	1233
596681	865	881	TCTGACAAGT TTAATAC	eekkddddddddkkeee	33	10015	10031	1234
596872	865	881	TCTGACAAGT TTAATAC	eekkddddddddkkee	20	10015	10031	1234

Table 23

Percent inhibition of SOD-1 mRNA by deoxy, MOE and cEt gapmers targeting SEQ ID NO: 1 and/or 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
333611	167	186	CCGTCGCCCT TCAGCACGCA	eeeeddddddddddeeeee	68	973	992	21
596720	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkeee	64	973	989	966
596911	167	183	TCGCCCTTCA GCACGCA	eekkddddddddkkee	71	973	989	966
596682	884	900	GCTTGAATGA CAAAGAA	eekkddddddddkkeee	24	10034	10050	1396
596873	884	900	GCTTGAATGA CAAAGAA	eekkddddddddkkee	32	10034	10050	1396
596683	885	901	GGCTTGAATG ACAAAGA	eekkddddddddkkeee	54	10035	10051	1397
596874	885	901	GGCTTGAATG ACAAAGA	eekkddddddddkkee	44	10035	10051	1397
596684	889	905	CACAGGCTTG AATGACA	eekkddddddddkkeee	34	10039	10055	1398
596875	889	905	CACAGGCTTG AATGACA	eekkddddddddkkee	47	10039	10055	1398
596685	890	906	TCACAGGCTT GAATGAC	eekkddddddddkkeee	28	10040	10056	1399
596876	890	906	TCACAGGCTT GAATGAC	eekkddddddddkkee	46	10040	10056	1399
596686	891	907	TTCACAGGCT TGAATGA	eekkddddddddkkeee	20	10041	10057	1242

596877	891	907	TTCACAGGCT TGAATGA	eekkddddddddkkee	16	10041	10057	1242
596687	892	908	ATTCACAGGC TTGAATG	eekkddddddddkkeee	19	10042	10058	1243
596878	892	908	ATTCACAGGC TTGAATG	eekkddddddddkkee	29	10042	10058	1243
596688	893	909	TATTCACAGG CTTGAAT	eekkddddddddkkeee	24	10043	10059	1244
596879	893	909	TATTCACAGG CTTGAAT	eekkddddddddkkee	11	10043	10059	1244
596689	894	910	TTATTCACAG GCTTGAA	eekkddddddddkkeee	26	10044	10060	1245
596880	894	910	TTATTCACAG GCTTGAA	eekkddddddddkkee	30	10044	10060	1245
596690	895	911	TTTATTCACA GGCTTGA	eekkddddddddkkeee	44	10045	10061	1246
596881	895	911	TTTATTCACA GGCTTGA	eekkddddddddkkee	55	10045	10061	1246
596691	896	912	TTTTATTCAC AGGCTTG	eekkddddddddkkeee	43	10046	10062	1247
596882	896	912	TTTTATTCAC AGGCTTG	eekkddddddddkkee	48	10046	10062	1247
596692	899	915	GGTTTTTATT CACAGGC	eekkddddddddkkeee	38	10049	10065	1250
596883	899	915	GGTTTTTATT CACAGGC	eekkddddddddkkee	57	10049	10065	1250
596693	903	919	ACAGGGTTTT TATTCAC	eekkddddddddkkeee	29	10053	10069	1254
596884	903	919	ACAGGGTTTT TATTCAC	eekkddddddddkkee	47	10053	10069	1254
596694	904	920	TACAGGGTTT TTATTCA	eekkddddddddkkeee	13	10054	10070	1255
596885	904	920	TACAGGGTTT TTATTCA	eekkddddddddkkee	31	10054	10070	1255
596695	907	923	CCATACAGGG TTTTTAT	eekkddddddddkkeee	13	10057	10073	1258
596886	907	923	CCATACAGGG TTTTTAT	eekkddddddddkkee	34	10057	10073	1258
596696	908	924	GCCATACAGG GTTTTTA	eekkddddddddkkeee	13	10058	10074	1259
596887	908	924	GCCATACAGG GTTTTTA	eekkddddddddkkee	26	10058	10074	1259

596697	909	925	TGCCATACAG GGTTTTT	eekkddddddddkkeee	21	10059	10075	1260
596888	909	925	TGCCATACAG GGTTTTT	eekkddddddddkkee	22	10059	10075	1260
596698	910	926	GTGCCATACA GGGTTTT	eekkddddddddkkeee	20	10060	10076	1261
596889	910	926	GTGCCATACA GGGTTTT	eekkddddddddkkee	28	10060	10076	1261
596699	911	927	AGTGCCATAC AGGGTTT	eekkddddddddkkeee	20	10061	10077	1262
596890	911	927	AGTGCCATAC AGGGTTT	eekkddddddddkkee	27	10061	10077	1262
596700	912	928	AAGTGCCATA CAGGGTT	eekkddddddddkkeee	15	10062	10078	1400
596891	912	928	AAGTGCCATA CAGGGTT	eekkddddddddkkee	21	10062	10078	1400
596701	913	929	TAAGTGCCAT ACAGGGT	eekkddddddddkkeee	26	10063	10079	1401
596892	913	929	TAAGTGCCAT ACAGGGT	eekkddddddddkkee	35	10063	10079	1401
596702	914	930	ATAAGTGCCA TACAGGG	eekkddddddddkkeee	36	10064	10080	1402
596893	914	930	ATAAGTGCCA TACAGGG	eekkddddddddkkee	46	10064	10080	1402
596703	915	931	AATAAGTGCC ATACAGG	eekkddddddddkkeee	40	10065	10081	1403
596894	915	931	AATAAGTGCC ATACAGG	eekkddddddddkkee	36	10065	10081	1403
596704	916	932	TAATAAGTGC CATACAG	eekkddddddddkkeee	22	10066	10082	1404
596895	916	932	TAATAAGTGC CATACAG	eekkddddddddkkee	30	10066	10082	1404
596705	917	933	ATAATAAGTG CCATACA	eekkddddddddkkeee	27	10067	10083	1405
596896	917	933	ATAATAAGTG CCATACA	eekkddddddddkkee	27	10067	10083	1405
596706	918	934	CATAATAAGT GCCATAC	eekkddddddddkkeee	32	10068	10084	1406
596897	918	934	CATAATAAGT GCCATAC	eekkddddddddkkee	34	10068	10084	1406
596707	919	935	TCATAATAAG TGCCATA	eekkddddddddkkeee	28	10069	10085	1407

596898	919	935	TCATAATAAG TGCCATA	eekkddddddddkkee	34	10069	10085	1407
596708	920	936	CTCATAATAA GTGCCAT	eekkddddddddkkeee	30	10070	10086	1408
596899	920	936	CTCATAATAA GTGCCAT	eekkddddddddkkee	44	10070	10086	1408
596709	921	937	CCTCATAATA AGTGCCA	eekkddddddddkkeee	29	10071	10087	1409
596900	921	937	CCTCATAATA AGTGCCA	eekkddddddddkkee	31	10071	10087	1409
596710	922	938	GCCTCATAAT AAGTGCC	eekkddddddddkkeee	41	10072	10088	1410
596901	922	938	GCCTCATAAT AAGTGCC	eekkddddddddkkee	33	10072	10088	1410
596711	923	939	AGCCTCATAA TAAGTGC	eekkddddddddkkeee	16	10073	10089	1411
596902	923	939	AGCCTCATAA TAAGTGC	eekkddddddddkkee	11	10073	10089	1411
596712	924	940	TAGCCTCATA ATAAGTG	eekkddddddddkkeee	11	10074	10090	1412
596903	924	940	TAGCCTCATA ATAAGTG	eekkddddddddkkee	27	10074	10090	1412
596713	925	941	ATAGCCTCAT AATAAGT	eekkddddddddkkeee	20	10075	10091	1413
596904	925	941	ATAGCCTCAT AATAAGT	eekkddddddddkkee	27	10075	10091	1413
596714	926	942	AATAGCCTCA TAATAAG	eekkddddddddkkeee	20	10076	10092	1414
596905	926	942	AATAGCCTCA TAATAAG	eekkddddddddkkee	25	10076	10092	1414
596715	931	947	CTTTTAATAG CCTCATA	eekkddddddddkkeee	45	10081	10097	1415
596906	931	947	CTTTTAATAG CCTCATA	eekkddddddddkkee	34	10081	10097	1415
596716	932	948	TCTTTTAATA GCCTCAT	eekkddddddddkkeee	52	10082	10098	1416
596907	932	948	TCTTTTAATA GCCTCAT	eekkddddddddkkee	56	10082	10098	1416
596717	936	952	GGATTCTTTT AATAGCC	eekkddddddddkkeee	14	10086	10102	1417
596908	936	952	GGATTCTTTT AATAGCC	eekkddddddddkkee	19	10086	10102	1417

596718	938	954	TTGGATTCTT TTAATAG	eekkddddddddkkeee	23	10088	10104	1263
596909	938	954	TTGGATTCTT TTAATAG	eekkddddddddkkee	8	10088	10104	1263
596719	949	965	TTAGTTTGAA TTTGGAT	eekkddddddddkkeee	31	10099	10115	1418
596910	949	965	TTAGTTTGAA TTTGGAT	eekkddddddddkkee	16	10099	10115	1418

Example 6: Dose-dependent inhibition of human SOD-1 with modified oligonucleotides in HepG2 cells

Gapmers from the studies described above exhibiting significant *in vitro* inhibition of SOD-1 mRNA were selected and tested at various doses in HepG2 cells. Benchmark compound ISIS 333611 and other compounds previously disclosed in WO 2005/040180, including ISIS 146144, 146145, 150445, 150446, 150447, 150454, 150463, 150465, 333606, 333609, and 333611 were also tested.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.813 μM, 1.625 μM, 3.250 μM, 6.500 μM, and 13.000 μM concentrations of modified oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is also presented. SOD-1 mRNA levels were significantly reduced in a dose-dependent manner in modified oligonucleotide treated cells.

Table 24
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.813 μM	1.625 μM	3.250 μM	6.500 μM	13.000 μM	IC_{50} (μM)
150445	7	21	44	56	82	4.4
150446	15	32	47	71	87	3.2
150447	26	43	68	81	93	2.0
150463	16	38	51	66	85	3.1
333611	18	39	57	66	79	3.0
393336	18	34	53	69	83	3.1
393343	24	32	53	73	42	5.1
436863	18	42	58	72	89	2.6

590089	28	59	70	82	90	1.5
590090	34	56	76	82	51	1.1
590091	30	44	68	84	88	1.9
590094	16	35	57	73	76	3.0
590113	34	35	57	73	84	2.3

Table 25
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.813 μM	1.625 μM	3.250 μM	6.500 μM	13.000 μM	IC_{50} (μM)
150465	42	59	77	82	87	1.0
333611	17	26	40	64	82	3.8
378879	14	35	63	72	86	2.8
393371	28	42	57	74	80	2.3
489520	28	44	64	72	84	2.2
590177	53	59	69	85	88	0.7
590178	40	53	71	73	87	1.3
590180	18	42	51	64	73	3.3
590187	34	51	68	80	92	1.6
590188	30	46	61	76	88	2.0
590189	37	49	68	78	88	1.6
590190	38	58	77	84	89	1.1
590191	29	56	71	77	84	1.6
590192	37	59	72	80	87	1.2

Table 26
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.813 μM	1.625 μM	3.250 μM	6.500 μM	13.000 μM	IC_{50} (μM)
146144	15	58	67	78	64	2.2
146145	31	53	67	81	90	1.6
333606	11	39	62	75	91	2.7
333609	13	37	57	71	85	2.9
333611	14	30	53	68	86	3.2
590250	8	19	47	64	84	3.9
590626	61	72	84	84	87	0.2
592630	24	33	58	70	85	2.7
592631	19	48	59	74	88	2.3
592645	20	31	53	74	89	2.8
592649	14	32	56	69	82	3.2

Table 27
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.813 μM	1.625 μM	3.250 μM	6.500 μM	13.000 μM	IC_{50} (μM)
150454	13	24	49	69	83	3.5
333611	28	28	53	68	82	3.0
489505	13	24	38	56	81	4.5
489516	25	16	39	61	79	4.3
592652	11	31	52	74	46	5.1
592714	8	25	45	69	82	3.8
592715	18	35	50	70	83	3.1
592762	44	66	74	81	89	0.8
592763	50	68	74	86	95	0.7
592764	26	43	48	76	87	2.5
592766	36	53	66	77	89	1.5
592767	25	31	54	70	79	2.9
592769	35	31	56	73	80	2.5
592771	34	43	58	70	80	2.2

Example 7: Dose-dependent inhibition of human SOD-1 with modified oligonucleotides in HepG2 cells

Gapmers from the studies described above exhibiting significant *in vitro* inhibition of SOD-1 mRNA were selected and tested at various doses in HepG2 cells. Benchmark compound, ISIS 333611, and ISIS 333625, both of which were previously disclosed in WO 2005/040180 were also tested.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.148 μM, 0.444 μM, 1.330 μM, 4.000 μM, and 12.000 μM concentrations of modified oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe sets RTS3898 or HTS90 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is also presented. SOD-1 mRNA levels were significantly reduced in a dose-dependent manner in modified oligonucleotide treated cells.

Table 28
Dose response assay with primer probe set RTS3898

ISIS No	0.148 μM	0.444 μM	1.330 μM	4.000 μM	12.000 μM	IC_{50} (μM)
333611	6	14	29	51	78	3.2
596911	8	12	23	54	74	3.6
596720	7	14	31	55	71	3.4
596800	44	60	75	84	82	0.2
596801	33	49	69	79	83	0.5
596610	16	44	65	78	84	0.8
596799	20	45	64	75	84	0.8
596609	17	54	65	75	81	0.7
596883	13	22	36	45	51	8.6
489523	16	40	62	78	90	0.9
590181	5	17	46	70	89	1.7
436868	10	35	47	69	82	1.4
596768	16	37	62	82	89	0.9
596775	36	50	66	83	89	0.4

Table 29
Dose response assay with primer probe set HTS90

ISIS No	0.148 μM	0.444 μM	1.330 μM	4.000 μM	12.000 μM	IC_{50} (μM)
333625	0	4	17	56	84	3.3
489532	54	70	78	86	96	0.1
590154	0	14	25	56	86	2.7
596173	0	5	25	63	92	2.4
596174	7	12	37	46	84	2.8
596178	2	16	40	68	82	2.1
596179	0	17	41	64	80	2.3
596308	0	5	22	56	80	3.3
596572	18	35	62	83	90	0.9
596589	10	45	61	77	91	0.9
596600	41	56	71	85	92	0.3
596602	14	51	74	86	95	0.6
596789	22	55	69	86	91	0.5
596795	16	43	64	82	93	0.8

Example 8: Dose-dependent inhibition of human SOD-1 with modified oligonucleotides in HepG2 cells

Gapmers from the studies described above exhibiting significant *in vitro* inhibition of SOD-1 mRNA were selected and tested at various doses in HepG2 cells. Benchmark compound, ISIS 333611, and

additional compounds including, ISIS 146143, 150442, 195753, 333607, and 333608, were previously disclosed in WO 2005/040180 were also tested.

The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.1875 μM, 0.7500 μM, 3.0000 μM, and 12.0000 μM concentrations of modified oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe sets RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is also presented. SOD-1 mRNA levels were significantly reduced in a dose-dependent manner in modified oligonucleotide treated cells.

Table 30
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.1875 μM	0.75 μM	3.00 μM	12.00 μM	IC_{50} (μM)
333611	0	27	60	91	2
596572	38	65	87	96	0.3
596583	62	89	95	95	<0.1
596590	40	79	89	94	0.2
596602	40	75	92	98	0.2
596603	51	79	92	96	0.1
596604	48	78	91	95	0.1
596605	50	86	90	97	0.1
596764	11	67	89	94	0.7
596768	27	49	82	92	0.7
596773	32	62	89	98	0.4
596774	56	89	93	96	<0.1
596775	31	75	90	97	0.3
596780	24	71	85	98	0.5
596781	30	80	93	97	0.3
596791	38	74	89	95	0.3
596794	43	75	91	97	0.2
596795	28	66	91	98	0.4
596796	43	78	93	98	0.2

Table 31
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.1875 μM	0.75 μM	3.00 μM	12.00 μM	IC_{50} (μM)
333611	0	15	68	95	2.1
596589	35	70	90	97	0.3
596789	38	71	89	97	0.3
596600	41	73	89	95	0.2
596582	30	71	87	95	0.4
596784	26	68	89	95	0.4
596787	44	67	89	94	0.2
596779	29	71	89	97	0.4
596792	37	63	83	95	0.4
596782	27	61	85	96	0.5
596765	34	59	87	95	0.4
596793	27	65	88	96	0.5
596570	25	60	84	91	0.6
596769	21	64	85	96	0.6
596783	10	57	84	94	0.9
596584	26	67	84	93	0.5
596571	37	71	81	92	0.3
596598	30	62	81	94	0.5
596588	11	64	87	95	0.7

Table 32
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.1875 μM	0.75 μM	3.00 μM	12.00 μM	IC_{50} (μM)
146143	6	12	51	88	2.5
150442	10	21	39	90	2.5
195753	13	23	48	77	2.8
333607	17	26	59	83	1.9
333608	0	2	28	92	3.7
333611	0	13	52	91	2.4
596573	26	51	77	91	0.8
596577	32	55	78	93	0.6
596591	23	51	74	91	0.8
596592	18	48	66	86	1.1
596593	16	58	78	87	0.8
596596	4	49	72	87	1.3
596761	28	55	74	91	0.7
596762	0	47	75	90	1.3
596763	0	40	78	92	1.5

596766	4	50	68	86	1.3
596785	10	47	77	91	1.1
596786	0	45	75	97	1.3
596788	9	52	81	95	1

Table 33
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.1875 μM	0.75 μM	3.00 μM	12.00 μM	IC_{50} (μM)
333611	3	22	60	92	2
596302	9	27	59	89	1.9
596308	29	47	82	96	0.7
596309	13	42	75	92	1.1
596310	13	16	48	81	2.8
596313	15	37	70	88	1.3
596314	18	45	74	92	1
596606	55	78	87	93	0.1
596607	44	71	83	84	0.2
596608	46	74	84	81	0.1
596609	30	61	79	87	0.5
596610	39	69	82	86	0.3
596612	16	50	62	77	1.4
596797	67	84	94	96	<0.1
596798	42	68	86	89	0.2
596799	35	66	83	87	0.4
596800	45	73	84	87	0.2
596801	40	67	86	88	0.3
596803	28	41	63	71	1.4

Table 34
Dose-dependent inhibition of SOD-1 mRNA

ISIS No	0.1875 μM	0.75 μM	3.00 μM	12.00 μM	IC_{50} (μM)
333611	0	30	56	69	3.1
590475	19	39	69	88	1.2
590625	19	51	74	85	1.0
590626	42	72	88	90	0.2
590627	16	42	70	84	1.0
590634	45	72	86	92	0.2
590635	39	60	80	90	0.4
590644	44	62	80	86	0.3
590650	34	56	82	93	0.5
590653	52	78	86	85	0.1

590655	35	71	79	82	0.3
596530	25	22	72	79	2.0
596531	8	38	74	96	1.2
596559	15	36	79	95	1.1
596721	14	47	82	97	0.9
596723	12	47	79	94	1.0
596726	24	42	80	94	0.9
596735	7	32	77	96	1.3
596736	25	52	82	97	0.7

Example 9: Dose-dependent inhibition of human SOD-1 in HepG2 cells by gapmers with mixed backbone chemistry

Additional gapmers were designed based on the sequences of the oligonucleotides disclosed in studies described above. The oligonucleotides were designed as 5-10-5 MOE, 5-8-5 MOE, and deoxy, MOE and cEt oligonucleotides. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of ten 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. The 5-8-5 MOE gapmers are 18 nucleosides in length, wherein the central gap segment is comprised of eight 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The deoxy, MOE and cEt oligonucleotides are 16 or 17 nucleosides in length wherein each nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety. The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose; and 'e' indicates a 2'-MOE modified sugar. The internucleoside linkages throughout each gapmer are either phosphodiester or phosphorothioate linkages. The internucleoside linkages of each oligonucleotide are denoted in the Backbone Chemistry column, where 'o' indicates a phosphodiester linkage and 's' denotes a phosphorothioate linkage. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000).

Table 35

Modified oligonucleotides targeting human SOD-1 with mixed backbone chemistry

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Sugar Modifications	Backbone Chemistry	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
611458	226	245	ACACCTTCAC TGGTCCATTA	eeeeeddddddddddeeeee	soooossssssssssooos	4980	4999	23
654335	233	248	CCCACACCTT CACTGG	ekddddddddekekee	sosssssssoooss	4987	5002	1420
611474	234	253	GCTTCCCCAC ACCTTCACTG	eeeeeddddddddddeeeee	soooossssssssssooos	4988	5007	149
654301	234	251	TTCCCCACAC CTTCACTG	eeeeeddddddddeeeee	sooossssssssooss	4988	5005	1421
654336	234	249	CCCCACACCT TCACTG	ekddddddddekekee	sosssssssoooss	4988	5003	1422
654302	235	252	CTTCCCCACA CCTTCACT	eeeeeddddddddeeeee	sooossssssssooss	4989	5006	1423
654319	235	250	TCCCCACACC TTCACT	kekeddddddddekek	sooosssssssoss	4989	5004	1424
654337	235	250	TCCCCACACC TTCACT	ekddddddddekekee	sosssssssoooss	4989	5004	1424
654303	236	253	GCTTCCCCAC ACCTTCAC	eeeeeddddddddeeeee	sooossssssssooss	4990	5007	1425
654320	236	251	TTCCCCACAC CTTCAC	kekeddddddddekek	sooosssssssoss	4990	5005	1426
654321	237	252	CTTCCCCACA CCTTCA	kekeddddddddekek	sooosssssssoss	4991	5006	1427
611475	321	340	GTGAGGACCT GCACTGGTAC	eeeeeddddddddddeeeee	soooossssssssssooos	7637	7656	172
611460	588	607	GGCGATCCCA ATTACACCAC	eeeeeddddddddddeeeee	soooossssssssssooos	9738	9757	47
654304	663	680	ATACATTTCT ACAGCTAG	eeeeeddddddddeeeee	sooossssssssooss	9813	9830	1429
654305	664	681	GATACATTTC TACAGCTA	eeeeeddddddddeeeee	sooossssssssooss	9814	9831	1430
654340	664	679	TACATTTCTA CAGCTA	ekddddddddekekee	sosssssssoooss	9814	9829	1431
611492	665	684	CAGGATACAT TTCTACAGCT	eeeeeddddddddddeeeee	soooossssssssssooos	9815	9834	725
654306	665	682	GGATACATTT CTACAGCT	eeeeeddddddddeeeee	sooossssssssooss	9815	9832	1432

654323	665	680	ATACATTTCT ACAGCT	kekeddddddddekek	soooosssssssoss	9815	9830	1433
654341	665	680	ATACATTTCT ACAGCT	ekddddddddekekee	sosssssssoooss	9815	9830	1433
611500	666	685	TCAGGATACA TTTCTACAGC	eeeeedddddddddeeeee	soooosssssssssooos	9816	9835	823
612941	666	682	GGATACATTT CTACAGC	eekkddddddddkkee	soooosssssssoss	9816	9832	1342
654307	666	683	AGGATACATT TCTACAGC	eeeeedddddddeeeee	soooosssssssooss	9816	9833	1434
654324	666	681	GATACATTTC TACAGC	kekeddddddddekek	soooosssssssoss	9816	9831	1435
654342	666	681	GATACATTTC TACAGC	ekddddddddekekee	sosssssssoooss	9816	9831	1435
654308	667	684	CAGGATACAT TTCTACAG	eeeeedddddddeeeee	soooosssssssooss	9817	9834	1436
612925	676	692	ATGTTTATCA GGATACA	eekkddddddddkkeee	soooosssssssooss	9826	9842	1348
612944	676	692	ATGTTTATCA GGATACA	eekkddddddddkkee	soooosssssssoss	9826	9842	1348
654343	677	692	ATGTTTATCA GGATAC	ekddddddddekekee	sosssssssoooss	9827	9842	1437
612927	678	694	TAATGTTTAT CAGGATA	eekkddddddddkkeee	soooosssssssooss	9828	9844	1350
654309	678	695	TTAATGTTTA TCAGGATA	eeeeedddddddeeeee	soooosssssssooss	9828	9845	1438
612928	679	695	TTAATGTTTA TCAGGAT	eekkddddddddkkeee	soooosssssssooss	9829	9845	1351
654310	679	696	TTTAATGTTT ATCAGGAT	eeeeedddddddeeeee	soooosssssssooss	9829	9846	1439
654311	680	697	GTTTAATGTT TATCAGGA	eeeeedddddddeeeee	soooosssssssooss	9830	9847	1440
654327	680	695	TTAATGTTTA TCAGGA	kekeddddddddekek	soooosssssssoss	9830	9845	1441
654346	680	695	TTAATGTTTA TCAGGA	ekddddddddekekee	sosssssssoooss	9830	9845	1441
611497	681	700	AGTGTTTAAT GTTTATCAGG	eeeeedddddddddeeeee	soooosssssssssooos	9831	9850	733
612948	681	697	GTTTAATGTT TATCAGG	eekkddddddddkkee	soooosssssssoss	9831	9847	1352
654312	681	698	TGTTTAATGT TTATCAGG	eeeeedddddddeeeee	soooosssssssooss	9831	9848	1442
654328	681	696	TTTAATGTTT ATCAGG	kekeddddddddekek	soooosssssssoss	9831	9846	1443

654347	681	696	TTTAATGTTT ATCAGG	ekddddddddekekee	sosssssssoooss	9831	9846	1443
654313	682	699	GTGTTTAATG TTTATCAG	eeeeeddddddddeeeee	sooossssssssooss	9832	9849	1444
654329	682	697	GTTTAATGTT TATCAG	kekeddddddddekek	sooosssssssoss	9832	9847	1445
654348	682	697	GTTTAATGTT TATCAG	ekddddddddekekee	sosssssssoooss	9832	9847	1445
612949	683	699	GTGTTTAATG TTTATCA	eekkddddddddkkee	sooossssssssoss	9833	9849	1172
654314	683	700	AGTGTTTAAT GTTTATCA	eeeeeddddddddeeeee	sooossssssssooss	9833	9850	1446
654330	683	698	TGTTTAATGT TTATCA	kekeddddddddekek	sooosssssssoss	9833	9848	1447
612931	684	700	AGTGTTTAAT GTTTATC	eekkddddddddkkeee	soosssssssssooss	9834	9850	1173
654315	684	701	CAGTGTTTAA TGTTTATC	eeeeeddddddddeeeee	sooossssssssooss	9834	9851	1448
654331	684	699	GTGTTTAATG TTTATC	kekeddddddddekek	sooosssssssoss	9834	9849	1449
654350	684	699	GTGTTTAATG TTTATC	ekddddddddekekee	sosssssssoooss	9834	9849	1449
654316	685	702	ACAGTGTTTA ATGTTTAT	eeeeeddddddddeeeee	sooossssssssooss	9835	9852	1450
612918	686	702	ACAGTGTTTA ATGTTTA	eeekkddddddddkkeee	soosssssssssooss	9836	9852	1175
612932	686	702	ACAGTGTTTA ATGTTTA	eekkddddddddkkeee	soosssssssssooss	9836	9852	1175
654317	686	703	TACAGTGTTT AATGTTTA	eeeeeddddddddeeeee	sooossssssssooss	9836	9853	1451
654333	686	701	CAGTGTTTAA TGTTTA	kekeddddddddekek	sooosssssssoss	9836	9851	1452
654352	686	701	CAGTGTTTAA TGTTTA	ekddddddddekekee	sosssssssoooss	9836	9851	1452
654318	687	704	TTACAGTGTT TAATGTTT	eeeeeddddddddeeeee	sooossssssssooss	9837	9854	1453
654334	687	702	ACAGTGTTTA ATGTTT	kekeddddddddekek	sooosssssssoss	9837	9852	1454

The newly designed oligonucleotides were tested at various doses in HepG2 cells. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.222 μM, 0.667 μM, 2.000 μM, and 6.000 μM

concentrations of modified oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe sets RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is also presented. SOD-1 mRNA levels were significantly reduced in a dose-dependent manner in modified oligonucleotide treated cells.

Table 36
Dose response assay

ISIS No	0.222 μM	0.667 μM	2.000 μM	6.000 μM	IC_{50} μM
333611	0	28	53	77	1.9
611458	0	21	50	79	2.0
611460	24	34	55	79	1.3
611474	14	32	55	79	1.5
611475	0	16	35	70	3.0
611492	38	70	88	95	0.3
611497	28	55	80	89	0.6
611500	25	50	73	92	0.7
612918	51	70	74	80	<0.2
612925	53	73	90	89	<0.2
612927	64	89	92	94	<0.2
612928	67	90	94	97	<0.2
612931	68	76	84	86	<0.2
612932	61	73	88	91	<0.2
612941	62	78	91	95	<0.2
612944	47	71	82	92	0.2
612948	76	90	93	94	<0.2
612949	58	68	83	96	<0.2
654301	7	4	17	42	>6.0

Table 37
Dose response assay

ISIS No	0.222 μM	0.667 μM	2.000 μM	6.000 μM	IC_{50} μM
333611	14	20	35	69	3.0
611458	11	27	36	68	2.9
654302	0	8	38	48	6.2
654303	8	29	46	76	1.9
654304	7	28	54	79	1.7

654305	28	59	73	85	0.6
654306	38	62	82	94	0.4
654307	9	43	65	86	1.1
654308	14	31	54	84	1.4
654309	0	17	47	72	2.4
654310	10	24	28	53	6.6
654311	45	73	78	87	0.2
654312	14	39	59	77	1.3
654313	20	43	56	81	1.2
654314	33	58	74	86	0.5
654315	21	47	64	84	0.9
654316	19	30	46	70	2.0
654317	13	46	57	70	1.4
654318	17	42	54	76	1.4

Table 38
Dose response assay

ISIS No	0.222 μM	0.667 μM	2.000 μM	6.000 μM	IC_{50} μM
333611	14	19	50	73	2.1
611458	9	22	39	72	2.5
654319	19	9	31	61	5.1
654320	6	16	20	59	5.9
654321	8	14	51	76	2.1
654323	55	73	89	95	<0.2
654324	54	78	89	96	<0.2
654327	53	82	91	96	<0.2
654328	73	90	93	97	<0.2
654329	58	78	86	94	<0.2
654330	42	54	69	86	0.4
654331	53	78	82	90	<0.2
654333	50	67	81	86	0.2
654334	55	68	78	88	<0.2
654335	15	31	58	81	1.4
654336	21	36	60	75	1.3
654337	16	34	58	80	1.4
654340	36	69	83	95	0.4
654341	43	58	79	91	0.3

Table 39
Dose response assay

ISIS No	0.222 μM	0.667 μM	2.00 μM	6.00 μM	IC_{50} μM
333611	0	6	38	64	3.6

611458	3	14	36	63	3.6
654342	40	60	80	93	0.4
654343	64	81	90	94	<0.2
654346	52	73	84	93	<0.2
654347	21	38	58	81	1.2
654348	44	63	82	94	0.3
654350	40	63	76	86	0.3
654352	54	79	84	88	<0.2

Example 10: Dose-dependent inhibition of human SOD-1 by gapmers with mixed backbone chemistry

Additional gapmers were designed based on the sequences of the oligonucleotides disclosed in studies described above. The oligonucleotides were designed as deoxy, MOE and cEt oligonucleotides. The deoxy, MOE and cEt oligonucleotides are 16 or 17 nucleosides in length wherein each nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety. The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose; and 'e' indicates a 2'-MOE modified sugar. The internucleoside linkages throughout each gapmer are either phosphodiester or phosphorothioate linkages. The internucleoside linkages of each oligonucleotide are denoted in the Backbone Chemistry column, where 'o' indicates a phosphodiester linkage and 's' indicates a phosphorothioate linkage. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000).

Table 40

Modified oligonucleotides targeting human SOD-1 with mixed backbone chemistry

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Sugar Modifications	Backbone Chemistry	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
612916	664	680	ATACATTTCTA CAGCTA	eeekkddddddkkeee	soosssssssssooss	9814	9830	1170
612947	679	695	TTAATGTTTAT CAGGAT	eekkddddddddkkee	sooosssssssssoss	9829	9845	1351

654322	664	679	TACATTTCTAC AGCTA	kekeddddddddekek	sooosssssssoss	9814	9829	1431
654325	667	682	GGATACATTT CTACAG	kekeddddddddekek	sooosssssssoss	9817	9832	1455
654326	679	694	TAATGTTTATC AGGAT	kekeddddddddekek	sooosssssssoss	9829	9844	1456
654332	685	700	AGTGTTTAAT GTTTAT	kekeddddddddekek	sooosssssssoss	9835	9850	1457
654338	662	677	CATTTCTACAG CTAGC	ekddddddddekekee	sosssssssooooss	9812	9827	1458
654339	663	678	ACATTTCTACA GCTAG	ekddddddddekekee	sosssssssooooss	9813	9828	1459
654344	678	693	AATGTTTATCA GGATA	ekddddddddekekee	sosssssssooooss	9828	9843	1460
654345	679	694	TAATGTTTATC AGGAT	ekddddddddekekee	sosssssssooooss	9829	9844	1456
654349	683	698	TGTTTAATGTT TATCA	ekddddddddekekee	sosssssssooooss	9833	9848	1447
654351	685	700	AGTGTTTAAT GTTTAT	ekddddddddekekee	sosssssssooooss	9835	9850	1457

The newly designed oligonucleotides were tested at various doses in A431 cells. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 5,000 cells per well and modified oligonucleotides were added to the media at 0.12 μM, 0.60 μM, 3.00 μM, and 15.00 μM concentrations of modified oligonucleotide for free uptake by the cells, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe sets RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

Table 41
Dose response assay

ISIS No	0.12 μM	0.60 μM	3.00 μM	15.00 μM
333611	0	7	17	31
611458	5	4	4	10
612916	4	13	26	37
612918	12	26	45	47
612944	1	4	21	29
612947	12	48	54	72
654305	7	15	39	52

654306	0	25	29	50
654313	1	15	36	50
654314	2	35	52	67
654321	0	8	8	18
654322	0	13	36	59
654329	7	7	41	66
654330	6	14	15	32
654337	0	0	7	21
654338	3	3	2	11
654345	1	9	22	46
654346	0	7	21	46

Table 42
Dose response assay

ISIS No	0.12 μM	0.60 μM	3.00 μM	15.00 μM
333611	0	0	0	2
611460	0	0	0	30
611474	0	0	11	0
612925	2	4	12	52
612927	0	38	54	68
612948	25	69	89	95
612949	22	57	73	84
654307	42	23	26	45
654308	2	31	9	18
654315	0	8	39	52
654316	0	18	26	45
654323	15	14	16	52
654324	12	22	21	34
654331	7	35	66	78
654332	2	31	47	61
654339	1	27	32	47
654340	37	0	22	12
654347	20	5	12	33
654348	2	19	33	62

Table 43
Dose response assay

ISIS No	0.12 μM	0.60 μM	3.00 μM	15.00 μM
333611	0	0	0	1
611475	0	17	0	16
611492	13	24	41	62

612928	12	36	49	72
612931	31	68	83	86
654301	2	0	0	9
654302	0	8	3	0
654309	18	7	11	9
654310	13	19	22	7
654317	3	0	1	20
654318	4	0	33	17
654325	0	0	0	14
654326	0	15	17	48
654333	19	18	36	55
654334	0	0	0	6
654341	0	9	0	25
654342	0	0	0	18
654349	0	13	31	49
654350	10	32	66	79

Table 44
Dose response assay

ISIS No	0.12 μM	0.60 μM	3.00 μM	15.00 μM
333611	5	0	7	3
611497	16	49	60	75
611500	9	8	21	49
612932	17	8	26	37
612941	4	12	36	51
654303	0	1	0	5
654304	9	10	27	43
654311	15	51	68	84
654312	6	26	29	33
654319	3	44	2	8
654320	4	12	5	12
654327	3	45	65	81
654328	15	44	73	85
654335	2	0	0	12
654336	0	0	0	0
654343	0	7	26	59
654344	10	30	51	72
654351	10	22	48	77
654352	8	26	57	76

Example 11: Dose-dependent inhibition of human SOD-1 by gapmers with mixed backbone chemistry

Additional gapmers were designed based on the sequences of the oligonucleotides disclosed in studies described above. The oligonucleotides were designed as 5-10-5 MOE gapmers, 4-8-5 MOE gapmers, 5-8-5 MOE gapmers, 5-8-7 MOE gapmers, 6-8-6 MOE gapmers, 6-9-5 MOE gapmers, or deoxy, MOE and cEt oligonucleotides.

The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of ten 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five nucleosides each. The 4-8-5 MOE gapmers are 17 nucleosides in length, wherein the central gap segment is comprised of eight 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising four and five nucleosides respectively. The 5-8-5 MOE gapmers are 18 nucleosides in length, wherein the central gap segment is comprised of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five nucleosides each. The 5-8-7 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five and seven nucleosides respectively. The 6-8-6 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of eight 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising six nucleosides each. The 6-9-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of nine 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising six and five nucleosides respectively. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification.

The deoxy, MOE and cEt oligonucleotides are 17 nucleosides in length wherein each nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety. The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose; and 'e' indicates a 2'-MOE modified sugar.

The internucleoside linkages throughout each gapmer are either phosphodiester or phosphorothioate linkages. The internucleoside linkages of each oligonucleotide are denoted in the Backbone Chemistry column, where 'o' indicates a phosphodiester linkage and 's' indicates a phosphorothioate linkage. All cytosine residues throughout each gapmer are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Tables below is targeted to either the human SOD-1 mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000).

Table 45

Modified oligonucleotides targeting human SOD-1 with mixed backbone chemistry

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	Sugar Modifications	Backbone Chemistry	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
666846	665	684	CAGGATACATTTCTACAGCT	5-10-5 MOE	eeeeeddddddddddeeeee	soooossssssssssooss	9815	9834	725
666849	665	684	CAGGATACATTTCTACAGCT	5-10-5 MOE	eeeeeddddddddddeeeee	sooossssssssssooss	9815	9834	725
666853	665	684	CAGGATACATTTCTACAGCT	5-10-5 MOE	eeeeeddddddddddeeeee	sososssssssssssosos	9815	9834	725
666859	679	695	TTAATGTTTATCAGGAT	Deoxy, MOE and cEt	eeeeddddddddkkeee	soossssssssooss	9829	9845	1351
666861	679	695	TTAATGTTTATCAGGAT	Deoxy, MOE and cEt	ekekddddddddeeeee	soossssssssooss	9829	9845	1351
666867	684	700	AGTGTTTAATGTTTATC	Deoxy, MOE and cEt	eekkddddddddeeeee	soossssssssooss	9834	9850	1173
666869	684	700	AGTGTTTAATGTTTATC	Deoxy, MOE and cEt	ekekddddddddkekee	soossssssssooss	9834	9850	1173
666870	684	700	AGTGTTTAATGTTTATC	Deoxy, MOE and cEt	ekekddddddddeeeee	soossssssssooss	9834	9850	1173
666919	666	682	GGATACATTTCTACAGC	Deoxy, MOE and cEt	eeeeddddddddkkee	sooossssssssoss	9816	9832	1342
666921	666	682	GGATACATTTCTACAGC	Deoxy, MOE and cEt	eeeeeddddddddkkee	sooossssssssoss	9816	9832	1342
666922	666	682	GGATACATTTCTACAGC	Deoxy, MOE and cEt	eeeekddddddddkeee	sooossssssssoss	9816	9832	1342
684059	676	692	ATGTTTATCAGGATACA	Deoxy, MOE and cEt	eeekddddddddkeeee	soossssssssooss	9826	9842	1348
684064	676	692	ATGTTTATCAGGATACA	Deoxy, MOE and cEt	eeeeddddddddkekee	soossssssssooss	9826	9842	1348
684068	676	692	ATGTTTATCAGGATACA	4-8-5 MOE	eeeeddddddddeeeee	soossssssssooss	9826	9842	1348
684087	590	607	GGCGATCCCAATTACACC	5-8-5 MOE	eeeeeddddddddeeeee	sooossssssssooss	9740	9757	613

684088	167	184	GTCGCCCTTC AGCACGCA	5-8-5 MOE	eeeeeddddddddeeeee	soooosssssssssooss	973	990	1419
684095	167	186	CCGTCGCCCT TCAGCACGCA	5-10-5 MOE	eeeeeddddddddddeeeee	soooossssssssssooss	973	992	21
684097	167	186	CCGTCGCCCT TCAGCACGCA	5-8-7 MOE	eeeeeddddddddeeeeeee	sooosssssssssoooss	973	992	21
684101	588	607	GGCGATCCCA ATTACACCAC	6-8-6 MOE	eeeeeeddddddddeeeeee	sooosssssssssoooss	9738	9757	47
684102	588	607	GGCGATCCCA ATTACACCAC	5-8-7 MOE	eeeeeddddddddeeeeeee	sooosssssssssoooss	9738	9757	47
684104	588	607	GGCGATCCCA ATTACACCAC	6-9-5 MOE	eeeeeeddddddddddeeeee	soooossssssssssooss	9738	9757	47

The newly designed oligonucleotides were tested at various doses in A431 cells. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 5,000 cells per well and modified oligonucleotides were added to the media at 0.062 μM, 0.185 μM, 0.556 μM, 1.667 μM, 5.000 μM, and 15.000 μM concentrations of modified oligonucleotide for free uptake by the cells, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe sets RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

Table 46
Dose response assay

ISIS No	0.062 μM	0.185 μM	0.556 μM	1.667 μM	5.000 μM	15.000 μM	IC_{50} (μM)
666846	18	28	45	70	69	81	0.8
666919	0	1	13	28	42	55	11.0
666849	33	29	52	62	74	82	0.6
666921	2	4	15	19	37	44	>15
666853	20	29	49	69	76	83	0.7
666922	8	7	30	33	66	59	4.1
666859	26	30	58	64	68	78	0.6
666861	6	21	44	76	68	77	1.1
666867	16	43	65	68	79	83	0.5
666869	52	68	79	88	89	91	<0.06
666870	24	37	57	77	81	86	0.4

Table 47
Dose response assay

ISIS No	0.062 μM	0.185 μM	0.556 μM	1.667 μM	5.000 μM	15.000 μM	IC_{50} (μM)
684059	7	18	38	53	68	79	1.5
684102	0	9	0	0	4	0	>15
684064	12	19	29	38	51	61	5.0
684104	0	0	0	0	0	4	>15
684068	0	4	10	33	50	56	8.0
684087	3	1	29	0	0	27	>15
684088	10	11	11	3	4	18	>15
684095	12	13	14	4	7	18	>15
684097	8	4	5	4	3	9	>15
684101	7	0	0	23	6	14	>15

The newly designed oligonucleotides were also tested at various doses in SH-SY5Y cells. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions. The results for each experiment are presented in separate tables shown below. Cells were plated at a density of 20,000 cells per well and modified oligonucleotides transfected using electroporation at 0.062 μM, 0.185 μM, 0.556 μM, 1.667 μM, 5.000 μM, and 15.000 μM concentrations of modified oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3898 was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells.

Table 48
Dose response assay

ISIS No	0.062 μM	0.185 μM	0.556 μM	1.667 μM	5.000 μM	15.000 μM	IC_{50} (μM)
666846	0	17	49	62	83	91	0.9
666919	10	3	23	35	77	78	2.2
666849	10	10	33	61	81	92	1.1
666921	0	0	12	30	56	68	4.8
666853	0	17	39	59	85	82	1.3
666922	9	0	12	33	65	76	3.2
666859	11	44	53	75	77	93	0.5
666861	0	0	34	61	81	90	1.4
666867	33	10	43	61	81	77	0.9
666869	38	49	61	83	81	84	0.2
666870	3	6	48	69	77	87	1.1

Table 49
Dose response assay

ISIS No	0.062 μM	0.185 μM	0.556 μM	1.667 μM	5.000 μM	15.000 μM	IC_{50} (μM)
684059	4	30	51	68	88	92	0.7
684102	5	2	16	25	36	61	12.0
684064	15	27	52	63	79	92	0.7
684104	0	3	20	38	61	84	2.6
684068	0	4	32	37	61	83	2.3
684087	0	3	21	31	47	66	5.8
684088	13	4	5	40	52	77	3.9
684095	16	5	19	36	68	80	2.4
684097	11	15	9	30	59	76	3.6
684101	0	0	8	23	49	66	6.6

Example 12: Inhibition of human SOD-1 in a transgenic rat model

Gapmers from the studies described above, including benchmark compound ISIS 333611, which was previously disclosed in WO 2005/040180, were tested in an SOD-1 transgenic rat model (Taconic, Cat# 2148-F and 2148-M). These hemizygous rats express mutant human SOD-1 in the spinal cord.

Additional gapmers were designed based on the sequences of the oligonucleotides disclosed in studies described above. The oligonucleotides were designed as 5-9-5 MOE gapmers, 5-10-5 MOE gapmers or deoxy, MOE and cEt oligonucleotides. The 5-9-5 MOE gapmers are 19 nucleosides in length, wherein the central gap segment is comprised of nine 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five nucleosides each. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment is comprised of ten 2'-deoxyribonucleosides and is flanked by wing segments on the 5' direction and the 3' directions comprising five nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-MOE modification. The deoxy, MOE and cEt oligonucleotides are 17 nucleosides in length wherein each nucleoside has a MOE sugar modification, a cEt sugar modification, or a deoxy moiety The sugar chemistry of each oligonucleotide is denoted as in the Chemistry column, where 'k' indicates a cEt modified sugar; 'd' indicates a 2'-deoxyribose; and 'e' indicates a 2'-MOE modified sugar. The internucleoside linkages throughout each gapmer are either phosphodiester or phosphorothioate linkages. The internucleoside linkages of each oligonucleotide is denoted in the Backbone Chemistry column, where 'o' indicates a phosphodiester linkage and 's' indicates a phosphorothioate linkage. All cytosine residues throughout each oligonucleotide are 5-methylcytosines. "Start site" indicates the 5'-most nucleoside to which the gapmer is targeted in the human gene sequence. "Stop site" indicates the 3'-most nucleoside to which the gapmer is targeted human gene sequence. Each gapmer listed in the Table below is targeted to either the human SOD-1 mRNA, designated

herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000454.4) or the human SOD-1 genomic sequence, designated herein as SEQ ID NO: 2 (GENBANK Accession No. NT_011512.10 truncated from nucleotides 18693000 to 18704000).

Table 50

Modified oligonucleotides targeting human SOD-1 with mixed backbone chemistry

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	Sugar Modifications	Backbone Chemistry	SEQ ID NO: 2 Start Site	SEQ ID NO: 2 Stop Site	SEQ ID NO
383872	167	186	CCGTCGCCCTTCAGCACGCA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	973	992	21
611457	165	184	GTCGCCCTTCAGCACGCACA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	971	990	54
611464	164	183	TCGCCCTTCAGCACGCACAC	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	970	989	67
611467	656	675	TTTCTACAGCTAGCAGGATA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9806	9825	272
611468	583	602	TCCCAATTACACCACAAGCC	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9733	9752	227
611472	230	249	CCCCACACCTTCACTGGTCC	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	4984	5003	145
611473	231	250	TCCCCACACCTTCACTGGTC	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	4985	5004	146
611478	644	663	GCAGGATAACAGATGAGTTA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9794	9813	260
611479	645	664	AGCAGGATAACAGATGAGTT	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9795	9814	261
611481	655	674	TTCTACAGCTAGCAGGATAA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9805	9824	271
611484	660	679	TACATTTCTACAGCTAGCAG	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9810	9829	276
611485	661	680	ATACATTTCTACAGCTAGCA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9811	9830	277
611488	124	143	GCTAGGCCACGCCGAGGTCC	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	930	949	593
611490	402	421	GTCAGCAGTCACATTGCCCA	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	8457	8476	666
611494	671	690	GTTTATCAGGATACATTTCT	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9821	9840	728
611495	673	692	ATGTTTATCAGGATACATTT	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9823	9842	729
611498	569	588	CAAGCCAAACGACTTCCAGC	5-10-5 MOE	eeeeedddddddddeeeee	sooosssssssssssooos	9719	9738	816

611499	664	683	AGGATACATTT CTACAGCTA	5-10-5 MOE	eeeeeddddddddddeeeee	sooosssssssssssooos	9814	9833	822
612912	621	637	CTCAGACTACA TCCAAG	Deoxy, MOE, and cEt	eeekkddddddddkkeee	soossssssssssooss	9771	9787	1146
612915	656	672	CTACAGCTAGC AGGATA	Deoxy, MOE, and cEt	eeekkddddddddkkeee	soossssssssssooss	9806	9822	1164
612917	684	700	AGTGTTTAATG TTTATC	Deoxy, MOE, and cEt	eeekkddddddddkkeee	soossssssssssooss	9834	9850	1173
612919	621	637	CTCAGACTACA TCCAAG	Deoxy, MOE, and cEt	eekkddddddddkkeee	soossssssssssooss	9771	9787	1146
612923	656	672	CTACAGCTAGC AGGATA	Deoxy, MOE, and cEt	eekkddddddddkkeee	soossssssssssooss	9806	9822	1164
612924	674	690	GTTTATCAGGA TACATT	Deoxy, MOE, and cEt	eekkddddddddkkeee	soossssssssssooss	9824	9840	1346
612934	170	186	CCGTCGCCCTT CAGCAC	Deoxy, MOE, and cEt	eekkddddddddkkee	sooossssssssssoss	976	992	969
612935	585	601	CCCAATTACAC CACAAG	Deoxy, MOE, and cEt	eekkddddddddkkee	sooossssssssssoss	9735	9751	1114
612940	659	675	TTTCTACAGCT AGCAGG	Deoxy, MOE, and cEt	eekkddddddddkkee	sooossssssssssoss	9809	9825	1167
612942	668	684	CAGGATACATT TCTACA	Deoxy, MOE, and cEt	eekkddddddddkkee	sooossssssssssoss	9818	9834	1344
612943	674	690	GTTTATCAGGA TACATT	Deoxy, MOE, and cEt	eekkddddddddkkee	sooossssssssssoss	9824	9840	1346
666854	665	681	AGGATACATTT CTACAGCT	5-9-5 MOE	eeeeeddddddddeeeee	sooosssssssssssooss	9815	9831	1428
666855	666	682	CAGGATACATT TCTACAGC	5-9-5 MOE	eeeeeddddddddeeeee	sooosssssssssssooss	9816	9832	1461
666857	679	695	TTAATGTTTAT CAGGAT	Deoxy, MOE, and cEt	eeekddddddddkeeee	soossssssssssooss	9829	9845	1351
666858	679	695	TTAATGTTTAT CAGGAT	Deoxy, MOE, and cEt	eekkddddddddeeeee	soossssssssssooss	9829	9845	1351
666864	679	695	TTAATGTTTAT CAGGAT	Deoxy, MOE, and cEt	kekeddddddddeeeee	soossssssssssooss	9829	9845	1351

666865	679	695	TTAATGTTTAT CAGGAT	Deoxy, MOE, and cEt	eeeeddddddddekeke	soosssssssssooss	9829	9845	1351
666866	684	700	AGTGTTTAATG TTTATC	Deoxy, MOE, and cEt	eeekddddddddkeeee	soosssssssssooss	9834	9850	1173
666908	686	702	ACAGTGTTTAA TGTTTA	Deoxy, MOE, and cEt	eeeekddddddddkeeee	sooosssssssssooss	9836	9852	1175
666923	666	682	GGATACATTTC TACAGC	Deoxy, MOE, and cEt	eeekddddddddkeeee	sooosssssssssooss	9816	9832	1342

The modified oligonucleotides were tested in a series of experiments that had similar conditions. The results for each experiment are presented in separate tables shown below. Rats were injected intrathecally with 30μL of a 16.67mg/ml solution of modified oligonucleotide diluted in PBS (500 μg final dose). A control group of rats was injected intrathecally with PBS. Inhibition levels of SOD-1 in the lumbar spinal cord, thoracic spinal cord and cervical spinal cord were assessed. The data is presented below and indicate that several modified oligonucleotides inhibited human SOD-1 levels in this model.

Table 51

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
333611	5-10-5 MOE with phosphorothioate backbone chemistry	51	51	47	21
383872	5-10-5 MOE with mixed backbone chemistry	29	36	26	21
611460	5-10-5 MOE with mixed backbone chemistry	55	53	25	1428
611464	5-10-5 MOE with mixed backbone chemistry	52	54	26	67
611468	5-10-5 MOE with mixed backbone chemistry	46	44	19	227
611481	5-10-5 MOE with mixed backbone chemistry	39	44	33	271

Table 52

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
611473	5-10-5 MOE with mixed backbone chemistry	47	42	5	146
611474	5-10-5 MOE with mixed backbone chemistry	75	65	65	149
611479	5-10-5 MOE with mixed backbone chemistry	24	13	20	261
611484	5-10-5 MOE with mixed backbone chemistry	51	31	41	276
611485	5-10-5 MOE with mixed backbone chemistry	52	40	35	277
611492	5-10-5 MOE with mixed backbone chemistry	57	44	43	725

Table 53

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
611472	5-10-5 MOE with mixed backbone chemistry	0	19	15	145
611478	5-10-5 MOE with mixed backbone chemistry	16	33	24	260
611490	5-10-5 MOE with mixed backbone chemistry	53	55	44	666
611494	5-10-5 MOE with mixed backbone chemistry	34	39	38	728
611495	5-10-5 MOE with mixed backbone chemistry	33	19	38	729

611498	5-10-5 MOE with mixed backbone chemistry	30	43	27	816
611499	5-10-5 MOE with mixed backbone chemistry	45	56	40	822
611500	5-10-5 MOE with mixed backbone chemistry	56	58	52	823

Table 54

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
611457	5-10-5 MOE with mixed backbone chemistry	56	46	43	54
611467	5-10-5 MOE with mixed backbone chemistry	21	28	22	272
611488	5-10-5 MOE with mixed backbone chemistry	14	23	4	593
612917	Deoxy, MOE, and cEt with mixed backbone chemistry	47	55	37	1173
612923	Deoxy, MOE, and cEt with mixed backbone chemistry	53	63	45	1164
612925	Deoxy, MOE, and cEt with mixed backbone chemistry	67	69	63	1348
612928	Deoxy, MOE, and cEt with mixed backbone chemistry	84	85	81	1351

Table 55

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
612912	Deoxy, MOE, and cEt with mixed backbone chemistry	59	60	48	1146
612919	Deoxy, MOE, and cEt with mixed backbone chemistry	60	60	58	1146

612916	Deoxy, MOE, and cEt with mixed backbone chemistry	72	69	69	1170
612931	Deoxy, MOE, and cEt with mixed backbone chemistry	81	79	72	1173
612932	Deoxy, MOE, and cEt with mixed backbone chemistry	21	26	24	1175

Table 56

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
612915	Deoxy, MOE, and cEt with mixed backbone chemistry	54	48	52	1164
612918	Deoxy, MOE, and cEt with mixed backbone chemistry	73	69	64	1175
612927	Deoxy, MOE, and cEt with mixed backbone chemistry	82	75	62	1350
612934	Deoxy, MOE, and cEt with mixed backbone chemistry	59	44	48	969
612935	Deoxy, MOE, and cEt with mixed backbone chemistry	64	54	62	1114
612940	Deoxy, MOE, and cEt with mixed backbone chemistry	11	26	17	1167
612941	Deoxy, MOE, and cEt with mixed backbone chemistry	81	75	71	1342
612942	Deoxy, MOE, and cEt with mixed backbone chemistry	40	42	41	1344
612943	Deoxy, MOE, and cEt with mixed backbone chemistry	61	54	51	1346
612944	Deoxy, MOE, and cEt with mixed backbone chemistry	59	52	51	1348

Table 57

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Thoracic	Cervical	SEQ ID NO
612924	Deoxy, MOE, and cEt with mixed backbone chemistry	42	64	53	1346
612947	Deoxy, MOE, and cEt with mixed backbone chemistry	68	75	74	1351
612948	Deoxy, MOE, and cEt with mixed backbone chemistry	80	90	87	1352
612949	Deoxy, MOE, and cEt with mixed backbone chemistry	73	82	85	1172

Table 58

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Cervical	SEQ ID NO
654304	5-8-5 MOE with mixed backbone chemistry	28	6	1429
654305	5-8-5 MOE with mixed backbone chemistry	14	0	1430
654306	5-8-5 MOE with mixed backbone chemistry	36	0	1432
654307	5-8-5 MOE with mixed backbone chemistry	17	0	1432

Table 59

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Cervical	SEQ ID NO
654334	Deoxy, MOE, and cEt with mixed backbone chemistry	39	19	1454
666854	5-9-5 MOE with mixed backbone chemistry	52	39	1428

666855	5-9-5 MOE with mixed backbone chemistry	37	17	1461
666857	Deoxy, MOE, and cEt with mixed backbone chemistry	59	39	1351
666858	Deoxy, MOE, and cEt with mixed backbone chemistry	38	22	1351
666859	Deoxy, MOE, and cEt with mixed backbone chemistry	79	64	1351
666864	Deoxy, MOE, and cEt with mixed backbone chemistry	50	40	1351
666865	Deoxy, MOE, and cEt with mixed backbone chemistry	73	44	1351
666866	Deoxy, MOE, and cEt with mixed backbone chemistry	67	56	1173
666908	Deoxy, MOE, and cEt with mixed backbone chemistry	38	13	1175
666923	Deoxy, MOE, and cEt with mixed backbone chemistry	45	26	1342

Table 60

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	Cervical	SEQ ID NO
654323	Deoxy, MOE, and cEt with mixed backbone chemistry	53	35	1433
666846	5-10-5 MOE with mixed backbone chemistry	64	50	725
666849	5-10-5 MOE with mixed backbone chemistry	63	55	725
666853	5-10-5 MOE with mixed backbone chemistry	81	74	725
666861	Deoxy, MOE, and cEt with mixed backbone chemistry	55	47	1351

666867	Deoxy, MOE, and cEt with mixed backbone chemistry	59	48	1173
666869	Deoxy, MOE, and cEt with mixed backbone chemistry	82	81	1173
666870	Deoxy, MOE, and cEt with mixed backbone chemistry	76	68	1173
666919	Deoxy, MOE, and cEt with mixed backbone chemistry	76	68	1342
666921	Deoxy, MOE, and cEt with mixed backbone chemistry	71	65	1342
666922	Deoxy, MOE, and cEt with mixed backbone chemistry	67	62	1342

Table 61

Percent inhibition of human SOD-1 in the spinal cord regions of transgenic rats

ISIS No	Chemistry	Lumbar	SEQ ID NO
684059	Deoxy, MOE, and cEt with mixed backbone chemistry	54	1348
684064	Deoxy, MOE, and cEt with mixed backbone chemistry	51	1348
684068	4-8-5 MOE with mixed backbone chemistry	18	1348
684087	5-8-5 MOE with mixed backbone chemistry	37	613
684088	5-8-5 MOE with mixed backbone chemistry	31	1419
684095	5-10-5 MOE with mixed backbone chemistry	34	21
684097	5-8-7 MOE with mixed backbone chemistry	22	21
684101	6-8-6 MOE with mixed backbone chemistry	22	47
684104	6-9-5 MOE with mixed backbone chemistry	11	47

Example 13: Dose-dependent inhibition of human SOD-1 with modified oligonucleotides in LLC-MK2 cells

Gapmers from the studies described above, including benchmark compound ISIS 333611, exhibiting significant *in vitro* inhibition of SOD-1 mRNA were selected and tested at various doses in LLC-MK2 cells. The cross-reactivity of the human modified oligonucleotides tested in this study with the rhesus monkey genomic sequence (the complement of GENBANK Accession No. NW_001114168.1 truncated from nucleotides 2258000 to 2271000, designated herein as SEQ ID NO: 3) is shown in the Table below.

Table 62
Cross-reactivity of antisense oligonucleotides targeting human SOD1with SEQ ID NO: 3

ISIS No	Start Site of SEQ ID NO: 3	Mismatches
333611	1572	2
436839	1564	0
436854	9049	0
436867	10347	0
666853	10375	1
666859	10389	1
666919	10376	1
666921	10376	1

Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.078 μM, 0.156 μM, 0.313 μM, 0.625 μM, 1.25 μM, 2.50 μM, 5.00 μM, and 10.000 μM concentrations of modified oligonucleotide, as specified in the Tables below. After a treatment period of approximately 16 hours, RNA was isolated from the cells and SOD-1 mRNA levels were measured by quantitative real-time PCR Primer probe set RTS3121 (forward sequence TGGAGATAATACACAAGGCTGTACCA, designated herein as SEQ ID NO: 17; reverse sequence CAACATGCCTCTCTTCATCCTTT, designated herein as SEQ ID NO: 18; probe sequence ATCCTCTATCCAGACAACACGGTGGGC, designated herein as SEQ ID NO: 19) was used to measure mRNA levels. SOD-1 mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. Results are presented as percent inhibition of SOD-1, relative to untreated control cells. The half maximal inhibitory concentration (IC_{50}) of each oligonucleotide is also presented. As presented in the Table, several of the newly designed oligonucleotides were more potent than the benchmark, ISIS 336611.

Table 63
Dose-dependent inhibition of SOD-1 rhesus monkey mRNA

ISIS No	0.078 μM	0.156 μM	0.313 μM	0.625 μM	1.25 μM	2.50 μM	5.00 μM	10.00 μM	IC_{50} (μM)
333611	3	2	0	0	17	15	19	40	>10
436839	0	0	5	0	20	22	37	61	7.1
436854	34	34	40	39	52	65	69	84	1.2
436867	3	0	11	18	34	49	70	87	2.2
666853	7	34	20	39	60	80	79	92	1.0
666859	0	9	20	18	15	25	30	44	>10
666919	11	15	16	36	51	65	73	84	1.4
666921	0	13	28	37	50	52	62	74	1.8

Example 14: Tolerability of SOD-1 modified oligonucleotides in a rat model

Gapmers from the studies described above, including benchmark compound ISIS 333611, which was previously disclosed in WO 2005/040180, were tested for tolerability in Sprague-Dawley rats.

The modified oligonucleotides were tested in a series of experiments that had similar conditions. Rats were injected intrathecally with3 mg of a single dose of ISIS oligonucleotide. A control group of rats was injected intrathecally with PBS. Acute tolerability was assessed 3 hours post-dose using a functional observational battery (FOB) . This score is used to evaluate the acute tolerability of a compound with lower scores denoting better tolerated compounds. Control animals usually have a score of '0' or '1'. At 3 hours post injection, the rats are observed by placing each rat on the cage top and evaluating certain functions, assigning a number of '0' or '1' depending on whether the rat exhibits normal function in the region of interest (0) or does not (1) for each function, and then adding the total scores. Seven regions are assessed, including tail, hind paws, hind legs, hind end, front posture, fore paws, and head. The results of the scoring are presented in the Table below. As presented in the Table, several newly designed oligonucleotides demonstrated more acute tolerability compared to the benchmark, ISIS 333611.

Table 64
FOB scores in Sprague-Dawley rats

ISIS No	Target Start Site on SEQ ID NO: 1	Chemistry	FOB score
333611	167	5-10-5 MOE with phosphorothioate backbone	4
684073	167	Deoxy, MOE, and cEt with mixed backbone	3
684081	167	Deoxy, MOE, and cEt with mixed backbone	1

684088	167	5-8-5 MOE with mixed backbone	0
684093	167	5-9-5 MOE with mixed backbone	0
684095	167	5-10-5 MOE with mixed backbone	0
684096	167	6-8-6 MOE with mixed backbone	0
684097	167	5-8-7 MOE with mixed backbone	0
684098	167	7-8-5 MOE with mixed backbone	0
684099	167	6-9-5 MOE with mixed backbone	0
684074	168	Deoxy, MOE, and cEt with mixed backbone	0
684082	168	Deoxy, MOE, and cEt with mixed backbone	1
684089	168	5-8-5 MOE with mixed backbone	0
684094	168	5-9-5 MOE with mixed backbone	1
684075	169	Deoxy, MOE, and cEt with mixed backbone	3
684083	169	Deoxy, MOE, and cEt with mixed backbone	3
684090	169	5-8-5 MOE with mixed backbone	2
684076	170	Deoxy, MOE, and cEt with mixed backbone	2
684084	170	Deoxy, MOE, and cEt with mixed backbone	4
611474	234	5-10-5 MOE with mixed backbone	4
654301	234	5-8-5 MOE with mixed backbone	3
654302	235	5-8-5 MOE with mixed backbone	1
654303	236	5-8-5 MOE with mixed backbone	0
684069	588	Deoxy, MOE, and cEt with mixed backbone	0
684077	588	Deoxy, MOE, and cEt with mixed backbone	1
684085	588	5-8-5 MOE with mixed backbone	0

684091	588	5-9-5 MOE with mixed backbone	0
684100	588	5-10-5 MOE with mixed backbone	0
684101	588	6-8-6 MOE with mixed backbone	0
684102	588	5-8-7 MOE with mixed backbone	0
684103	588	7-8-5 MOE with mixed backbone	0
684104	588	6-9-5 MOE with mixed backbone	0
684070	589	Deoxy, MOE, and cEt with mixed backbone	0
684078	589	Deoxy, MOE, and cEt with mixed backbone	0
684086	589	5-8-5 MOE with mixed backbone	0
684092	589	5-9-5 MOE with mixed backbone	0
684071	590	Deoxy, MOE, and cEt with mixed backbone	0
684079	590	Deoxy, MOE, and cEt with mixed backbone	0
684087	590	5-8-5 MOE with mixed backbone	0
684072	591	Deoxy, MOE, and cEt with mixed backbone	1
684080	591	Deoxy, MOE, and cEt with mixed backbone	1
654304	663	5-8-5 MOE with mixed backbone	3
612916	664	Deoxy, MOE, and cEt with mixed backbone	0
654305	664	5-8-5 MOE with mixed backbone	2
611492	665	5-10-5 MOE with mixed backbone	0
654306	665	5-8-5 MOE with mixed backbone	3
654323	665	Deoxy, MOE, and cEt with mixed backbone	0
654341	665	Deoxy, MOE, and cEt with mixed backbone	0
666846	665	5-10-5 MOE with mixed backbone	0

666849	665	5-10-5 MOE with mixed backbone	0
666851	665	5-10-5 MOE with mixed backbone	1
666853	665	5-10-5 MOE with mixed backbone	0
666854	665	5-9-5 MOE with mixed backbone	1
611500	666	5-10-5 MOE with mixed backbone	0
612941	666	Deoxy, MOE, and cEt with mixed backbone	3
654307	666	5-8-5 MOE with mixed backbone	2
654342	666	Deoxy, MOE, and cEt with mixed backbone	2
666845	666	5-10-5 MOE with mixed backbone	0
666848	666	5-10-5 MOE with mixed backbone	1
666850	666	5-10-5 MOE with mixed backbone	0
666852	666	5-10-5 MOE with mixed backbone	1
666855	666	5-9-5 MOE with mixed backbone	1
666917	666	Deoxy, MOE, and cEt with mixed backbone	3
666918	666	Deoxy, MOE, and cEt with mixed backbone	3
666919	666	Deoxy, MOE, and cEt with mixed backbone	2
666920	666	Deoxy, MOE, and cEt with mixed backbone	1
666921	666	Deoxy, MOE, and cEt with mixed backbone	2
666922	666	Deoxy, MOE, and cEt with mixed backbone	3
666923	666	Deoxy, MOE, and cEt with mixed backbone	2
666856	667	5-9-5 MOE with mixed backbone	3
612925	676	Deoxy, MOE, and cEt with mixed backbone	4
684059	676	Deoxy, MOE, and cEt with mixed backbone	4

684060	676	Deoxy, MOE, and cEt with mixed backbone	3
684061	676	Deoxy, MOE, and cEt with mixed backbone	4
684062	676	Deoxy, MOE, and cEt with mixed backbone	4
684063	676	Deoxy, MOE, and cEt with mixed backbone	5
684064	676	Deoxy, MOE, and cEt with mixed backbone	4
684065	676	Deoxy, MOE, and cEt with mixed backbone	4
684066	676	Deoxy, MOE, and cEt with mixed backbone	4
684067	676	Deoxy, MOE, and cEt with mixed backbone	5
684068	676	4-8-5 MOE with mixed backbone	4
612927	678	Deoxy, MOE, and cEt with mixed backbone	4
654309	678	5-8-5 MOE with mixed backbone	4
612928	679	Deoxy, MOE, and cEt with mixed backbone	2
612947	679	Deoxy, MOE, and cEt with mixed backbone	7
654310	679	5-8-5 MOE with mixed backbone	3
666857	679	Deoxy, MOE, and cEt with mixed backbone	1
666858	679	Deoxy, MOE, and cEt with mixed backbone	1
666859	679	Deoxy, MOE, and cEt with mixed backbone	1
666860	679	Deoxy, MOE, and cEt with mixed backbone	0
666861	679	Deoxy, MOE, and cEt with mixed backbone	5
666862	679	Deoxy, MOE, and cEt with mixed backbone	1
666863	679	Deoxy, MOE, and cEt with mixed backbone	4
666864	679	Deoxy, MOE, and cEt with mixed backbone	4
666865	679	Deoxy, MOE, and cEt with mixed backbone	5

611497	681	5-10-5 MOE with mixed backbone	5
612948	681	Deoxy, MOE, and cEt with mixed backbone	3
666847	681	5-10-5 MOE with mixed backbone	7
612949	683	Deoxy, MOE, and cEt with mixed backbone	4
612931	684	Deoxy, MOE, and cEt with mixed backbone	4
666866	684	Deoxy, MOE, and cEt with mixed backbone	6
666867	684	Deoxy, MOE, and cEt with mixed backbone	6
666868	684	Deoxy, MOE, and cEt with mixed backbone	6
666869	684	Deoxy, MOE, and cEt with mixed backbone	6
666870	684	Deoxy, MOE, and cEt with mixed backbone	6
666871	684	Deoxy, MOE, and cEt with mixed backbone	6
666872	684	Deoxy, MOE, and cEt with mixed backbone	6
666873	684	Deoxy, MOE, and cEt with mixed backbone	6
666874	684	Deoxy, MOE, and cEt with mixed backbone	5
612918	686	Deoxy, MOE, and cEt with mixed backbone	4
612932	686	Deoxy, MOE, and cEt with mixed backbone	2
666906	686	Deoxy, MOE, and cEt with mixed backbone	2
666907	686	Deoxy, MOE, and cEt with mixed backbone	3
666908	686	Deoxy, MOE, and cEt with mixed backbone	1
666909	686	Deoxy, MOE, and cEt with mixed backbone	0
666910	686	Deoxy, MOE, and cEt with mixed backbone	2
666911	686	Deoxy, MOE, and cEt with mixed backbone	0
666912	686	Deoxy, MOE, and cEt with mixed backbone	0

666913	686	Deoxy, MOE, and cEt with mixed backbone	0
666914	686	Deoxy, MOE, and cEt with mixed backbone	0
666915	686	Deoxy, MOE, and cEt with mixed backbone	1
666916	686	Deoxy, MOE, and cEt with mixed backbone	1
654318	687	5-8-5 MOE with mixed backbone	1
654334	687	Deoxy, MOE, and cEt with mixed backbone	3

Tolerability was also assessed 8 weeks post-dose by measuring the levels of IBA1, a microglial marker, and GFAP, an astrocytic marker, in the lumbar spinal cord region. Both IBA1 and GFAP are markers of CNS inflammation (Frank, MG, *Brain Behav. Immun.* **2007**, 21, 47-59), hence the higher the level of either marker, the less tolerable the antisense oligonucleotide is deemed to be in this rat model.

IBA1 mRNA levels were measured with primer probe set rAIF1_LTS00219 (forward sequence AGGAGAAAAACAAAGAACACCAGAA, designated herein as SEQ ID NO: 5; reverse sequence CAATTAGGGCAACTCAGAAATAGCT, designated herein as SEQ ID NO: 6; probe sequence CCAACTGGTCCCCCAGCCAAGA, designated herein as SEQ ID NO: 7). GFAP mRNA levels were measured with primer probe set mGFAP_LTS00370 (forward sequence GAAACCAGCCTGGACACCAA, designated herein as SEQ ID NO: 8; reverse sequence TCCACAGTCTTTACCACGATGTTC, designated herein as SEQ ID NO: 9; probe sequence TCCGTGTCAGAAGGCCACCTCAAGA, designated herein as SEQ ID NO: 10).

The results are presented in the Table below. As presented in the Table, several newly designed oligonucleotides were more tolerable compared to the benchmark, ISIS 333611.

Table 65

IBA1 and GFAP mRNA levels (% control) in the lumbar regions of Sprague-Dawley rats

ISIS No.	IBA1	GFAP
333611	341	314
654301	149	137
654302	261	129
654303	110	80
654304	143	130
654305	185	158

654306	110	106
654307	152	144
654309	195	169
654310	119	141
654318	93	81
654323	125	113
654334	114	75
654341	209	224
654342	473	485
666845	389	416
666846	173	171
666847	271	297
666848	399	377
666849	140	150
666850	246	252
666851	246	199
666852	282	266
666853	168	147
666854	135	123
666855	238	221
666856	253	209
666857	242	182
666858	169	134
666859	185	162
666861	161	152
666862	254	285
666863	216	185
666864	174	154
666865	251	232
666866	281	135
666867	132	112
666868	199	211
666869	262	207
666870	201	189
666871	192	214
666872	441	136
666873	340	277
666874	204	199
666917	292	244
666919	115	85
666920	155	102

666921	108	82
666922	123	82
666923	118	93
684059	168	162
684060	158	141
684061	335	263
684062	218	265
684064	191	168
684065	245	304
684066	313	376
684067	171	151
684068	157	135
684085	459	586
684086	187	227
684087	215	263
684088	151	183
684089	507	667
684090	130	170
684091	350	426
684092	366	333
684093	412	264
684094	294	373
684095	213	215
684096	404	335
684097	217	206
684098	378	438
684099	534	473
684100	276	259
684101	153	125
684102	237	242
684103	588	416
684104	221	193

Example 15: Dose dependent inhibition of human SOD-1 in a transgenic rat model

Gapmers from the studies described above, including benchmark compound ISIS 333611, were tested in an SOD-1 transgenic rat model (Taconic, Cat# 2148-F and 2148-M). These hemizygous rats express mutant human SOD-1 in the spinal cord, many brain regions, and peripheral organs.

Rats were injected intrathecally with 10, 30, 100, 300, 1000, or 3000 μg of a gapmer listed in the table below or with only PBS. Two weeks later, the animals were sacrificed. Inhibition of SOD-1 mRNA in the lumbar spinal cord, cervical spinal cord, rostral cortex, and caudal cortex was assessed by RT-PCR using

primer probe set RTS3898, described in Example 1. The data is presented below as ED_{50} values, and indicates that the oligonucleotides inhibited SOD1 mRNA in multiple CNS tissues more potently than Isis 333611. Indeed, ED_{50} values for Isis No. 333611 could not even be calculated, as indicated by an entry of "n/a," because even the highest concentration tested (3000 μg) did not inhibit SOD-1 mRNA greater than 55-65%. "n.d." indicates that there is no data available for the indicated sample.

Table 66
Inhibition of human SOD1 in transgenic rats

Isis No.	ED_{50} (μg)				SEQ ID NO.
	Lumbar	Cervical	Rostral	Caudal	
333611	n/a	n/a	n.d.	n.d.	21
666853	81.3	242.6	6434	931	725
666859	74.0	358.8	2360	1113	1351
666870	139.4	1111	5511	2105	1173
666919	104.1	613.5	> 6000	2655	1342

Example 16: Tolerability of SOD-1 modified oligonucleotides in rats

Gapmers from the studies described above, including benchmark compound ISIS 333611, were tested for tolerability in Sprague-Dawley rats. Groups of 4 to 6 rats were injected intrathecally with 1 mg or 3 mg of a single dose of an ISIS oligonucleotide. A control group of rats was injected intrathecally with PBS. Acute tolerability was assessed 3 hours post-dose, as described in Example 14. The results for the 1 mg dose are the averages for each group following one experiment. The results for the 3 mg dose are the averages for each group across two replicate experiments. The results of the study, presented in the table below, indicate that several newly designed oligonucleotides were more tolerable than the benchmark, ISIS 333611.

Table 67
FOB values

Isis No.	3 hour FOB		8 week FOB	
	1 mg	3 mg	1 mg	3 mg
333611	3.0	4.9	0.0	1.2
666853	0.0	0.5	0.0	0.0
666859	0.0	2.1	0.0	0.3
666870	2.3	5.8	0.0	0.8
666919	1.3	3.5	0.0	0.1

Example 17: Dose dependent inhibition of human SOD-1 in a transgenic mouse model

In order to confirm the results obtained in transgenic rats in another species, gapmers from the studies described above were tested in an SOD-1 transgenic mouse model that expresses the same G93A human mutant SOD1 gene that the transgenic rat expresses (see Examples 12 and 15).

Mice received an intracerebral ventricular bolus (ICVB) of 10, 30, 100, 300, or 700 µg of a gapmer listed in the table below, or PBS. Two weeks later, the animals were sacrificed. Inhibition of SOD-1 mRNA in the lumbar spinal cord and cortex was assessed by RT-PCR using primer probe set RTS3898, described in Example 1. The data is presented below as ED_{50} values, and indicates that the oligonucleotides inhibited SOD1 mRNA more potently than Isis 333611 in both rats and mice.

Table 68
Inhibition of human SOD1 in transgenic mice

Isis No.	Lumbar ED_{50} (µg)	Cortex ED_{50} (µg)
333611	401	786
666853	136	188
666859	106	206
666870	148	409
666919	168	1211

Example 18: Tolerability of SOD-1 modified oligonucleotides in mice

Gapmers from the studies described above, including benchmark compound ISIS 333611, were tested for tolerability in C57bl6 mice. Mice were injected stereotaxically into the cerebral ventricles with 700ug of a single dose of ISIS oligonucleotide. A control group of mice was injected into the cerebral ventricle with PBS. Acute tolerability was assessed at 3 hours post injection using a functional observation battery (FOB) different from that used for the rats. Each mouse was evaluated according to 7 different criteria. The 7 criteria are (1) the mouse was bright, alert, and responsive; (2) the mouse was standing or hunched without stimuli; (3) the mouse shows any movement without stimuli (4) the mouse demonstrates forward movement after its lifted; (5) the mouse demonstrates any movement after its lifted; (6) the mouse responds to a tail pinch; (7) regular breathing. For each of the 7 different criteria, each mouse was given a sub-score of 0 if it met the criteria or 1 if it did not. After all of the 7 criteria were evaluated, the sub-scores were summed for each mouse and then averaged for each group. For example, if a mouse was bright, alert, and responsive 3 hours after the 700 µg ICV dose, and met all other other criteria, it would get a summed score of 0. If another mouse was not bright, alert, and responsive 3 hours after the 700 µg ICV dose but met

all other criteria, it would receive a score of 1. Saline treated mice generally receive a score of 0. A score at the top end of the range would be suggestive of acute toxicity.

Body weights were measured throughout the study and are reported below as percent change at 8 weeks relative to baseline. Long term tolerability was assessed 8 weeks post-dose by measuring the levels of IBA1 and GFAP, as described in Example 14. IBA1 and GFAP mRNA levels are reported relative to PBS treated animals. The results of the study, presented in the tables below, indicate that several newly designed oligonucleotides were more tolerable, in rats and mice, compared to the benchmark, ISIS 333611.

Table 69

FOB values and body weight change

Isis No.	3 hour FOB	Body weight (% change)
333611	6.5	3.8
666853	1.25	8.0
666859	1.75	14.0
666870	4.75	7.3
666919	0.0	5.2

Table 70

Inflammation markers

Isis No.	IBA1 (% PBS)		GFAP (% PBS)	
	Lumbar	Cortex	Lumbar	Cortex
333611	130.3	134.3	117.5	207.7
666853	102.8	109.3	103.3	103.7
666859	110.4	98.2	109.0	72.8
666870	158.8	117.8	106.7	128.6
666919	115.0	97.9	99.8	84.3

Example 19: Dose dependent inhibition of monkey SOD-1 in cynomolgus monkey

Isis No. 666853 was tested in cynomolgus monkey. There is one mismatch between Isis No. 666853 and cynomolgus monkey SOD-1, and there are 17 contiguous bases in Isis No. 666853 that are 100% complementary to cynomolgus monkey SOD-1.

Groups of 6-10 male and female monkeys received an intrathecal lumbar bolus of PBS or 4, 12, or 35 mg of Isis No. 666853 on days 1, 14, 28, 56, and 84 of the study. Each group received the same dose on all

five dosing days. On day 91, the animals were sacrificed. Inhibition of SOD-1 mRNA in the lumbar, thoracic, and cervical spinal cord and frontal cortex, motor cortex, hippocampus, pons, and cerebellum was assessed by RT-PCR using primer probe set RTS3898. The data is presented below as the average percent inhibition for each treatment group, relative to the PBS treated group. The results indicate that Isis No. 666853 inhibited SOD-1 mRNA in multiple target tissues in cynomolgus monkey.

Treatment with 666853 was well tolerated for the duration of the 13 week study and there were no clinical observations of adverse reactions in monkeys.

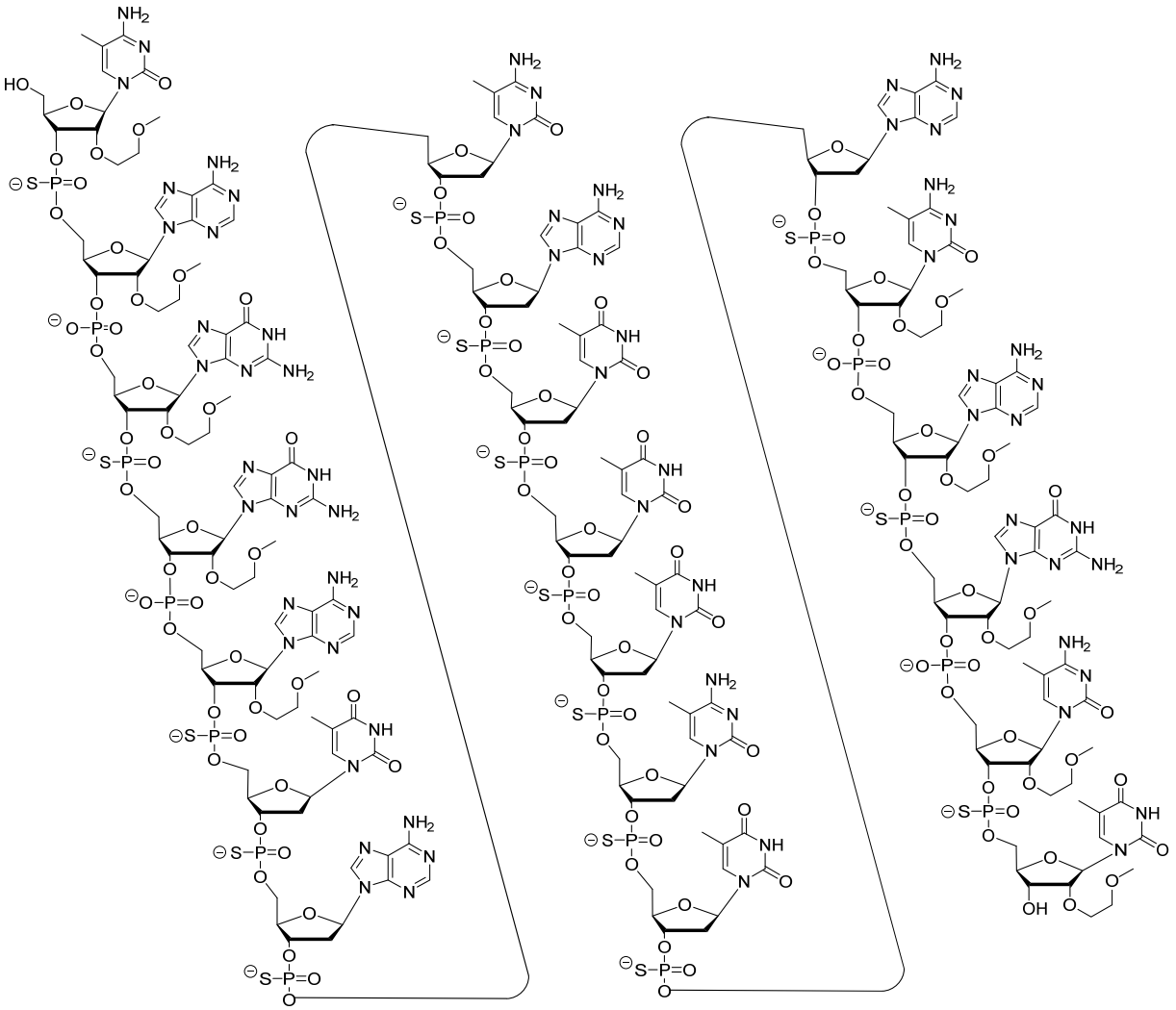
Table 71

Inhibition of SOD-1 mRNA in monkeys

Amount of 666853 per dose (mg)	Inhibition (%)							
	Lumbar	Thoracic	Cervical	Frontal cortex	Motor cortex	Hippocampus	Pons	Cerebellum
4	44.4	27.1	20.1	21.5	21.6	32.0	6.8	15.4
12	75.4	69.0	42.1	56.7	55.7	31.8	13.2	33.3
35	87.0	74.8	72.1	80.5	82.6	80.1	48.6	48.4

CLAIMS

1. A salt of an antisense compound, wherein the anion of the antisense compound has the following formula:



.

2. The salt of the antisense compound of claim 1, wherein the salt is a sodium salt.

3. An antisense compound according to the following formula:

mCes Aeo Ges Geo Aes Tds Ads mCds Ads Tds Tds Tds mCds Tds Ads mCeo Aes Geo mCes Te (nucleobase sequence of SEQ ID NO:725), wherein,

A = an adenine,

mC = a 5-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethylribose modified sugar,

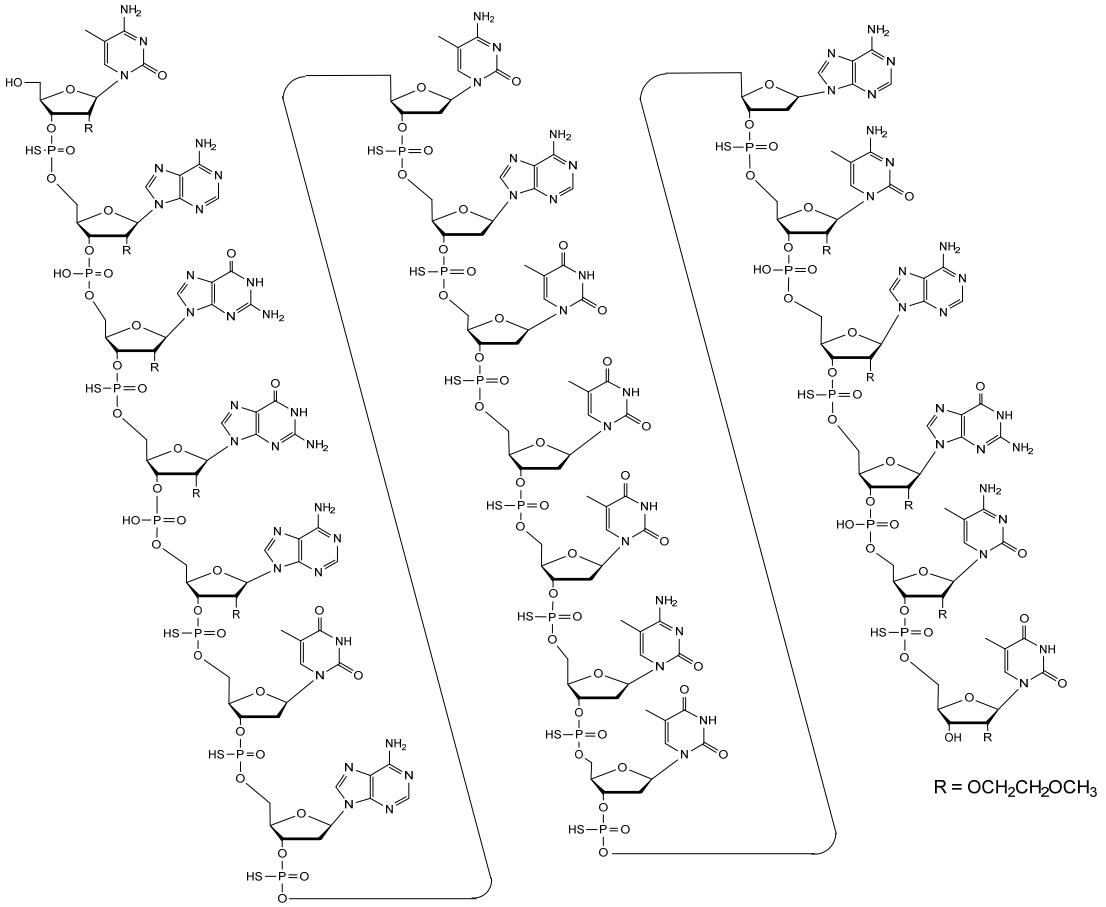
d = a 2'-deoxyribose sugar,

s = a phosphorothioate internucleoside linkage, and

o = a phosphodiester internucleoside linkage;

or a pharmaceutically acceptable salt thereof.

4. An antisense compound according to the following formula:



or a pharmaceutically acceptable salt thereof.

5. The antisense compound of claim 3 or 4.

6. The pharmaceutically acceptable salt of the antisense compound of claim 3 or 4.

7. A pharmaceutical composition comprising the pharmaceutically acceptable salt of claim 1, 2, or 6, the antisense compound or pharmaceutically acceptable salt of claim 3 or 4, or the antisense compound of claim 5 and at least one of a pharmaceutically acceptable carrier or diluent.

8. The pharmaceutical composition of claim 7, wherein the pharmaceutically acceptable diluent is phosphate-buffered saline (PBS).

9. The pharmaceutical composition of claim 7 or 8, which is formulated for intrathecal administration.

10. The antisense compound or pharmaceutically acceptable salt of claim 3 or 4, the antisense compound of claim 5, or the pharmaceutical composition of any one of claims 7 to 9, for use as a medicament.

11. Use of the pharmaceutically acceptable salt of claim 1, 2, or 6, the antisense compound or pharmaceutically acceptable salt of claim 3 or 4, the antisense compound of claim 5, or the pharmaceutical composition of any one of claims 7 to 9 for the manufacture of a medicament for treating a SOD-1 associated neurodegenerative disorder.

12. Use of the pharmaceutically acceptable salt of claim 1, 2, or 6, the antisense compound or pharmaceutically acceptable salt of claim 3 or 4, the antisense compound of claim 5, or the pharmaceutical composition of any one of claims 7 to 9 for the manufacture of a medicament for preventing a SOD-1 associated neurodegenerative disorder.

13. Use of the pharmaceutically acceptable salt of claim 1, 2, or 6, the antisense compound or pharmaceutically acceptable salt of claim 3 or 4, the antisense compound of claim 5, or the pharmaceutical composition of any one of claims 7 to 9 for the manufacture of a medicament for treating SOD-1 associated amyotrophic lateral sclerosis (ALS).

14. Use of the pharmaceutically acceptable salt of claim 1, 2, or 6, the antisense compound or pharmaceutically acceptable salt of claim 3 or 4, the antisense compound of claim 5, or the pharmaceutical composition of any one of claims 7 to 9 for the manufacture of a medicament for preventing SOD-1 associated ALS.

15. The use of any one of claims 11 to 14, wherein the medicament is administered intrathecally.