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(54) **Title:** MODULATION OF PREKALLIKREIN (PKK) EXPRESSION

(57) **Abstract:** Disclosed herein are antisense compounds and methods for decreasing PKK mRNA and protein expression. Such methods, compounds, and compositions are useful to treat, prevent, or ameliorate PKK-associated diseases, disorders, and conditions.



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MODULATION OF PREKALLIKREIN (PKK) EXPRESSION

Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The
5 Sequence Listing is provided as a file entitled BIOL0172WOSEQ_ST25.txt created August 15, 2014, which
is approximately 632 KB in size. The information in the electronic format of the sequence listing is
incorporated herein by reference in its entirety.

Field

10 Provided are compounds, compositions, and methods for reducing expression of human plasma
prekallikrein (PKK) mRNA and protein in an animal. Such compositions and methods are useful to treat,
prevent, or ameliorate inflammatory and thromboembolic conditions.

Background

Plasma prekallikrein (PKK) is the precursor of plasma kallikrein (PK), which is encoded by the
KLKB1 gene. PKK is a glycoprotein that participates in the surface-dependent activation of blood
15 coagulation, fibrinolysis, kinin generation, and inflammation. PKK is converted to PK by Factor XIIa by the
cleavage of an internal Arg-Ile peptide bond. PK liberates kinins from kininogens and also generates plasmin
from plasminogen. PK is a member of the kinin-kallikrein pathway, which consists of several proteins that
play a role in inflammation, blood pressure control, coagulation, and pain.

Summary

20 Provided herein are compounds, compositions, and methods for modulating expression of PKK
mRNA and protein. In certain embodiments, compounds useful for modulating expression of PKK mRNA
and protein are antisense compounds. In certain embodiments, the antisense compounds are antisense
oligonucleotides.

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

Also provided are compounds, compositions, and methods useful for preventing, treating, and
ameliorating diseases, disorders, and conditions associated with PKK. In certain embodiments, such PKK
30 associated diseases, disorders, and conditions are inflammatory diseases. In certain embodiments, the
inflammatory disease may be an acute or chronic inflammatory disease. In certain embodiments, such
inflammatory diseases may include hereditary angioedema (HAE), edema, angioedema, swelling,

angioedema of the lids, ocular edema, macular edema, and cerebral edema. In certain embodiments, such PKK associated diseases, disorders, and conditions are thromboembolic diseases. In certain embodiments, such thromboembolic diseases may include thrombosis, embolism, thromboembolism, deep vein thrombosis, pulmonary embolism, myocardial infarction, stroke, and infarct.

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 an inflammatory disease include genetic predisposition to an inflammatory disease and environmental factors. In certain embodiments, the subject has a mutated complement 1 esterase inhibitor (C1-INH) gene or mutated Factor 12 gene. In certain embodiments, the subject has taken or is on angiotensin-converting enzyme inhibitors (ACE inhibitors) or angiotensin II receptor blockers (ARBs). In certain embodiments, the subject has had an allergic reaction leading to angioedema. In certain embodiments, the subject has type I HAE. In certain embodiments, the subject has type II HAE. In certain embodiments, the subject has type III HAE.

Certain outcomes associated with development of an inflammatory disease include edema/swelling in various body parts including the extremities (i.e., hands, feet, arms, legs), the intestines (abdomen), the face, the genitals, the larynx (i.e., voice box); vascular permeability; vascular leakage; generalized inflammation; abdominal pain; bloating; vomiting; diarrhea; itchy skin; respiratory (asthmatic) reactions; rhinitis; anaphylaxis; bronchoconstriction; hypotension; coma; and death.

Certain risk factors and causes for development of a thromboembolic disease include genetic predisposition to a thromboembolic disease, immobility, surgery (particularly orthopedic surgery), malignancy, pregnancy, older age, use of oral contraceptives, atrial fibrillation, previous thromboembolic condition, chronic inflammatory disease, and inherited or acquired prothrombotic clotting disorders. Certain outcomes associated with development of a thromboembolic condition include decreased blood flow through an affected vessel, death of tissue, and death.

In certain embodiments, methods of treatment include administering a PKK antisense compound to an individual in need thereof. In certain embodiments, methods of treatment include administering a PKK antisense oligonucleotide to an individual in need thereof.

Listing of Figures

Figure 1 is a Western blot quantification of HMWK from blood samples as described in Example 11.

Figure 2 is a Western blot quantification of HMWK from blood samples as described in Example 14.

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. 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.

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 application, including, but not limited to, patents, patent applications, articles, books, and treatises, 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. Where permitted, all patents, applications, published applications and other publications, 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 incorporated by reference for the portions of the document discussed herein, as well as in their entirety.

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

“2'-O-methoxyethyl” (also 2'-MOE and 2'-OCH₂CH₂-OCH₃ and MOE) refers to an O-methoxyethyl modification of the 2' position of a furanose ring. A 2'-O-methoxyethyl modified sugar is a modified sugar.

“2'-O-methoxyethyl modified nucleoside” (also “2'-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.

“2'-deoxynucleoside” means a nucleoside comprising a hydrogen at the 2' position of the sugar portion of the nucleoside.

“3' target site” refers to the nucleotide of a target nucleic acid which is complementary to the 3'-most nucleotide of a particular antisense compound.

“5' target site” refers to the nucleotide of a target nucleic acid which is complementary to the 5'-most nucleotide of a particular antisense compound.

“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 $\pm 7\%$ of a value. For example, if it is stated, “the compounds affected at least about 70% inhibition of PKK”, it is implied that the PKK levels are inhibited within a range of 63% and 77%.

5 “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
10 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
15 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.

“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
20 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.

25 “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.

30 “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 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 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 antisense 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.

“Base complementarity” refers to the capacity for the precise base pairing of nucleobases of an antisense 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 nucleoside” (also bicyclic nucleic acid or BNA) means a nucleoside having a sugar moiety comprising a bridge connecting two carbon atoms of the sugar ring, thereby forming a bicyclic ring system. In certain embodiments, the bridge connects the 4'-carbon and the 2'-carbon of the sugar ring.

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

“cEt” or “constrained ethyl” 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(CH₃)-O-2'.

“cEt modified nucleoside” (also “constrained ethyl nucleoside”) means a nucleoside comprising a bicyclic sugar moiety comprising a 4'-CH(CH₃)-O-2' bridge.

“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 creating 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.

“Downstream” refers to the relative direction toward the 3' end or C-terminal end of a nucleic acid.

“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.

5 “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.

10 “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.”

15 “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 antisense oligonucleotide and a nucleic acid target.

20 “Identifying an animal having an inflammatory disease” means identifying an animal having been diagnosed with an inflammatory disease or predisposed to develop an inflammatory disease. Individuals predisposed to develop an inflammatory disease include those having one or more risk factors for developing an inflammatory disease including environmental factors, having a personal or family history, or genetic predisposition to one or more inflammatory disease. 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.

25 “Identifying an animal having a PKK associated disease” means identifying an animal having been diagnosed with a PKK associated disease or predisposed to develop a PKK associated disease. Individuals predisposed to develop a PKK associated disease include those having one or more risk factors for developing a PKK associated disease including having a personal or family history, or genetic predisposition of one or more PKK 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.

30 “Identifying an animal having a thromboembolic disease” means identifying an animal having been diagnosed with a thromboembolic disease or predisposed to develop a thromboembolic disease. Individuals predisposed to develop a thromboembolic disease include those having one or more risk factors for developing a thromboembolic disease including having a personal or family history, or genetic predisposition of one or more thromboembolic diseases, immobility, surgery (particularly orthopedic surgery), malignancy,

pregnancy, older age, use of oral contraceptives, atrial fibrillation, previous thromboembolic condition, chronic inflammatory disease, and inherited or acquired prothrombotic clotting disorders. 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.

5 “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.

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

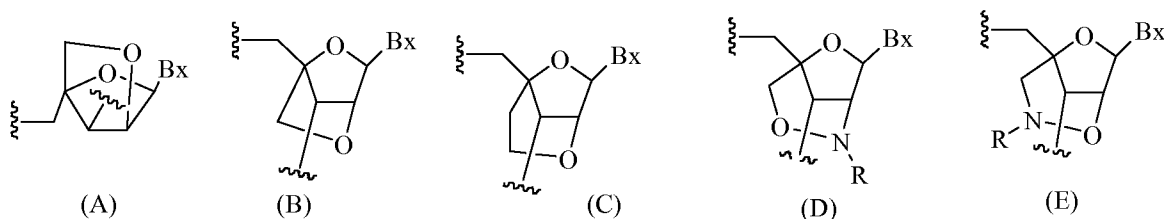
10 “Inhibiting PKK” means reducing the level or expression of a PKK mRNA and/or protein. In certain embodiments, PKK mRNA and/or protein levels are inhibited in the presence of an antisense compound targeting PKK, including an antisense oligonucleotide targeting PKK, as compared to expression of PKK mRNA and/or protein levels in the absence of a PKK antisense compound, such as an antisense 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.

15 “Internucleoside linkage” refers to the chemical bond between nucleosides.

“Linked nucleosides” means adjacent nucleosides linked together by an internucleoside linkage.

20 “Locked nucleic acid” or “LNA” or “LNA nucleosides” means nucleic acid monomers having a bridge connecting two carbon atoms between the 4' and 2' position of the nucleoside sugar unit, thereby forming a bicyclic sugar. Examples of such bicyclic sugar include, but are not limited to (A) α -L-Methyleneoxy (4'-CH₂-O-2') LNA, (B) β -D-Methyleneoxy (4'-CH₂-O-2') LNA, (C) Ethyleneoxy (4'-(CH₂)₂-O-2') LNA, (D) Aminooxy (4'-CH₂-O-N(R)-2') LNA and (E) Oxyamino (4'-CH₂-N(R)-O-2') LNA, as depicted below.



25 As used herein, LNA compounds include, but are not limited to, compounds having at least one bridge between the 4' and the 2' position of the sugar wherein each of the bridges independently comprises 1 or from 2 to 4 linked groups independently selected from -[C(R₁)(R₂)]_n-, -C(R₁)=C(R₂)-, -C(R₁)=N-, -C(=NR₁)-, -C(=O)-, -C(=S)-, -O-, -Si(R₁)₂-, -S(=O)_x- and -N(R₁)-; wherein: x is 0, 1, or 2; n is 1, 2, 3, or 4; each R₁ and R₂ is, independently, H, a protecting group, hydroxyl, C₁-C₁₂ alkyl, substituted C₁-C₁₂ alkyl, C₂-C₁₂ alkenyl, substituted C₂-C₁₂ alkenyl, C₂-C₁₂ alkynyl, substituted C₂-C₁₂ alkynyl, C₅-C₂₀ aryl,

substituted C₅-C₂₀ aryl, a heterocycle radical, a substituted heterocycle radical, heteroaryl, substituted heteroaryl, C₅-C₇ alicyclic radical, substituted C₅-C₇ alicyclic radical, halogen, OJ₁, NJ₁J₂, SJ₁, N₃, COOJ₁, acyl (C(=O)-H), substituted acyl, CN, sulfonyl (S(=O)₂-J₁), or sulfoxyl (S(=O)-J₁); and each J₁ and J₂ is, independently, H, C₁-C₁₂ alkyl, substituted C₁-C₁₂ alkyl, C₂-C₁₂ alkenyl, substituted C₂-C₁₂ alkenyl, C₂-C₁₂ alkynyl, substituted C₂-C₁₂ alkynyl, C₅-C₂₀ aryl, substituted C₅-C₂₀ aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C₁-C₁₂ aminoalkyl, substituted C₁-C₁₂ aminoalkyl or a protecting group.

Examples of 4'-2' bridging groups encompassed within the definition of LNA include, but are not limited to one of formulae: -[C(R₁)(R₂)]_n-, -[C(R₁)(R₂)]_n-O-, -C(R₁R₂)-N(R₁)-O- or -C(R₁R₂)-O-N(R₁)-. Furthermore, other bridging groups encompassed with the definition of LNA are 4'-CH₂-2', 4'-(CH₂)₂-2', 4'-(CH₂)₃-2', 4'-CH₂-O-2', 4'-(CH₂)₂-O-2', 4'-CH₂-O-N(R₁)-2' and 4'-CH₂-N(R₁)-O-2'- bridges, wherein each R₁ and R₂ is, independently, H, a protecting group or C₁-C₁₂ alkyl.

Also included within the definition of LNA according to the invention are LNAs in which the 2'-hydroxyl group of the ribosyl sugar ring is connected to the 4' carbon atom of the sugar ring, thereby forming a methyleneoxy (4'-CH₂-O-2') bridge to form the bicyclic sugar moiety. The bridge can also be a methylene (-CH₂-) group connecting the 2' oxygen atom and the 4' carbon atom, for which the term methyleneoxy (4'-CH₂-O-2') LNA is used. Furthermore; in the case of the bicyclic sugar moiety having an ethylene bridging group in this position, the term ethyleneoxy (4'-CH₂CH₂-O-2') LNA is used. α-L- methyleneoxy (4'-CH₂-O-2'), an isomer of methyleneoxy (4'-CH₂-O-2') LNA is also encompassed within the definition of LNA, as used herein.

"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.

"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 (also known as 5-methyluracil), 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).

"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.

5 “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.

10 “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.

15 “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.

20 “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.

25 “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 tetrahydropyran 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.

5 “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.

10 “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.

15 “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.

20 “Pharmaceutical agent” means a substance that provides a therapeutic benefit when administered to an individual. For example, in certain embodiments, an antisense oligonucleotide targeted to PKK is a pharmaceutical agent.

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

25 “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.

5 “PKK” means mammalian plasma prekallikrein, including human plasma prekallikrein. Plasma prekallikrein (PKK) is the precursor of plasma kallikrein (PK), which is encoded by the KLKB1 gene.

“PKK associated disease” means any disease associated with any PKK nucleic acid or expression product thereof. Such diseases may include an inflammatory disease or a thromboembolic disease. Such diseases may include hereditary angioedema (HAE).

“PKK mRNA” means any messenger RNA expression product of a DNA sequence encoding PKK.

10 “PKK nucleic acid” means any nucleic acid encoding PKK. For example, in certain embodiments, a PKK nucleic acid includes a DNA sequence encoding PKK, an RNA sequence transcribed from DNA encoding PKK (including genomic DNA comprising introns and exons), and an mRNA sequence encoding PKK. “PKK mRNA” means an mRNA encoding a PKK protein.

“PKK protein” means the polypeptide expression product of a PKK nucleic acid.

15 “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.

20 “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.

25 “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.

30 “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.

“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.

“Specifically hybridizable” or “specifically hybridizes” refers to an antisense compound having a sufficient degree of complementarity between an antisense 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.

“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 to administering a composition to effect an 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 occurring 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).

“Upstream” refers to the relative direction toward the 5' end or N-terminal end of a nucleic acid.

“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.

10 *Certain Embodiments*

Certain embodiments provide compounds, compositions, and methods for inhibiting plasma prekallikrein (PKK) mRNA and protein expression. Certain embodiments provide compounds, compositions, and methods for decreasing PKK mRNA and protein levels.

Certain embodiments provide antisense compounds targeted to a plasma prekallikrein (PKK) nucleic acid. In certain embodiments, the PKK nucleic acid is the sequence set forth in GENBANK Accession No. NM_000892.3 (incorporated herein as SEQ ID NO: 1), GENBANK Accession No. DC412984.1 (incorporated herein as SEQ ID NO: 2), GENBANK Accession No. CN265612.1 (incorporated herein as SEQ ID NO: 3), GENBANK Accession No. AK297672.1 (incorporated herein as SEQ ID NO: 4), GENBANK Accession No. DC413312.1 (incorporated herein as SEQ ID NO: 5), GENBANK Accession No. AV688858.2 (incorporated herein as SEQ ID NO: 6), GENBANK Accession No. CD652077.1 (incorporated herein as SEQ ID NO: 7), GENBANK Accession No. BC143911.1 (incorporated herein as SEQ ID NO: 8), GENBANK Accession No. CB162532.1 (incorporated herein as SEQ ID NO: 9), GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000 (incorporated herein as SEQ ID NO: 10), GENBANK Accession No. NM_008455.2 (incorporated herein as SEQ ID NO: 11), GENBANK Accession No. BB598673.1 (incorporated herein as SEQ ID NO: 12), GENBANK Accession No. NT_039460.7 truncated from nucleobases 6114001 to 6144000 (incorporated herein as SEQ ID NO: 13), GENBANK Accession No. NM_012725.2 (incorporated herein as SEQ ID NO: 14), GENBANK Accession No. NW_047473.1 truncated from nucleobases 10952001 to 10982000 (incorporated herein as SEQ ID NO: 15), GENBANK Accession No. XM_002804276.1 (incorporated herein as SEQ ID NO: 17), and GENBANK Accession No. NW_001118167.1 truncated from nucleobases 2358000 to 2391000 (incorporated herein as SEQ ID NO: 18).

Certain embodiments provide compounds, 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: 30-2226.

Certain embodiments provide compounds, 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 the nucleobase sequence of SEQ ID NO: 570.

Certain embodiments provide compounds, 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 the nucleobase sequence of SEQ ID NO: 705.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of the nucleobase sequence of SEQ ID NO: 1666.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 20 linked nucleosides and having the nucleobase sequence of SEQ ID NO: 570.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 20 linked nucleosides and having the nucleobase sequence of SEQ ID NO: 705.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 16 linked nucleosides and having the nucleobase sequence of SEQ ID NO: 1666.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 62, 72, 103, 213, 312, 334-339, 344, 345, 346, 348, 349, 351, 369, 373, 381, 382, 383, 385, 387-391, 399, 411, 412, 414, 416, 444, 446-449, 452, 453, 454, 459, 460, 462-472, 473, 476, 477, 479, 480, 481, 484, 489-495, 497, 500, 504, 506, 522, 526, 535, 558, 559, 560, 564, 566, 568-571, 573, 576, 577, 578, 587, 595, 597-604, 607, 608, 610, 613, 615, 618, 619, 622, 623, 624, 633, 635, 636, 638, 639, 640, 642, 643, 645, 652, 655-658, 660, 661, 670, 674-679, 684, 685, 698, 704, 705, 707, 708, 713, 716, 717, 728, 734, 736, 767, 768, 776, 797, 798, 800, 802, 810, 815, 876, 880, 882, 883, 886, 891, 901-905, 908-911, 922, 923, 924, 931, 942, 950-957, 972, 974, 978, 979, 980, 987-991, 1005, 1017-1021, 1025, 1026, 1029, 1030, 1032, 1034, 1035, 1037, 1040, 1041, 1045, 1046, 1051, 1054, 1059, 1060, 1061, 1064, 1065, 1066, 1075, 1076, 1087, 1089, 1111, 1114, 1116, 1117, 1125, 1133, 1153, 1169, 1177, 1181, 1182, 1187, 1196, 1200, 1214, 1222, 1267, 1276, 1277, 1285, 1286, 1289, 1290, 1291, 1303, 1367, 1389, 1393, 1398-

1401, 1406, 1407, 1408, 1411, 1419-1422, 1426, 1430, 1431, 1432, 1434-1437, 1439, 1440, 1443, 1444, 1451, 1452, 1471, 1516, 1527, 1535, 1537, 1538, 1539, 1540, 1541, 1563, 1564, 1567, 1568, 1616, 1617, 1623, 1629, 1664, 1665, 1666, 1679, 1687, 1734, 1804, 1876, 1886, 1915, 2008, 2018, 2100, 2101, 2115, and 2116. In certain embodiments, the modified oligonucleotide achieves at least 80% mRNA inhibition of PKK.

5 Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 62, 72, 103, 213, 334-339, 344, 346, 348, 349, 351, 381, 382, 383, 385, 389, 390, 391, 446, 448, 452, 453, 454, 466-473, 476, 481, 484, 491, 492, 494, 495, 497, 504, 526, 558, 10 559, 566, 568-571, 576, 578, 587, 595, 597, 598, 600-604, 607, 610, 613, 618, 619, 624, 635, 638, 639, 645, 652, 656, 657, 658, 660, 674, 675, 676, 684, 698, 704, 705, 707, 713, 716, 768, 876, 880, 901-905, 908-911, 922, 923, 924, 931, 942, 951, 954-957, 972, 974, 978, 979, 987, 988, 990, 1005, 1019, 1020, 1021, 1025, 1032, 1037, 1040, 1041, 1045, 1054, 1059, 1060, 1061, 1064, 1065, 1066, 1075, 1111, 1116, 1117, 1125, 1133, 1153, 1169, 1177, 1200, 1222, 1267, 1285, 1290, 1291, 1303, 1367, 1398, 1399, 1401, 1406, 1408, 15 1411, 1419, 1420, 1421, 1426, 1430, 1431, 1432, 1434-1437, 1440, 1443, 1444, 1451, 1537-1540, 1563, 1616, 1679, 1687, 1804, 2008, 2101, 2115, and 2116. In certain embodiments, the modified oligonucleotide achieves at least 85% mRNA inhibition of PKK.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 346, 351, 382, 390, 391, 446, 448, 452, 453, 468, 469, 470, 471, 20 472, 476, 481, 491, 495, 504, 558, 566, 568, 570, 571, 578, 587, 597, 598, 600, 604, 613, 635, 638, 645, 656, 658, 660, 674, 675, 684, 704, 705, 880, 901-905, 909, 922, 931, 951, 954, 956, 990, 1005, 1020, 1032, 1037, 1040, 1041, 1045, 1054, 1075, 1111, 1125, 1133, 1153, 1200, 1267, 1291, 1303, 1398, 1399, 1401, 1406, 25 1420, 1426, 1430, 1431, 1434, 1435, 1436, 1440, 1443, 1451, 1537-1540, 2115, and 2116. In certain embodiments, the modified oligonucleotide achieves at least 90% mRNA inhibition of PKK.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 391, 448, 468, 469, 568, 570, 598, 635, 658, 674, 684, 705, 901, 30 903, 904, 922, 990, 1267, 1291, 1420, 1430, 1431, 1434, 1435, 1436, 1537, 1538, and 1540. In certain embodiments, the modified oligonucleotide achieves at least 95% mRNA inhibition of PKK.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 338, 346, 349, 382, 383, 390, 448, 452, 453, 454, 495, 526, 559, 570, 587, 598, 635, 660, 705, 901, 903, 904, 908, 923, 931, 955, 974, 988, 990, 1020, 1039, 1040, 1111, 1117, 1267, 1291, 1349, 1352, 1367, 1389, 1393, 1399, 1401, 1408, 1411, 1426, 1499, 1516, 1535, 1544, 1548, 1563, 1564, 1568, 1569, 1598, 1616, 1617, 1623, 1624, 1643, 1661, 1665, 1666, 1673, 1679, 1695, 1720, 1804, 1817, 1876, 1881, 1886, 1940, 1947, 2008, 2018, 2019, 2031, 2044, 2100, 2101, 2115, and 2116. In certain embodiments, the modified oligonucleotide achieves an IC_{50} (μM) of 0.4 or less.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 346, 349, 382, 453, 454, 495, 526, 570, 587, 598, 635, 660, 901, 903, 904, 931, 955, 990, 1020, 1111, 1267, 1349, 1352, 1367, 1389, 1399, 1408, 1411, 1426, 1516, 1535, 1544, 1548, 1563, 1564, 1568, 1569, 1598, 1616, 1617, 1623, 1643, 1661, 1665, 1666, 1673, 1695, 1804, 1876, 1881, 2019, 2044, 2100, 2101, 2115, and 2116. In certain embodiments, the modified oligonucleotide achieves an IC_{50} (μM) of 0.3 or less.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 346, 382, 453, 495, 526, 570, 587, 598, 635, 901, 904, 931, 955, 1020, 1111, 1349, 1352, 1389, 1426, 1516, 1535, 1544, 1548, 1564, 1569, 1598, 1616, 1617, 1665, 1666, 1804, 1876, 1881, 2019, 2044, 2101, and 2116. In certain embodiments, the modified oligonucleotide achieves an IC_{50} (μM) of 0.2 or less.

Certain embodiments provide compounds, 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 495, 587, 598, 635, 1349, 1352, 1389, 1516, 1544, 1548, 1569, 1598, 1617, 1665, 1666, 1804, 1881, and 2019. In certain embodiments, the modified oligonucleotide achieves an IC_{50} (μM) of less than 0.2.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 27427-27466 of SEQ ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 33183-33242 of SEQ

ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 30570-30610 of SEQ

ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 27427-27520 of SEQ

ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 33085-33247 of SEQ

ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 30475-30639 of SEQ

ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 27362-27524 of SEQ

ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 33101-33240 of SEQ ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 30463-30638 of SEQ ID NO: 10.

Certain embodiments provide compounds, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of exon 9, exon 12, or exon 14 of a PKK nucleic acid.

In certain embodiments 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: 10.

In certain embodiments, the compound consists of a single-stranded modified oligonucleotide.

In certain embodiments, at least one internucleoside linkage of the modified oligonucleotide is a modified internucleoside linkage.

In certain embodiments, at least one modified internucleoside linkage of the modified oligonucleotide is a phosphorothioate internucleoside linkage.

In certain embodiments, each internucleoside linkage of the modified oligonucleotide is a phosphorothioate linkage.

In certain embodiments, at least one nucleoside of the modified oligonucleotide comprises a modified nucleobase.

In certain embodiments, the modified nucleobase is a 5-methylcytosine.

In certain embodiments, the modified oligonucleotide comprises at least one modified sugar.

In certain embodiments, the modified sugar is a 2' modified sugar, a BNA, or a THP.

In certain embodiments, the modified sugar is any of a 2'-O-methoxyethyl, 2'-O-methyl, a constrained ethyl, a LNA, or a 3'-fluoro-HNA.

In certain embodiments, the compound comprises at least one 2'-O-methoxyethyl nucleoside, 2'-O-methyl nucleoside, constrained ethyl nucleoside, LNA nucleoside, or 3'-fluoro-HNA nucleoside.

In certain embodiments, the modified oligonucleotide comprises:

a gap segment consisting of 10 linked deoxynucleosides;

5 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.

In certain embodiments, the modified oligonucleotide consists of 20 linked nucleosides.

10 In certain embodiments, the modified oligonucleotide consists of 19 linked nucleosides.

In certain embodiments, the modified oligonucleotide consists of 18 linked nucleosides.

Certain embodiments provide compounds consisting of a modified oligonucleotide according to the following formula: Tes Ges mCes Aes Aes Gds Tds mCds Tds mCds Tds Tds Gds Gds mCds Aes Aes Aes mCes Ae; wherein,

15 A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethyl modified nucleoside,

20 d = a 2'-deoxynucleoside, and

s = a phosphorothioate internucleoside linkage.

Certain embodiments provide compounds consisting of a modified oligonucleotide according to the following formula: mCes mCes mCes mCes mCes Tds Tds mCds Tds Tds Tds Ads Tds Ads Gds mCes mCes Aes Ges mCe; wherein,

25 A = an adenine,

mC = a 5'-methylcytosine;

G = a guanine,

T = a thymine,

e = a 2'-O-methoxyethyl modified nucleoside,

d = a 2'-deoxynucleoside, and

s = a phosphorothioate internucleoside linkage.

5 Certain embodiments provide compounds consisting of a modified oligonucleotide according to the following formula: mCes Ges Aks Tds Ads Tds mCds Ads Tds Gds Ads Tds Tds mCks mCks mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine;

G = a guanine,

T = a thymine,

10 e = a 2'-O-methoxyethyl modified nucleoside,

k = a cEt modified nucleoside,

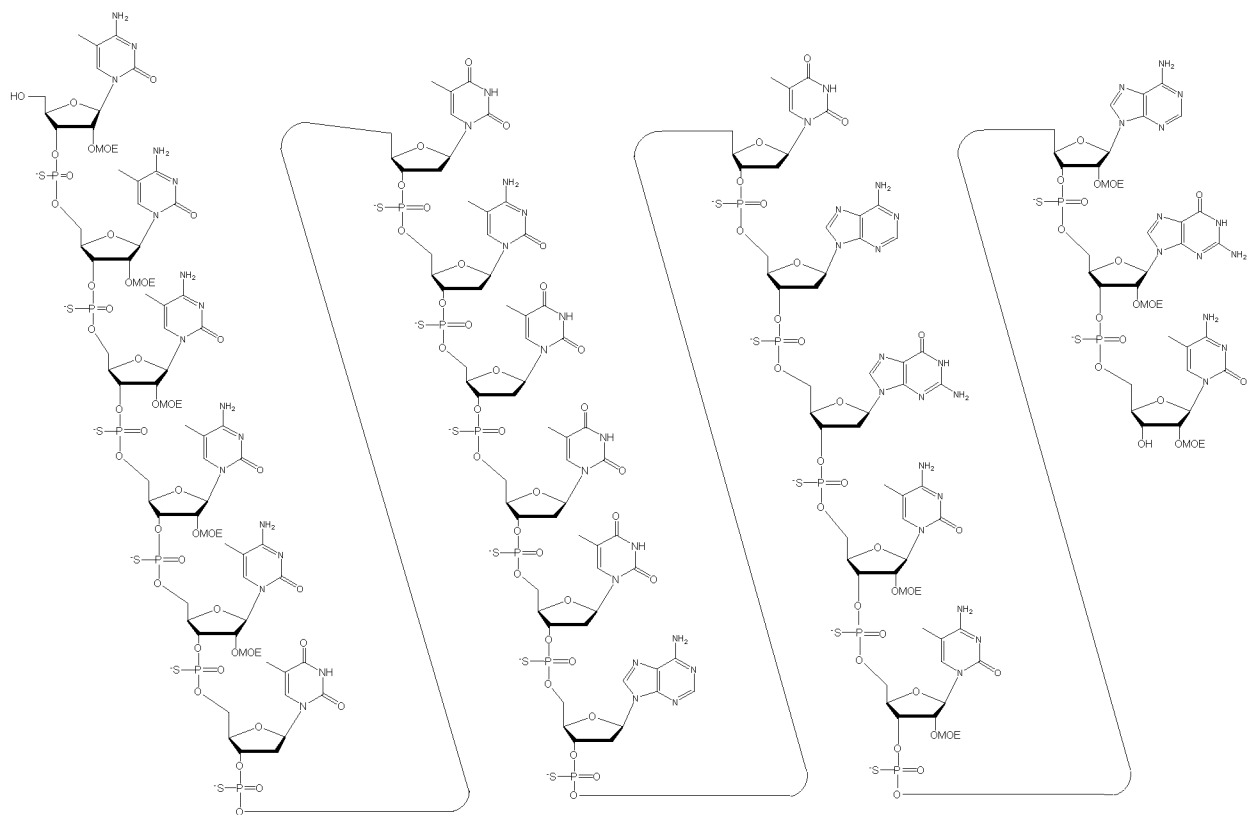
d = a 2'-deoxynucleoside, and

s = a phosphorothioate internucleoside linkage.

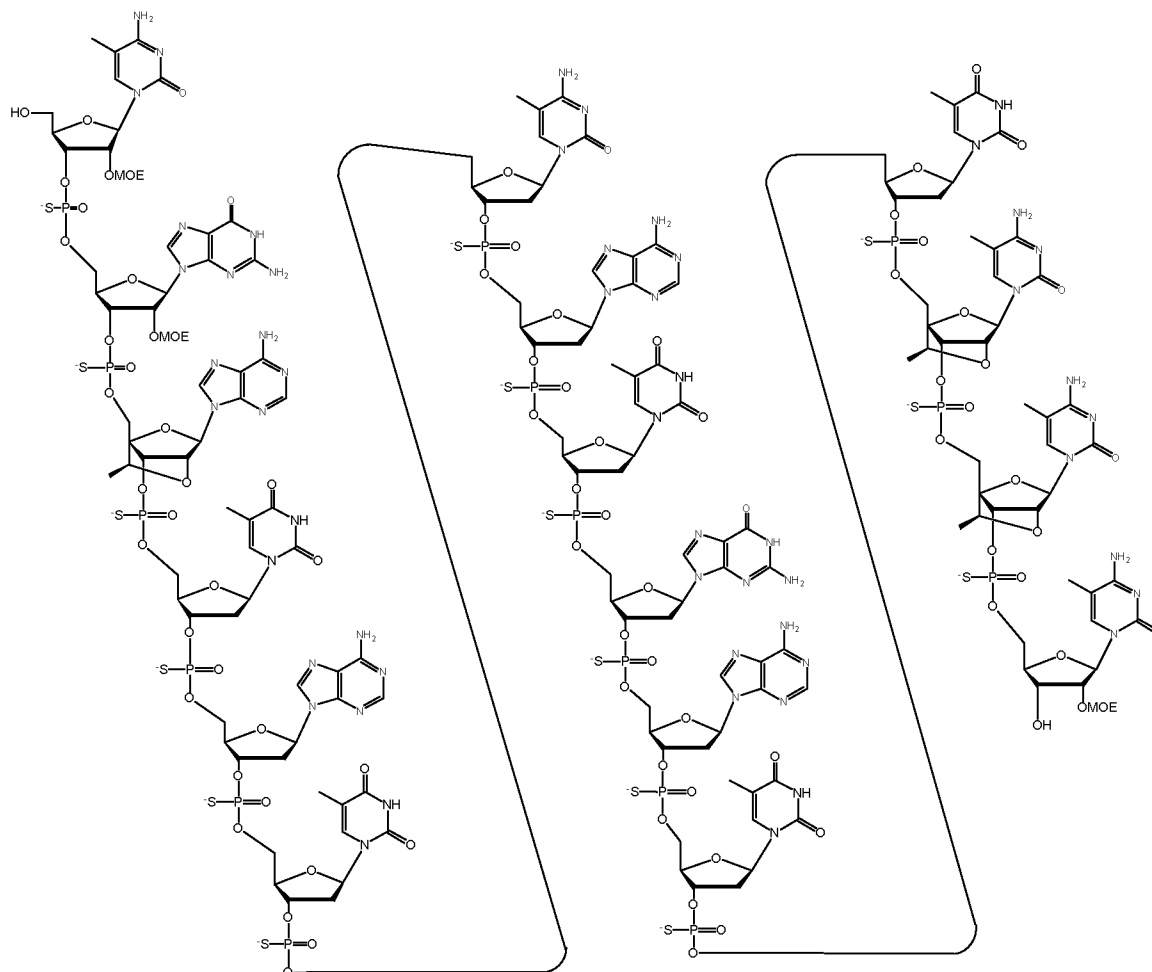
Certain embodiments provide compounds according to the following formula:



Certain embodiments provide compounds according to the following formula:



Certain embodiments provide compounds according to the following formula:



Certain embodiments provide compositions comprising the compound of any preceding claim or salt thereof and at least one of a pharmaceutically acceptable carrier or diluent.

- 5 Certain embodiments provide methods comprising administering to an animal the compound or composition of any preceding claim.

In certain embodiments, the animal is a human.

In certain embodiments, administering the compound prevents, treats, or ameliorates a PKK associated disease, disorder or condition.

- 10 In certain embodiments, the PKK associated disease, disorder or condition is a hereditary angioedema (HAE), edema, angioedema, swelling, angioedema of the lids, ocular edema, macular edema, cerebral edema, thrombosis, embolism, thromboembolism, deep vein thrombosis, pulmonary embolism, myocardial infarction, stroke, or infarct.

Certain embodiments provide use of the compound or composition of any preceding claim for the manufacture of a medicament for treating an inflammatory disease or a thromboembolic disease.

Antisense Compounds

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

10 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 antisense 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.

15 In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 12 to 30 subunits in length. In certain embodiments, an antisense compound targeted to PKK nucleic acid is 12 to 25 subunits in length. In certain embodiments, an antisense compound targeted to PKK nucleic acid is 12 to 22 subunits in length. In certain embodiments, an antisense compound targeted to PKK nucleic acid is 14 to 20 subunits in length. In certain embodiments, an antisense compound targeted to PKK nucleic acid is 15 to 25 subunits in length. In certain embodiments, an antisense compound targeted to PKK nucleic acid is 18 to 22 subunits in length. In certain embodiments, an antisense compound targeted to PKK 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.

25 In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 12 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 13 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 14 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 15 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 16 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 17 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 18 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 19 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 20 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 21 subunits in length.

length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 22 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 23 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 24 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 25 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 26 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 27 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 28 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 29 subunits in length. In certain embodiments, an antisense compound targeted to a PKK nucleic acid is 30 subunits in length. In certain embodiments, the antisense compound targeted to a PKK 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 an antisense oligonucleotide, and the linked subunits are nucleosides.

In certain embodiments antisense oligonucleotides targeted to a PKK 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 PKK 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 an antisense 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 antisense oligonucleotides 13-25 nucleobases in length were tested for their ability to induce cleavage of a target RNA in an oocyte injection model. Antisense oligonucleotides 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the antisense oligonucleotides were able to direct specific cleavage of the target mRNA, albeit to a lesser extent

than the antisense oligonucleotides that contained no mismatches. Similarly, target specific cleavage was achieved using 13 nucleobase antisense 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.

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

Antisense Compound Motifs

In certain embodiments, antisense compounds targeted to a PKK 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 antisense 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-CH₃, among others), and bicyclic sugar modified nucleosides (such bicyclic sugar modified nucleosides may include those having a 4'-(CH₂)_n-O-2' bridge, where n=1 or n=2 and 4'-CH₂-O-CH₂-2'). 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.

5 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
10 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.

15 *Target Nucleic Acids, Target Regions and Nucleotide Sequences*

Nucleotide sequences that encode human plasma prekallikrein (PKK) include, without limitation, the following: GENBANK Accession No. NM_000892.3 (incorporated herein as SEQ ID NO: 1), GENBANK Accession No. DC412984.1 (incorporated herein as SEQ ID NO: 2), GENBANK Accession No. CN265612.1 (incorporated herein as SEQ ID NO: 3), GENBANK Accession No. AK297672.1 (incorporated
20 herein as SEQ ID NO: 4), GENBANK Accession No. DC413312.1 (incorporated herein as SEQ ID NO: 5), GENBANK Accession No. AV688858.2 (incorporated herein as SEQ ID NO: 6), GENBANK Accession No. CD652077.1 (incorporated herein as SEQ ID NO: 7), GENBANK Accession No. BC143911.1 (incorporated herein as SEQ ID NO: 8), GENBANK Accession No. CB162532.1 (incorporated herein as SEQ ID NO: 9), GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000
25 (incorporated herein as SEQ ID NO: 10), GENBANK Accession No. NM_008455.2 (incorporated herein as SEQ ID NO: 11), GENBANK Accession No. BB598673.1 (incorporated herein as SEQ ID NO: 12), GENBANK Accession No. NT_039460.7 truncated from nucleobases 6114001 to 6144000 (incorporated herein as SEQ ID NO: 13), GENBANK Accession No. NM_012725.2 (incorporated herein as SEQ ID NO: 14), GENBANK Accession No. NW_047473.1 truncated from nucleobases 10952001 to 10982000
30 (incorporated herein as SEQ ID NO: 15), GENBANK Accession No. XM_002804276.1 (incorporated herein as SEQ ID NO: 17), and GENBANK Accession No. NW_001118167.1 truncated from nucleobases 2358000 to 2391000 (incorporated herein as SEQ ID NO: 18).

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.

5 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 PKK 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
10 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.

15 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 embodiments, 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
20 nucleic acid, or is a range defined by any two of the preceding 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.

25 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 specifically exclude a certain structurally defined region such as the start codon or stop codon.

30 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 PKK mRNA levels are indicative of inhibition of PKK expression. Reductions in levels of a PKK protein are also indicative of inhibition of target mRNA expression. Further, phenotypic changes are indicative of inhibition of PKK expression. For example, reduced or prevented inflammation can be indicative of inhibition of PKK expression. In another example, reduced or prevented edema/swelling can be indicative of inhibition of PKK expression. In another example, reduced or prevented vascular permeability can be indicative of inhibition of PKK expression. In another example, reduced or prevented vascular leakage can be indicative of inhibition of PKK expression. In certain embodiments, vascular permeability is measured by quantification of a dye, such as Evans Blue.

Hybridization

In some embodiments, hybridization occurs between an antisense compound disclosed herein and a target 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 target 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 PKK nucleic acid).

Non-complementary nucleobases between an antisense compound and a PKK 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 PKK 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%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% complementary to an PKK 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 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 plasma prekallikrein 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 antisense 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 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 or specified portion thereof.

The antisense compounds provided 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 antisense 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 antisense 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 occurring 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, antisense compounds targeted to a plasma prekallikrein nucleic acid comprise one or more modified internucleoside linkages. In certain embodiments, the modified internucleoside linkages are phosphorothioate linkages. In certain embodiments, each internucleoside linkage of an antisense compound is a phosphorothioate internucleoside linkage.

Modified Sugar Moieties

Antisense compounds 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 substituent 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(R₁)(R₂) (R, R₁ and R₂ are each independently H, C₁-C₁₂ 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).

5 Examples of nucleosides having modified sugar moieties include without limitation nucleosides comprising 5'-vinyl, 5'-methyl (*R* or *S*), 4'-S, 2'-F, 2'-OCH₃, 2'-OCH₂CH₃, 2'-OCH₂CH₂F and 2'-O(CH₂)₂OCH₃ substituent groups. The substituent at the 2' position can also be selected from allyl, amino, azido, thio, O-allyl, O-C₁-C₁₀ alkyl, OCF₃, OCH₂F, O(CH₂)₂SCH₃, O(CH₂)₂-O-N(R_m)(R_n), O-CH₂-C(=O)-N(R_m)(R_n), and O-CH₂-C(=O)-N(R₁)-(CH₂)₂-N(R_m)(R_n), where each R₁, R_m and R_n is, independently, H or
10 substituted or unsubstituted C₁-C₁₀ alkyl.

As used herein, "bicyclic nucleosides" refer to modified nucleosides comprising a bicyclic sugar moiety. Examples of bicyclic nucleosides 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 bicyclic nucleosides comprising a 4' to 2' bridge. Examples of such 4' to 2' bridged
15 bicyclic nucleosides, include but are not limited to one of the formulas: 4'-(CH₂)-O-2' (LNA); 4'-(CH₂)-S-2'; 4'-(CH₂)₂-O-2' (ENA); 4'-CH(CH₃)-O-2' (also referred to as constrained ethyl or cEt) and 4'-CH(CH₂OCH₃)-O-2' (and analogs thereof see U.S. Patent 7,399,845, issued on July 15, 2008); 4'-C(CH₃)(CH₃)-O-2' (and analogs thereof see PCT/US2008/068922 published as WO/2009/006478, published January 8, 2009); 4'-CH₂-N(OCH₃)-2' (and analogs thereof see PCT/US2008/064591 published as WO/2008/150729, published
20 December 11, 2008); 4'-CH₂-O-N(CH₃)-2' (see published U.S. Patent Application US2004-0171570, published September 2, 2004); 4'-CH₂-N(R)-O-2', wherein R is H, C₁-C₁₂ alkyl, or a protecting group (see U.S. Patent 7,427,672, issued on September 23, 2008); 4'-CH₂-C(H)(CH₃)-2' (see Chattopadhyaya *et al.*, *J. Org. Chem.*, 2009, 74, 118-134); and 4'-CH₂-C(=CH₂)-2' (and analogs thereof see PCT/US2008/066154 published as WO 2008/154401, published on December 8, 2008).

25 Further reports related to bicyclic nucleosides can also be found in published literature (see for example: Frieden *et al.*, *Nucleic Acids Research*, 2003, 21, 6365-6372; Singh *et al.*, *Chem. Commun.*, 1998, 4, 455-456; Koshkin *et al.*, *Tetrahedron*, 1998, 54, 3607-3630; Wahlestedt *et al.*, *Proc. Natl. Acad. Sci. U. S. A.*, 2000, 97, 5633-5638; Kumar *et al.*, *Bioorg. Med. Chem. Lett.*, 1998, 8, 2219-2222; Singh *et al.*, *J. Org. Chem.*, 1998, 63, 10035-10039; Srivastava *et al.*, *J. Am. Chem. Soc.*, 2007, 129(26) 8362-8379; Elayadi *et al.*,
30 *Curr. Opinion Invest. Drugs*, 2001, 2, 558-561; Braasch *et al.*, *Chem. Biol.*, 2001, 8, 1-7; and Orum *et al.*, *Curr. Opinion Mol. Ther.*, 2001, 3, 239-243; U.S. Patent Nos. 6,268,490; 6,525,191; 6,670,461; 6,770,748; 6,794,499; 7,034,133; 7,053,207; 7,399,845; 7,547,684; and 7,696,345; U.S. Patent Publication No. US2008-0039618; US2009-0012281; US2007-0287831; US2004-0171570; U.S. Patent Application Serial Nos. 12/129,154; 60/989,574; 61/026,995; 61/026,998; 61/056,564; 61/086,231; 61/097,787; and 61/099,844;

Published PCT International applications WO 1994/014226; WO 2004/106356; WO 2005/021570; WO 2007/134181; WO 2008/150729; WO 2008/154401; and WO 2009/006478. 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).

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' position of the pentofuranosyl sugar moiety wherein such bridges independently comprise 1 or from 2 to 4 linked groups independently selected from - $[C(R_a)(R_b)]_n$ -, $-C(R_a)=C(R_b)$ -, $-C(R_a)=N$ -, $-C(=O)$ -, $-C(=NR_a)$ -, $-C(=S)$ -, $-O$ -, $-Si(R_a)_2$ -, $-S(=O)_x$ -, 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 ($S(=O)_2J_1$), or sulfoxyl ($S(=O)J_1$); and

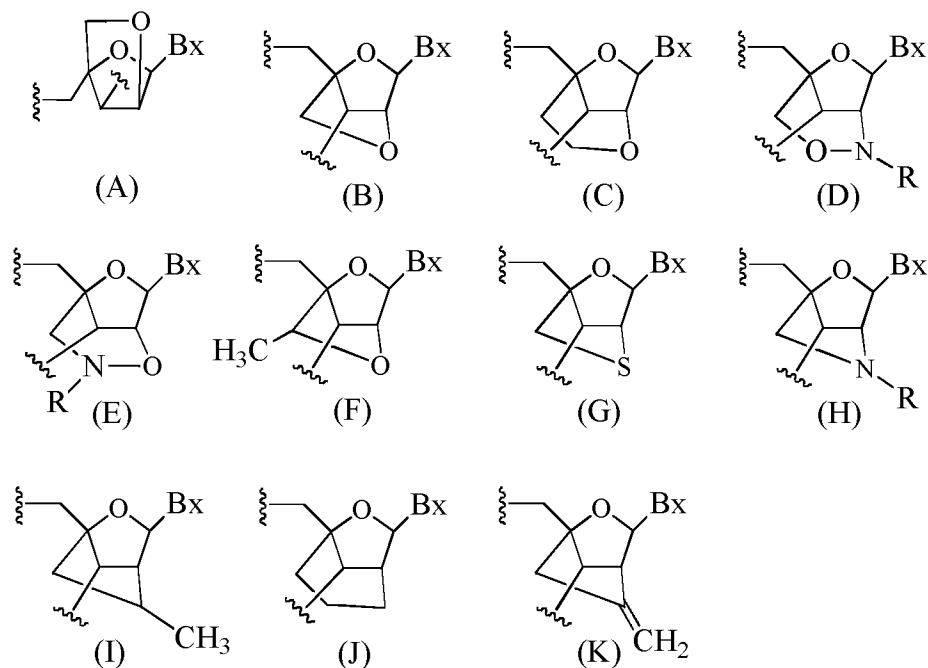
each J_1 and J_2 is, independently, H, C_1 - C_{12} alkyl, substituted C_1 - C_{12} alkyl, C_2 - C_{12} alkenyl, substituted C_2 - C_{12} alkenyl, C_2 - C_{12} alkynyl, substituted C_2 - C_{12} alkynyl, C_5 - C_{20} aryl, substituted C_5 - C_{20} aryl, acyl ($C(=O)$ -H), substituted acyl, a heterocycle 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'-2' methylene-oxy 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, 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,

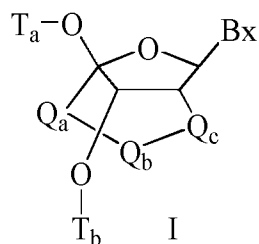
(D) aminooxy ($4'-\text{CH}_2\text{-O-N(R)-2}'$) BNA, (E) oxyamino ($4'-\text{CH}_2\text{-N(R)-O-2}'$) BNA, and (F) methyl(methyleneoxy) ($4'-\text{CH}(\text{CH}_3)\text{-O-2}'$) BNA, (G) methylene-thio ($4'-\text{CH}_2\text{-S-2}'$) BNA, (H) methylene-amino ($4'-\text{CH}_2\text{-N(R)-2}'$) BNA, (I) methyl carbocyclic ($4'-\text{CH}_2\text{-CH}(\text{CH}_3)\text{-2}'$) BNA, (J) propylene carbocyclic ($4'-(\text{CH}_2)_3\text{-2}'$) BNA and (K) vinyl BNA as depicted below:



5

wherein Bx is the base moiety and R is independently H, a protecting group, $\text{C}_1\text{-C}_{12}$ alkyl or $\text{C}_1\text{-C}_{12}$ alkoxy.

In certain embodiments, bicyclic nucleosides are provided having Formula I:



10 wherein:

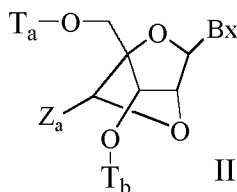
Bx is a heterocyclic base moiety;

$-\text{Q}_a\text{-Q}_b\text{-Q}_c-$ is $-\text{CH}_2\text{-N(R}_c\text{)-CH}_2-$, $-\text{C(=O)-N(R}_c\text{)-CH}_2-$, $-\text{CH}_2\text{-O-N(R}_c\text{)-}$, $-\text{CH}_2\text{-N(R}_c\text{)-O-}$ or $-\text{N(R}_c\text{)-O-CH}_2-$;

R_c is $\text{C}_1\text{-C}_{12}$ 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 are provided having Formula II:



5 wherein:

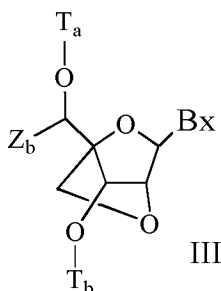
Bx is a heterocyclic base moiety;

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;

10 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 thio.

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 $NJ_cC(=X)NJ_cJ_d$, 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 .

15 In certain embodiments, bicyclic nucleosides are provided having Formula III:



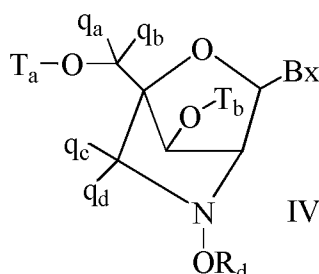
wherein:

Bx is a heterocyclic base moiety;

20 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 are provided having Formula IV:



5 wherein:

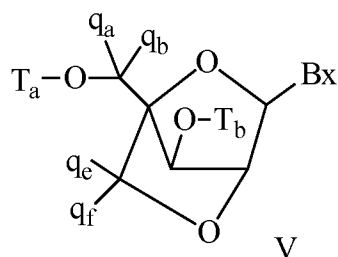
Bx is a heterocyclic base moiety;

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;

10 R_d is C₁-C₆ alkyl, substituted C₁-C₆ alkyl, C₂-C₆ alkenyl, substituted C₂-C₆ alkenyl, C₂-C₆ alkynyl or substituted C₂-C₆ alkynyl;

each q_a, q_b, q_c and q_d is, independently, H, halogen, C₁-C₆ alkyl, substituted C₁-C₆ alkyl, C₂-C₆ alkenyl, substituted C₂-C₆ alkenyl, C₂-C₆ alkynyl or substituted C₂-C₆ alkynyl, C₁-C₆ alkoxy, substituted C₁-C₆ alkoxy, acyl, substituted acyl, C₁-C₆ aminoalkyl or substituted C₁-C₆ aminoalkyl;

In certain embodiments, bicyclic nucleosides are provided having Formula V:



15

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;

20 q_a, q_b, q_e and q_f are each, independently, hydrogen, halogen, C₁-C₁₂ alkyl, substituted C₁-C₁₂ alkyl, C₂-C₁₂ alkenyl, substituted C₂-C₁₂ alkenyl, C₂-C₁₂ alkynyl, substituted C₂-C₁₂ alkynyl, C₁-C₁₂ alkoxy, substituted

C₁-C₁₂ alkoxy, OJ_j, SJ_j, SOJ_j, SO₂J_j, NJ_jJ_k, N₃, 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;

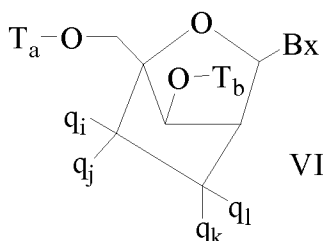
or q_e and q_f together are =C(q_g)(q_h);

q_g and q_h are each, independently, H, halogen, C₁-C₁₂ alkyl or substituted C₁-C₁₂ alkyl.

- 5 The synthesis and preparation of the methyleneoxy (4'-CH₂-O-2') BNA monomers adenine, cytosine, guanine, 5-methyl-cytosine, thymine and uracil, along with their oligomerization, and nucleic acid recognition properties have been described (Koshkin *et al.*, *Tetrahedron*, 1998, 54, 3607-3630). BNAs and preparation thereof are also described in WO 98/39352 and WO 99/14226.

10 Analogs of methyleneoxy (4'-CH₂-O-2') BNA and 2'-thio-BNAs, have also been prepared (Kumar *et al.*, *Bioorg. Med. Chem. Lett.*, 1998, 8, 2219-2222). Preparation of locked nucleoside analogs comprising oligodeoxyribonucleotide duplexes 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'-methyldamino-BNA's have been prepared and the
15 thermal stability of their duplexes with complementary RNA and DNA strands has been previously reported.

In certain embodiments, bicyclic nucleosides are provided having Formula VI:



wherein:

Bx is a heterocyclic base moiety;

- 20 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, C₁-C₁₂ alkyl, substituted C₁-C₁₂ alkyl, C₂-C₁₂ alkenyl, substituted C₂-C₁₂ alkenyl, C₂-C₁₂ alkynyl, substituted C₂-C₁₂ alkynyl, C₁-C₁₂ alkoxy, substituted C₁-C₁₂ alkoxy, OJ_j, SJ_j, SOJ_j, SO₂J_j, NJ_jJ_k, N₃, CN, C(=O)OJ_j, C(=O)NJ_jJ_k, C(=O)J_j, O-C(=O)NJ_jJ_k,

- 25 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_i and q_k together are =C(q_g)(q_h), wherein q_g and q_h are each, independently, H, halogen, C₁-C₁₂ alkyl or substituted C₁-C₁₂ alkyl.

One carbocyclic bicyclic nucleoside having a 4'-(CH₂)₃-2' bridge and the alkenyl analog bridge 4'-CH=CH-CH₂-2' have been described (Freier *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).

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.

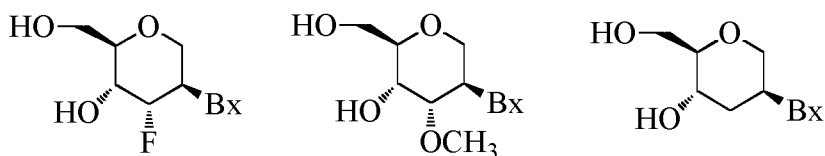
As used herein, "monocyclic nucleosides" refer to nucleosides comprising modified sugar moieties that are not bicyclic sugar moieties. In certain embodiments, the sugar moiety, or sugar moiety analogue, of a nucleoside may be modified or substituted at any position.

As used herein, "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[(CH₂)_nO]_mCH₃, O(CH₂)_nNH₂, O(CH₂)_nCH₃, O(CH₂)_nF, O(CH₂)_nONH₂, OCH₂C(=O)N(H)CH₃, and O(CH₂)_nON[(CH₂)_nCH₃]₂, where n and m are from 1 to about 10. Other 2'-substituent groups can also be selected from: C₁-C₁₂ alkyl, substituted alkyl, alkenyl, alkynyl, alkaryl, aralkyl, O-alkaryl or O-aralkyl, SH, SCH₃, OCN, Cl, Br, CN, F, CF₃, OCF₃, SOCH₃, SO₂CH₃, ONO₂, NO₂, N₃, NH₂, 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, modified 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).

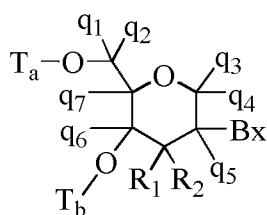
As used herein, a "modified tetrahydropyran nucleoside" or "modified THP nucleoside" means a nucleoside having a six-membered tetrahydropyran "sugar" substituted in for the pentofuranosyl residue in normal nucleosides (a sugar surrogate). Modified THP nucleosides include, but are not limited to, what 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, 841-1954) or fluoro HNA (F-HNA) having a tetrahydropyran

ring system as illustrated below:



In certain embodiments, sugar surrogates are selected having Formula VII:



VII

wherein independently for each of said at least one tetrahydropyran nucleoside analog of Formula VII:

Bx is a heterocyclic base moiety;

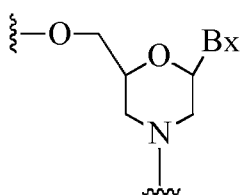
T_a and T_b are each, independently, an internucleoside linking group linking the tetrahydropyran nucleoside analog to the antisense compound or one of T_a and T_b is an internucleoside linking group linking the tetrahydropyran nucleoside analog to the antisense compound and the other of T_a and T_b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

q₁, q₂, q₃, q₄, q₅, q₆ and q₇ are each independently, H, C₁-C₆ alkyl, substituted C₁-C₆ alkyl, C₂-C₆ alkenyl, substituted C₂-C₆ alkenyl, C₂-C₆ alkynyl or substituted C₂-C₆ alkynyl; and each of R₁ and R₂ is selected from hydrogen, hydroxyl, halogen, substituted or unsubstituted alkoxy, NJ₁J₂, SJ₁, N₃, OC(=X)J₁, OC(=X)NJ₁J₂, NJ₃C(=X)NJ₁J₂ and CN, wherein X is O, S or NJ₁ and each J₁, J₂ and J₃ is, independently, H or C₁-C₆ alkyl.

In certain embodiments, the modified THP nucleosides of Formula VII are provided wherein q₁, q₂, q₃, q₄, q₅, q₆ and q₇ are each H. In certain embodiments, at least one of q₁, q₂, q₃, q₄, q₅, q₆ and q₇ is other than H. In certain embodiments, at least one of q₁, q₂, q₃, q₄, q₅, q₆ and q₇ is methyl. In certain embodiments, THP nucleosides of Formula VII are provided wherein one of R₁ and R₂ is fluoro. In certain embodiments, R₁ is fluoro and R₂ is H; R₁ is methoxy and R₂ is H, and R₁ is methoxyethoxy and R₂ 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 “modified morpholinos.”

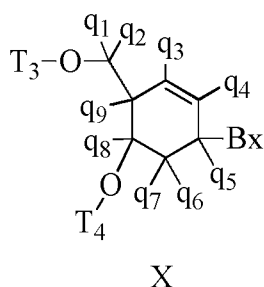
Combinations of modifications are also provided without limitation, such as 2'-F-5'-methyl substituted nucleosides (see PCT International Application WO 2008/101157 published on 8/21/08 for other disclosed 5', 2'-bis substituted nucleosides) and replacement of the ribosyl ring oxygen atom with S and 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'-CH₂-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

5

modified cyclohexenyl nucleosides have Formula X.



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

Bx is a heterocyclic base moiety;

10 T₃ and T₄ are each, independently, an internucleoside linking group linking the cyclohexenyl nucleoside analog to an antisense compound or one of T₃ and T₄ is an internucleoside linking group linking the tetrahydropyran nucleoside analog to an antisense compound and the other of T₃ and T₄ is H, a hydroxyl protecting group, a linked conjugate group, or a 5'-or 3'-terminal group; and

15 q₁, q₂, q₃, q₄, q₅, q₆, q₇, q₈ and q₉ are each, independently, H, C₁-C₆ alkyl, substituted C₁-C₆ alkyl, C₂-C₆ alkenyl, substituted C₂-C₆ alkenyl, C₂-C₆ alkynyl, substituted C₂-C₆ alkynyl or other sugar substituent group.

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

20 allyl, amino, azido, thio, O-allyl, O-C₁-C₁₀ alkyl, -OCF₃, O-(CH₂)₂-O-CH₃, 2'-O(CH₂)₂SCH₃, O-(CH₂)₂-O-N(R_m)(R_n), or O-CH₂-C(=O)-N(R_m)(R_n), where each R_m and R_n is, independently, H or substituted or unsubstituted C₁-C₁₀ alkyl. 2'-modified nucleosides may further comprise other modifications, for example at other positions of the sugar and/or at the nucleobase.

25 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'-OCH₃" or "2'-O-methyl" each refers to a nucleoside comprising a sugar comprising an -OCH₃ group at the 2' position of the sugar ring.

As used herein, "MOE" or "2'-MOE" or "2'-OCH₂CH₂OCH₃" or "2'-O-methoxyethyl" each refers to a nucleoside comprising a sugar comprising a -OCH₂CH₂OCH₃ group at the 2' position of the sugar ring.

5 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).

Many other monocyclo, bicyclo and tricyclo sugar surrogate ring systems are also known in the art that can be used to modify nucleosides for incorporation into antisense compounds as provided herein (see
10 for example review article: Leumann, *Bioorg. Med. Chem.*, 2002, 10, 841-1954). Such ring systems can undergo various additional substitutions to enhance activity.

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;
15 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.

In nucleotides having modified sugar moieties, the nucleobase moieties (natural, modified or a
20 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(CH₃)-O-2') bridging group. In certain embodiments, the (4'-
25 CH(CH₃)-O-2') modified nucleosides are arranged throughout the wings of a gapmer motif.

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 antisense oligonucleotides.
30 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 PKK nucleic acids can be tested in vitro in a variety of cell types. Cell types used for such analyses are available from commercial 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., Life Technologies, Carlsbad, CA). Illustrative cell types include, but are not limited to, HepaRG^{TMT} cells and mouse primary hepatocytes.

In vitro testing of antisense oligonucleotides

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

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

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

Another reagent used to introduce antisense oligonucleotides into cultured cells includes LIPOFECTAMINE (Life Technologies, Carlsbad, CA). Antisense oligonucleotide is mixed with LIPOFECTAMINE in OPTI-MEM 1 reduced serum medium (Life Technologies, Carlsbad, CA) to achieve

the desired concentration of antisense oligonucleotide and a LIPOFECTAMINE concentration that may range from 2 to 12 ug/mL per 100 nM antisense oligonucleotide.

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

5 Yet another technique used to introduce antisense oligonucleotides into cultured cells includes free uptake of the oligonucleotides by the cells.

Cells are treated with antisense oligonucleotides by routine methods. Cells may be harvested 16-24 hours after antisense 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
10 in multiple replicates, the data are presented as the average of the replicate treatments.

The concentration of antisense oligonucleotide used varies from cell line to cell line. Methods to determine the optimal antisense oligonucleotide concentration for a particular cell line are well known in the art. Antisense oligonucleotides are typically used at concentrations ranging from 1 nM to 300 nM when transfected with LIPOFECTAMINE. Antisense oligonucleotides are used at higher concentrations ranging
15 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
20 the TRIZOL Reagent (Life Technologies, Carlsbad, CA) according to the manufacturer's recommended protocols.

Analysis of inhibition of target levels or expression

Inhibition of levels or expression of a PKK nucleic acid can be assayed in a variety of ways known
25 in the art. For example, target nucleic acid levels can be quantitated by, e.g., Northern blot analysis, competitive polymerase chain reaction (PCR), or quantitative 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-
30 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.

5 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 Life Technologies (Carlsbad, CA). RT real-time-PCR reactions are carried out by methods well known to those skilled in the art.

10 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 (Life Technologies, 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
15 quantification by RIBOGREEN are taught 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 PKK 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
20 PRIMER EXPRESS Software (Applied Biosystems, Foster City, CA).

Analysis of Protein Levels

Antisense inhibition of PKK nucleic acids can be assessed by measuring PKK protein levels. Protein levels of PKK can be evaluated or quantitated in a variety of ways well known in the art, such as
25 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
30 polyclonal antibody generation methods well known in the art.

In vivo testing of antisense compounds

Antisense compounds, for example, antisense oligonucleotides, are tested in animals to assess their ability to inhibit expression of PKK and produce phenotypic changes.

In certain embodiments, such phenotypic changes include those associated with an inflammatory disease, such as, reduced inflammation, edema/swelling, vascular permeability, and vascular leakage. In certain embodiments, inflammation is measured by measuring the increase or decrease of edema, temperature, pain, color of tissue, and abdominal function in the animal.

In certain embodiments, such phenotypic changes include those associated with a thromboembolic disease, such as, prolonged aPTT, prolonged aPTT time in conjunction with a normal PT, decreased quantity of Platelet Factor 4 (PF-4), and reduced formation of thrombus or increased time for thrombus formation.

Testing may be performed in normal animals, or in experimental disease models. For administration to animals, antisense 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. Calculation of antisense oligonucleotide dosage and dosing frequency is within the abilities of those skilled in the art, and depends upon factors such as route of administration and animal body weight. Following a period of treatment with antisense oligonucleotides, RNA is isolated from liver tissue and changes in PKK nucleic acid expression are measured.

Certain Indications

In certain embodiments, the invention provides methods of treating an individual comprising administering one or more pharmaceutical compositions as described herein.

In certain embodiments, the individual has an inflammatory disease. In certain embodiments, the individual is at risk for developing an inflammatory condition, including, but not limited to hereditary angioedema (HAE), edema, angioedema, swelling, angioedema of the lids, ocular edema, macular edema, and cerebral edema. This includes individuals with an acquired problem, disease, or disorder that leads to a risk of inflammation, for example, genetic predisposition to an inflammatory condition, environmental factors, and exposure to certain medications, including, for example, ACE inhibitors and ARBs. In certain embodiments, the individual has been identified as in need of anti-inflammation therapy. Examples of such individuals include, but are not limited to those having a mutation in the genetic code for complement 1 esterase inhibitor (i.e., C1-INH) or Factor 12. In certain embodiments, an abnormal code can lead to a deficiency in C1-INH (i.e., type I HAE), an inability of existing C1-INH to function properly (type II HAE), or hyperfunctional Factor 12 (i.e., type III HAE).

In certain embodiments, the individual has a thromboembolic disease. In certain embodiments, the individual is at risk for a blood clotting disorder, including, but not limited to, infarct, thrombosis, embolism, thromboembolism such as deep vein thrombosis, pulmonary embolism, myocardial

infarction, and stroke. This includes individuals with an acquired problem, disease, or disorder that leads to a risk of thrombosis, for example, surgery, cancer, immobility, sepsis, atherosclerosis atrial fibrillation, as well as genetic predisposition, for example, antiphospholipid syndrome and the autosomal dominant condition, Factor V Leiden. In certain embodiments, the individual has been identified as in need of anticoagulation therapy. Examples of such individuals include, but are not limited to, those undergoing major orthopedic surgery (e.g., hip/knee replacement or hip fracture surgery) and patients in need of chronic treatment, such as those suffering from arterial fibrillation to prevent stroke.

In certain embodiments the invention provides methods for prophylactically reducing PKK 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 PKK nucleic acid.

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

In certain embodiments, administration of an antisense compound targeted to a PKK nucleic acid results in reduction of PKK expression by at least 15, 20, 25, 30, 35, 40, 45, 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, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99%, or a range defined by any two of these values. In certain embodiments, pharmaceutical compositions comprising an antisense compound targeted to PKK are used for the preparation of a medicament for treating a patient suffering or susceptible to an inflammatory disease or thromboembolic disease.

Certain Compositions

1. ISIS 546254

In certain embodiments, ISIS 546254 is characterized as a 5-10-5 MOE gapmer, having a sequence of (from 5' to 3') TGCAAGTCTCTTGGCAAACA (incorporated herein as SEQ ID NO: 570), wherein each internucleoside linkage is a phosphorothioate linkage, each cytosine is a 5'-methylcytosine, each of nucleosides 1-5 and 16-20 are 2'-O-methoxyethyl modified nucleosides, and each of nucleosides 6-15 are 2'-deoxynucleosides.

In certain embodiments, ISIS 546254 is described by the following chemical notation: Tes Ges mCes Aes Aes Gds Tds mCds Tds mCds Tds Tds Gds Gds mCds Aes Aes Aes mCes Ae; wherein,

A = an adenine,

mC = a 5'-methylcytosine

G = a guanine,

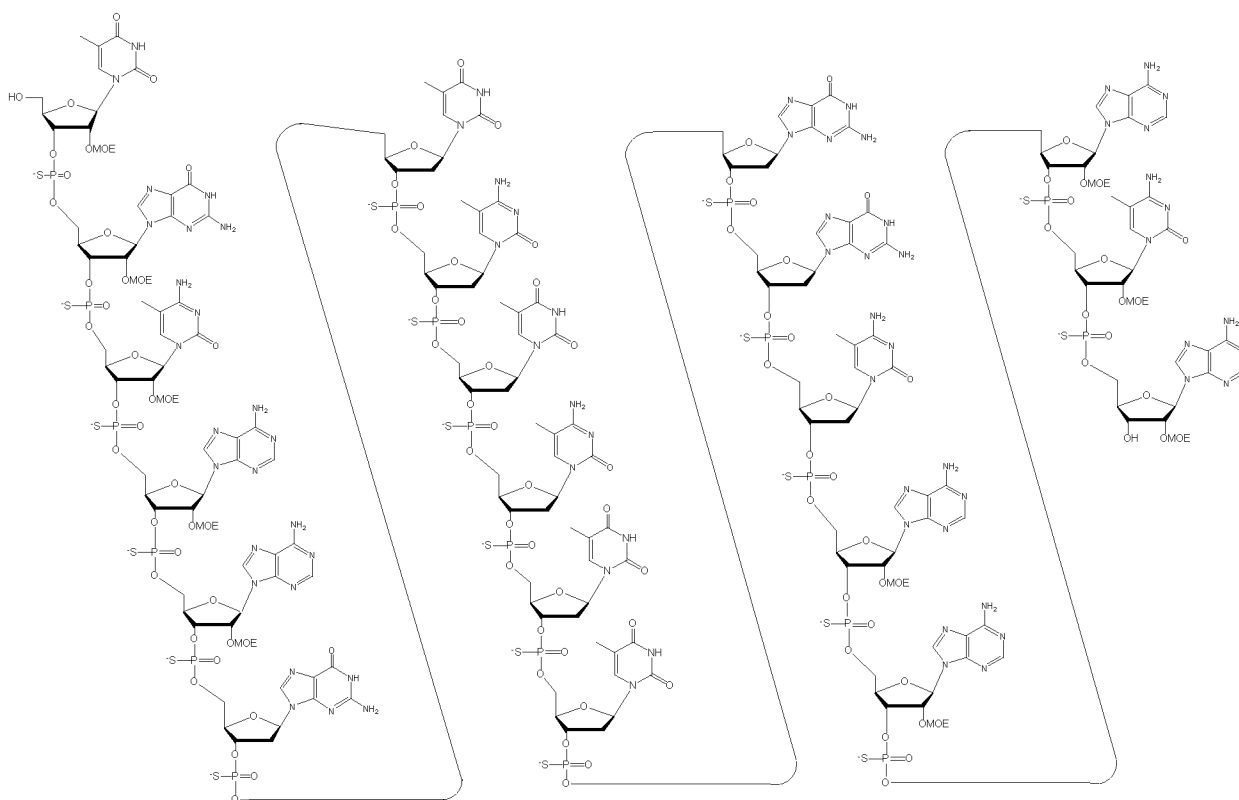
T = a thymine,

e = a 2'-O-methoxyethyl modified nucleoside,

d = a 2'-deoxynucleoside, and

s = a phosphorothioate internucleoside linkage.

In certain embodiments, ISIS 546254 is described by the following chemical structure:



10 **Structure 1.** ISIS 546254

In certain embodiments, as provided in Example 2 (hereinbelow), ISIS 546254 achieved 95% inhibition of human PKK mRNA in cultured HepaRG™ cells (density of 20,000 cells per well) when transfected using electroporation with 5,000 nM antisense oligonucleotide after a treatment period of 24 hours and measured by quantitative real-time PCR using human primer probe set RTS3454 and adjusted according to total RNA content, as measured by RIBOGREEN®.

In certain embodiments, as provided in Example 5 (see Tables 34 and 41 hereinbelow), ISIS 546254 achieved an IC₅₀ of 0.2μM and 0.3μM in a 4 point dose response curve (0.19 μM, 0.56 μM, 1.67 μM, and 5.0 μM) in cultured HepaRG™ cells (density of 20,000 cells per well) when transfected using electroporation

after a treatment period of 16 and measured by quantitative real-time PCR using human primer probe set RTS3454 and adjusted according to total RNA content, as measured by RIBOGREEN®.

In certain embodiments, as provided in Example 7 (hereinbelow), ISIS 546254 achieved 31%, 55%, 84%, and 83% human PKK mRNA inhibition and 0%, 36%, 51%, and 76% human PKK protein inhibition in transgenic mice harboring the human PKK gene sequence when injected subcutaneously twice a week for 3 weeks with 2.5 mg/kg/week, 5.0 mg/kg/week, 10 mg/kg/week or 20 mg/kg/week with ISIS 546254.

In certain embodiments, as provided in Example 8 (hereinbelow), ISIS 546254 is effective for inhibiting PKK mRNA and protein expression and is tolerable in primates.

2. ISIS 546343

In certain embodiments, ISIS 546343 is characterized as a 5-10-5 MOE gapmer, having a sequence of (from 5' to 3') CCCCCTTCTTTATAGCCAGC (incorporated herein as SEQ ID NO: 705), wherein each internucleoside linkage is a phosphorothioate linkage, each cytosine is a 5'-methylcytosine, each of nucleosides 1-5 and 16-20 are 2'-O-methoxyethyl modified nucleosides, and each of nucleosides 6-15 are 2'-deoxynucleosides.

In certain embodiments, ISIS 546343 is described by the following chemical notation: mCes mCes mCes mCes Tds Tds mCds Tds Tds Tds Ads Tds Ads Gds mCes mCes Aes Ges mCe; wherein,

A = an adenine,

mC = a 5'-methylcytosine;

G = a guanine,

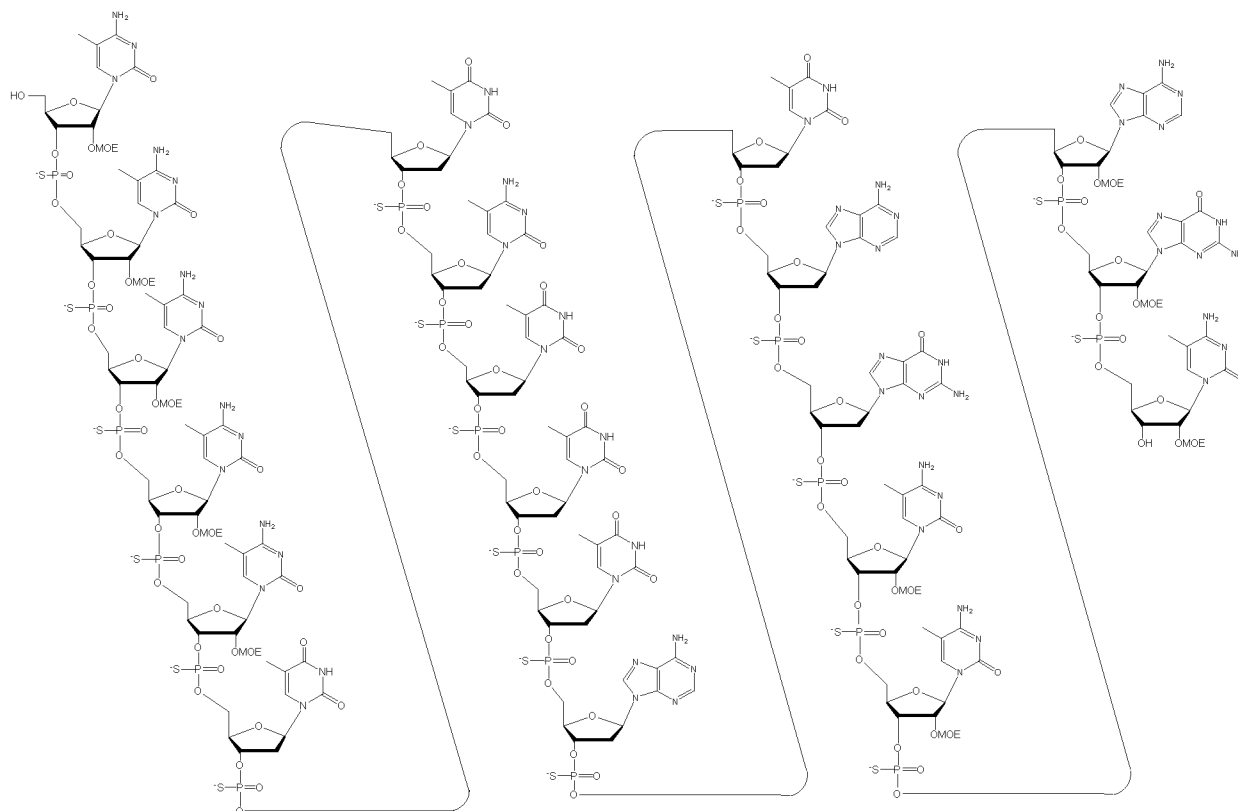
T = a thymine,

e = a 2'-O-methoxyethyl modified nucleoside,

d = a 2'-deoxynucleoside, and

s = a phosphorothioate internucleoside linkage.

In certain embodiments, ISIS 546343 is described by the following chemical structure:



Structure 2. ISIS 546343

In certain embodiments, as provided in Example 2 (see Tables 9 and 10 hereinbelow), ISIS 546343 achieved 97% and 91% human PKK mRNA inhibition in cultured HepaRG™ cells (density of 20,000 cells per well) when transfected using electroporation with 5,000 nM antisense oligonucleotide after a treatment period of 24 hours and measured by quantitative real-time PCR using human primer probe set RTS3454 and adjusted according to total RNA content, as measured by RIBOGREEN®.

In certain embodiments, as provided twice in Example 5 (see Tables 34 and 41 hereinbelow), ISIS 546343 achieved an IC₅₀ of 0.4 μM in a 4 point dose response curve (0.19 μM, 0.56 μM, 1.67 μM, and 5.0 μM) in cultured HepaRG™ cells (density of 20,000 cells per well) when transfected using electroporation after a treatment period of 16 and measured by quantitative real-time PCR using human primer probe set RTS3454 and adjusted according to total RNA content, as measured by RIBOGREEN®.

In certain embodiments, as provided in Example 7 (hereinbelow), ISIS 546343 achieved 46%, 66%, and 86% human PKK mRNA inhibition and 0%, 38%, and 79% human PKK protein inhibition in transgenic mice harboring the human PKK gene sequence when injected subcutaneously twice a week for 3 weeks with 2.5 mg/kg/week, 5.0 mg/kg/week, 10 mg/kg/week or 20 mg/kg/week with ISIS 546343.

In certain embodiments, as provided in Example 8 (hereinbelow), ISIS 546343 is effective for inhibiting PKK mRNA and protein expression and is tolerable in primates.

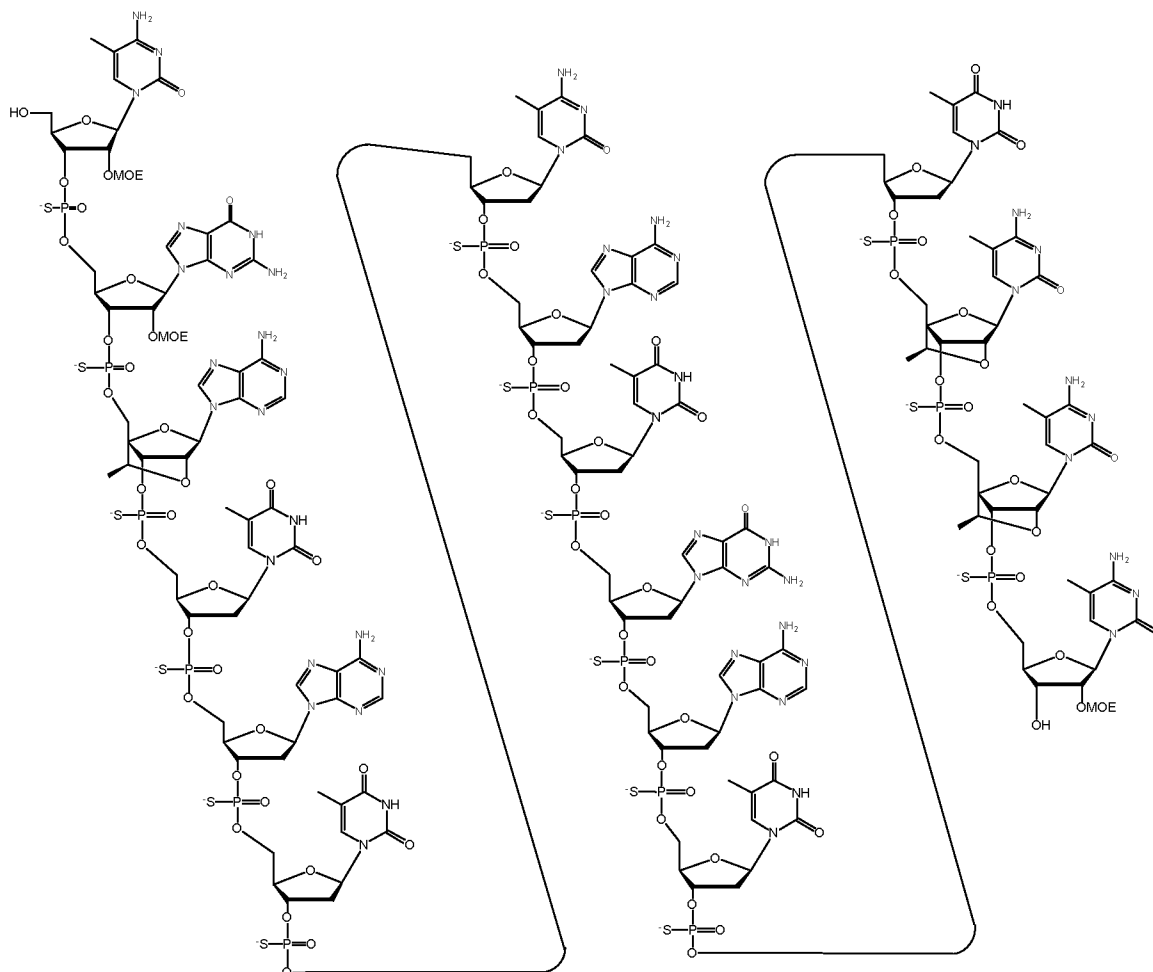
3. ISIS 548048

5 In certain embodiments, ISIS 548048 is characterized as a modified antisense oligonucleotide having the nucleobase sequence (from 5' to 3') CGATATCATGATTCCC (incorporated herein as SEQ ID NO: 1666), consisting of a combination of sixteen 2'-deoxynucleosides, 2'-O-methoxyethyl modified nucleosides, and cEt modified nucleosides, wherein each of nucleosides 1, 2, and 16 are 2'-O-methoxyethyl modified nucleosides, wherein each of nucleosides 3, 14, and 15 are cEt modified nucleosides, wherein each of
10 nucleosides 4-13 are 2'-deoxynucleosides, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage, and wherein each cytosine is a 5'-methylcytosine.

In certain embodiments, ISIS 548048 is described by the following chemical notation: mCes Ges Aks Tds Ads Tds mCds Ads Tds Gds Ads Tds Tds mCks mCks mCe; wherein,

15 A = an adenine,
 mC = a 5'-methylcytosine;
 G = a guanine,
 T = a thymine,
 e = a 2'-O-methoxyethyl modified nucleoside,
 k = a cEt modified nucleoside,
20 d = a 2'-deoxynucleoside, and
 s = a phosphorothioate internucleoside linkage.

In certain embodiments, ISIS 548048 is described by the following chemical structure:



Structure 3. ISIS 548048

In certain embodiments, as provided in Example 3 (hereinbelow), ISIS 548048 achieved 84% mRNA inhibition in cultured HepaRG™ cells (density of 20,000 cells per well) when transfected using electroporation with 1,000 nM antisense oligonucleotide after a treatment period of 24 hours and measured by quantitative real-time PCR using human primer probe set RTS3454 and adjusted according to total RNA content, as measured by RIBOGREEN®.

In certain embodiments, as provided in Example 6 (hereinbelow), ISIS 548048 achieved an IC₅₀ of 0.1 μM in a 4 point dose response curve (0.11 μM, 0.33 μM, 1.00 μM, and 3.00 μM) in cultured HepaRG™ cells (density of 20,000 cells per well) when transfected using electroporation after a treatment period of 16 and measured by quantitative real-time PCR using human primer probe set RTS3454 and adjusted according to total RNA content, as measured by RIBOGREEN®.

In certain embodiments, as provided in Example 7 (hereinbelow), ISIS 548048 achieved 7%, 77%, 72% and 80% human PKK mRNA inhibition and 23%, 70%, 89%, and 98% human PKK protein inhibition in transgenic mice harboring the human PKK gene sequence when injected subcutaneously twice a week for 3 weeks with 2.5 mg/kg/week, 5.0 mg/kg/week, 10 mg/kg/week or 20 mg/kg/week with ISIS 548048.

5 In certain embodiments, as provided in Example 8 (hereinbelow), ISIS 548048 is effective for inhibiting PKK mRNA and protein expression and is tolerable in primates.

Certain Hotspot Regions

1. Nucleobases 27427-27466 of SEQ ID NO: 10

10 In certain embodiments, antisense oligonucleotides are designed to target nucleobases 27427-27466 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 27427-27466 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 27427-27466 of SEQ ID NO: 10 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20
15 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the
20 nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 27427-27466 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 530993, 530994, 530995, 546251, 546252, 546253, 546254, 546255, 546256, 547410, 547411, 547978, 547979, 547980, and 547981.

25 In certain embodiments, nucleobases nucleobases 27427-27466 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 94, 95, 96, 566, 567, 568, 569, 570, 571, 572, 573, 1597, 1598, 1599, and 1600.

In certain embodiments, antisense oligonucleotides targeting nucleobases 27427-27466 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at
30 least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at

least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

5 2. Nucleobases 33183-33242 of SEQ ID NO: 10

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 33183-33242 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 33183-33242 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 33183-33242 of SEQ ID NO: 10 are targeted by antisense
 10 oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and
 15 cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 33183-33242 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 531052, 531053, 531054, 531055, 531056, 531057, 531158, 546343, 546345, 547480, 547481, 547482, and 547483.

20 In certain embodiments, nucleobases nucleobases 33183-33242 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 155, 156, 157, 158, 159, 160, 261, 702, 703, 704, 705, 706, and 707.

In certain embodiments, antisense oligonucleotides targeting nucleobases 33183-33242 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at
 25 least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at
 30 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%, or at least 99% reduction of PKK mRNA and/or protein levels in vitro and/or in vivo.

3. Nucleobases 30570-30610 of SEQ ID NO: 10

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 30570-30610 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 30570-30610 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 30570-30610 of SEQ ID NO: 10 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 30570-30610 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 531026, 546309, 546310, 546311, 546313, 547453, 547454, 547455, 547456, 547457, 547458, 548046, 548047, 548048, 548049, and 548050.

In certain embodiments, nucleobases 30570-30610 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 129, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 1664, 1665, 1666, 1667, and 1668.

In certain embodiments, antisense oligonucleotides targeting nucleobases 30570-30610 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK mRNA and/or protein levels in vitro and/or in vivo.

4. Nucleobases 27427-27520 of SEQ ID NO: 10

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 27427-27520 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 27427-27520 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 27427-27520 of SEQ ID NO: 10 are targeted by antisense

oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 27427-27520 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 530993-530999, 546251-546256, 546258-546260, 546263, 546265-546268, 547410-547417, and 547978-547992.

In certain embodiments, nucleobases 27427-27520 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 94-100, 566-587, and 1597-1611.

In certain embodiments, antisense oligonucleotides targeting nucleobases 27427-27520 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

5. Nucleobases 33085-33247 of SEQ ID NO: 10

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 33085-33247 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 33085-33247 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 33085-33247 of SEQ ID NO: 10 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and

cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 33085-33247 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 531041-531158, 546336, 546339, 546340, 546343, 546345, 547474-547483, 547778, 548077-
5 548082, and 548677-548678.

In certain embodiments, nucleobases 33085-33247 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 144-160, 261, 693-707, 1256, 1320-1325, 2214, and 2215.

In certain embodiments, antisense oligonucleotides targeting nucleobases 33085-33247 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%,
10 at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at
15 least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

6. Nucleobases 30475-30639 of SEQ ID NO: 10

20 In certain embodiments, antisense oligonucleotides are designed to target nucleobases 30475-30639 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 30475-30639 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 30475-30639 of SEQ ID NO: 10 are targeted by antisense
25 oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the
30 nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 30475-30639 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 531021-531029, 531146, 546297, 546299-546304, 546306-546311, 546313, 546316-546319, 547444-547462, 548031, 548032, and 548034-548056.

In certain embodiments, nucleobases 30475-30639 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 124-132, 249, 633-669, and 1650-1674.

In certain embodiments, antisense oligonucleotides targeting nucleobases 30475-30639 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%,
5 at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at
10 least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

7. Nucleobases 27362-27524 of SEQ ID NO: 10

15 In certain embodiments, antisense oligonucleotides are designed to target nucleobases 27362-27524 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 27362-27524 correspond to exon 9 of PKK (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain
20 embodiments, nucleobases 27362-27524 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 27362-27524 of SEQ ID NO: 10 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE
25 and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 27361-27524 of SEQ ID NO: 10 are targeted by the following
30 ISIS numbers: 530985-530999, 546244, 546247-546256, 546258-546260, 546263, 546265-546268, 547403-547417, 547723, 547968-547970, and 547972-547992.

In certain embodiments, nucleobases 27361-27524 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 86-100, 554-587, 1217, and 1588-1611.

In certain embodiments, antisense oligonucleotides targeting nucleobases 27362-27524 of SEQ ID

NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

8. Nucleobases 33101-33240 of SEQ ID NO: 10

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 33101-33240 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 33101-33240 correspond to exon 14 of PKK (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 33101-33240 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 33101-33240 of SEQ ID NO: 10 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 33101-33240 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 531041-531158, 546336, 546339, 546340, 546343, 546345, 547474-547483, 548077-548082, and 548678-548678.

In certain embodiments, nucleobases 33101-33240 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 144-160, 261, 693-707, 1320-1325, and 2215.

In certain embodiments, antisense oligonucleotides targeting nucleobases 33101-33240 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at

least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

9. Nucleobases 30463-30638 of SEQ ID NO: 10

In certain embodiments, antisense oligonucleotides are designed to target nucleobases 30463-30638 of SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 30463-30638 correspond to exon 12 of PKK (GENBANK Accession No. NT_016354.19 truncated from nucleobases 111693001 to 111730000). In certain embodiments, nucleobases 30463-30638 of SEQ ID NO: 10 are a hotspot region. In certain embodiments, nucleobases 30463-30638 of SEQ ID NO: 10 are targeted by antisense oligonucleotides. In certain embodiments, the antisense oligonucleotides are 15, 16, 17, 18, 19, or 20 nucleobases in length. In certain embodiments, the antisense oligonucleotides are gapmers. In certain embodiments, the gapmers are 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. In certain embodiments, the gapmers are 5-10-5 MOE and cEt gapmers, 4-9-4 MOE and cEt gapmers, 4-10-4 MOE and cEt gapmers, 4-10-3 MOE and cEt gapmers, 3-10-4 MOE and cEt gapmers, or 3-10-3 MOE and cEt gapmers. In certain embodiments, the nucleosides of the antisense oligonucleotides are linked by phosphorothioate internucleoside linkages.

In certain embodiments, nucleobases 30463-30638 of SEQ ID NO: 10 are targeted by the following ISIS numbers: 531021-531029, 531146, 546297, 546299-546304, 546306-546311, 546313, 546316-546319, 547444-547462, 548031, 548032, and 548034-548056.

In certain embodiments, nucleobases 30463-30638 of SEQ ID NO: 10 are targeted by the following SEQ ID NOs: 124-132, 249, 633-669, and 1650-1674.

In certain embodiments, antisense oligonucleotides targeting nucleobases 30463-30638 of SEQ ID NO: 10 achieve at least 30%, at least 31%, at least 32%, at least 33%, at least 34%, at least 35%, at least 36%, at least 37%, at least 38%, at least 39%, at least 40%, at least 41%, at least 42%, at least 43%, at least 44%, at least 45%, at least 46%, at least 47%, at least 48%, at least 49%, at least 50%, at least 51%, at least 52%, at least 53%, at least 54%, at least 55%, at least 56%, at least 57%, at least 58%, at least 59%, at least 60%, at least 61%, at least 62%, at least 63%, at least 64%, at least 65%, at least 66%, at least 67%, at least 68%, at least 69%, at least 70%, at least 71%, at least 72%, at least 73%, at least 74%, at least 75%, at least 76%, at

least 77%, at least 78%, at least 79%, 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%, or at least 99% reduction of PKK and/or protein levels in vitro and/or in vivo.

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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.

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Example 1: Antisense inhibition of human PKK in HepaRGTM cells by antisense oligonucleotides with 2'-MOE sugar modifications

Antisense oligonucleotides were designed targeting a PKK nucleic acid and were tested for their effects on PKK mRNA *in vitro*. HepaRGTM cells, which are terminally differentiated hepatic cells derived from a human hepatic progenitor cell line and retain many characteristics of primary human hepatocytes (Lubberstedt M. et al., J. Pharmacol. Toxicol. Methods 2011 63: 59-68), were used in the screen.

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The chimeric antisense oligonucleotides in the tables below were designed as 5-10-5 MOE gapmers. The gapmers are 20 nucleosides in length, wherein the central gap segment comprises of ten 2'-deoxynucleosides 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'-O-methoxyethyl 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 in the human gene sequence. Each gapmer listed in the tables below is targeted to either the human PKK mRNA, designated herein as SEQ ID NO: 1 (GENBANK Accession No. NM_000892.3) or the human PKK genomic sequence, designated herein as SEQ ID NO: 10 (GENBANK Accession No. NT_016354.19 truncated from nucleotides 111693001 to 111730000). 'n/a' indicates that the antisense oligonucleotide does not target that particular gene sequence.

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Cultured HepaRGTM cells at a density of 20,000 cells per well were transfected using electroporation with 3,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and PKK mRNA levels were measured by quantitative real-time PCR. Human primer

probe set RTS3454 (forward sequence CCAAAAAAGGTGCACCAGTAACA, designated herein as SEQ ID NO: 20; reverse sequence CCTCCGGGACTGTACTTTAATAGG, designated herein as SEQ ID NO: 21; probe sequence CACGCAAACATTTTACAAGGCAGAGTACC, designated herein as SEQ ID NO: 22) was used to measure mRNA levels. PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. The antisense 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. Results are presented as percent inhibition of PKK, relative to untreated control cells.

Table 1

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
530929	1	20	AACGGTCTTCAAGCTGTTCT	59	3393	3412	30
530930	6	25	AAATGAACGGTCTTCAAGCT	17	3398	3417	31
530931	11	30	CTTAAAAATGAACGGTCTTC	29	3403	3422	32
530932	16	35	TGTCACCTAAAAATGAACGG	52	3408	3427	33
530933	31	50	TGGAGGTGAGTCTCTTGTC	76	3423	3442	34
530934	36	55	CTTCTTGGAGGTGAGTCTCT	54	3428	3447	35
530935	68	87	GCTTGAATAAAATCATTCTG	0	n/a	n/a	36
530936	73	92	TGCTTGCTTGAATAAAATCA	27	4072	4091	37
530937	78	97	TAAGTTGCTTGCTTGAATAA	0	4077	4096	38
530938	88	107	GGAAATGAAATAAGTTGCTT	11	4087	4106	39
530939	93	112	AACAAGGAAATGAAATAAGT	0	4092	4111	40
530940	98	117	TAGCAAACAAGGAAATGAAA	7	4097	4116	41
530941	103	122	AACTGTAGCAAACAAGGAAA	22	4102	4121	42
530942	108	127	CAGGAACTGTAGCAAACAA	22	4107	4126	43
530943	113	132	ATCCACAGGAACTGTAGCA	56	n/a	n/a	44
530944	118	137	CAGACATCCACAGGAACTG	0	n/a	n/a	45
530945	157	176	ATCCCCACCTCTGAAGAAGG	0	8029	8048	46
530946	160	179	TACATCCCCACCTCTGAAGA	0	8032	8051	47
530947	165	184	GAAGCTACATCCCCACCTCT	27	8037	8056	48
530948	170	189	ACATGGAAGCTACATCCCCA	35	8042	8061	49
530949	175	194	GGTGTACATGGAAGCTACAT	31	8047	8066	50
530950	221	240	ACCTTGGGTGGAATGTGCAC	47	8093	8112	51
530951	226	245	CAAACACCTTGGGTGGAATG	49	8098	8117	52
530952	234	253	CTGAATAGCAAACACCTTGG	38	8106	8125	53
530953	239	258	GAAACTGAATAGCAAACAC	7	8111	8130	54
530954	244	263	TGGAAGAAAACCTGAATAGCA	47	8116	8135	55
530955	278	297	CAAACCTTTTCTCCATGTCA	55	n/a	n/a	56
530956	300	319	ACACTATCTTTCAAGAAGCA	57	9834	9853	57
530957	386	405	GGCAAGCACTTATTTGATGA	56	n/a	n/a	58

530958	432	451	TTAAAATTGACTCCTCTCAT	60	12688	12707	59
530959	456	475	TCAACACTGCTAACCTTAGA	60	12712	12731	60
530960	461	480	ATTCTTCAACACTGCTAACC	58	12717	12736	61
530961	466	485	TTGGCATTCTTCAACACTGC	88	12722	12741	62
530962	472	491	CCTTTTTTGGCATTCTTCAA	64	12728	12747	63
530963	479	498	TGGTGCACCTTTTTTGGCAT	78	12735	12754	64
530964	628	647	CTTCAGTGAGAATCCAGATT	44	14199	14218	65
530965	637	656	GGCACAGGGCTTCAGTGAGA	73	14208	14227	66
530966	649	668	AATTTCTGAAAGGGCACAGG	58	14220	14239	67
530967	654	673	CAACCAATTTCTGAAAGGGC	69	n/a	n/a	68
530968	680	699	CAAGATGCTGGAAGATGTTC	18	26128	26147	69
530969	846	865	GTGCCACTTTCAGATGTTTT	0	27110	27129	70
530970	851	870	TTGGTGTGCCACTTTCAGAT	74	27115	27134	71
530971	856	875	GGAAC TTGGTGTGCCACTTT	85	27120	27139	72
530972	861	880	GTAGAGGAACTTGGTGTGCC	42	27125	27144	73
530973	866	885	GAGGAGTAGAGGAACTTGGT	52	27130	27149	74
530974	871	890	TTCTTGAGGAGTAGAGGAAC	18	27135	27154	75
530975	876	895	GTGTTTTCTTGAGGAGTAGA	41	27140	27159	76
530976	881	900	ATATGGTGT TTTCTTGAGGA	26	27145	27164	77
530977	886	905	TCCAGATATGGTGT TTTCTT	55	27150	27169	78
530978	891	910	CTATATCCAGATATGGTGTT	0	27155	27174	79
530979	901	920	GGTTAAAAGGCTATATCCAG	35	27165	27184	80
530980	906	925	TTGCAGGTTAAAAGGCTATA	29	27170	27189	81
530981	911	930	TTCTTTTGCAGGTTAAAAGG	0	27175	27194	82
530982	916	935	TAAAGTTCTTTTGCAGGTTA	0	27180	27199	83
530983	931	950	ATGGCAGGGTTCAGGTAAAG	9	n/a	n/a	84
530984	936	955	TTAGAATGGCAGGGTTCAGG	25	n/a	n/a	85
530985	941	960	AAATTTTAGAATGGCAGGGT	32	27363	27382	86
530986	946	965	CGGGTAAATTTTAGAATGGC	62	27368	27387	87
530987	951	970	ACTCCCGGGTAAATTTTAGA	0	27373	27392	88
530988	961	980	TCCAAAGTCAACTCCCGGGT	76	27383	27402	89
530989	966	985	TCTCCTCCAAAGTCAACTCC	28	27388	27407	90
530990	971	990	ATTCTTCTCCTCCAAAGTCA	32	27393	27412	91
530991	976	995	ATTCAATTCTTCTCCTCCAA	43	27398	27417	92
530992	981	1000	GTCACATTCAATTCTTCTCC	70	27403	27422	93
530993	1005	1024	CAAACATTCACTCCTTTAAC	30	27427	27446	94
530994	1010	1029	CTTGGCAAACATTCACTCCT	50	27432	27451	95
530995	1015	1034	AGTCTCTTGGCAAACATTCA	49	27437	27456	96
530996	1038	1057	TGACAGCGAATCATCTTTGT	51	27460	27479	97
530997	1043	1062	AAAAGTACAGCGAATCATC	39	27465	27484	98
530998	1048	1067	AGTGAAAACTGACAGCGAA	0	27470	27489	99
530999	1071	1090	CAGTCTTCTGGGAGTAAAGA	31	27493	27512	100

531000	1098	1117	AAGAAACACTTACACTTCTC	1	n/a	n/a	101
531001	1108	1127	AGATAATCTTAAGAAACACT	44	27629	27648	102
531002	1155	1174	GAGCTCCCTTGTGTCCCATA	85	27676	27695	103
531003	1160	1179	AACCAGAGCTCCCTTGTGTC	49	27681	27700	104
531004	1165	1184	AGAGTAACCAGAGCTCCCTT	76	27686	27705	105
531005	1170	1189	CTCAAAGAGTAACCAGAGCT	76	27691	27710	106
531006	1216	1235	GCTTGTTTTTGTGTGCAGA	49	27892	27911	107

Table 2

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
482586	1608	1627	ACCCAACAGTTGGTATAAAT	0	31914	31933	108
486847	1563	1582	AGGCATATTGGTTTTTGGAA	78	31869	31888	109
531007	46	65	AACACAATTGCTTCTTGAG	51	3438	3457	110
531008	675	694	TGCTGGAAGATGTTCATGTG	51	26123	26142	111
531009	1239	1258	TTTGTTCCCTCCAACAATGCG	65	27915	27934	112
531010	1244	1263	AAGAGTTTGTTCCTCCAACA	52	27920	27939	113
531011	1249	1268	CCAAGAAGAGTTTGTTCCTC	0	27925	27944	114
531012	1254	1273	TCTCCCCAAGAAGAGTTTGT	48	27930	27949	115
531013	1264	1283	CCAGGGCCACTCTCCCCAAG	56	27940	27959	116
531014	1287	1306	AGCTTCACCTGCAGGCTCAC	0	27963	27982	117
531015	1324	1343	TATGAGTGACCCTCCACACA	52	28000	28019	118
531016	1329	1348	TGTCCTATGAGTGACCCTCC	39	28005	28024	119
531017	1334	1353	ACTGGTGTCTATGAGTGAC	31	28010	28029	120
531018	1339	1358	GACCCACTGGTGTCTATGA	54	28015	28034	121
531019	1344	1363	GTGAGGACCCACTGGTGTCC	28	28020	28039	122
531020	1369	1388	AAGCCCATCAAAGCAGTGGG	0	n/a	n/a	123
531021	1420	1439	GTCTGACAGATTTAAAATGC	50	30498	30517	124
531022	1425	1444	GTAATGTCTGACAGATTTAA	74	30503	30522	125
531023	1430	1449	CTTTTGTAAATGTCTGACAGA	71	30508	30527	126
531024	1452	1471	TTTATTTGTGAGAAAGGTGT	69	30530	30549	127
531025	1457	1476	TCTCTTTTATTTGTGAGAAA	34	30535	30554	128
531026	1501	1520	ATCATGATTCCTTCTGAGA	73	30579	30598	129
531027	1530	1549	AAAGGAGCCTGGAGTTTTAT	0	30608	30627	130
531028	1535	1554	AATTCAAAGGAGCCTGGAGT	56	30613	30632	131
531029	1540	1559	AGTGTAATTCAAAGGAGCCT	59	30618	30637	132
531030	1545	1564	AATTCAGTGTAATTCAAAGG	24	n/a	n/a	133
531031	1550	1569	TTTGGAATTCAGTGTAATTC	59	n/a	n/a	134
531032	1555	1574	TGGTTTTTGAATTCAGTGT	67	n/a	n/a	135
531033	1557	1576	ATTGGTTTTTGAATTCAGT	53	n/a	n/a	136

531034	1560	1579	CATATTGGTTTTTGAATTC	36	31866	31885	137
531035	1565	1584	GTAGGCATATTGGTTTTTGG	46	31871	31890	138
531036	1581	1600	GTGTCACCTTTGGAAGGTAG	71	31887	31906	139
531037	1604	1623	AACAGTTGGTATAAATTGTG	35	31910	31929	140
531038	1605	1624	CAACAGTTGGTATAAATTGT	22	31911	31930	141
531039	1609	1628	TACCCAACAGTTGGTATAAA	36	31915	31934	142
531040	1632	1651	TCCTTCGAGAAGCCCCATCC	27	31938	31957	143
531041	1677	1696	AAAGGAATATTTACCTTTTG	68	33121	33140	144
531042	1682	1701	TTACCAAAGGAATATTTACC	11	33126	33145	145
531043	1687	1706	ATTTGTTACCAAAGGAATAT	27	33131	33150	146
531044	1697	1716	GGCATTCTTCATTTGTTACC	68	33141	33160	147
531045	1702	1721	TTTCTGGCATTCTTCATTTG	37	33146	33165	148
531046	1709	1728	GATATCTTTTCTGGCATTCT	54	33153	33172	149
531047	1714	1733	ATCTTGATATCTTTTCTGGC	68	33158	33177	150
531048	1719	1738	TTATAATCTTGATATCTTTT	42	33163	33182	151
531049	1724	1743	TTATTTTATAATCTTGATAT	2	33168	33187	152
531050	1729	1748	TTGGGTTATTTTATAATCTT	18	33173	33192	153
531051	1734	1753	ATCCGTTGGGTTATTTTATA	51	33178	33197	154
531052	1739	1758	AGACCATCCGTTGGGTTATT	60	33183	33202	155
531053	1744	1763	AGCACAGACCATCCGTTGGG	49	33188	33207	156
531054	1754	1773	CTTTATAGCCAGCACAGACC	48	33198	33217	157
531055	1759	1778	CCCTTCTTTATAGCCAGCAC	68	33203	33222	158
531056	1764	1783	TTTCCCCCTTCTTTATAGCC	45	33208	33227	159
531057	1769	1788	CATCTTTTCCCCCTTCTTTA	48	33213	33232	160
531058	1779	1798	CCCTTACAAGCATCTTTTCC	60	n/a	n/a	161
531059	n/a	n/a	ACATTCCATTGTGTTTGCAA	55	33919	33938	162
531060	n/a	n/a	TGGTGATGCCACCAAACGC	35	33940	33959	163
531061	1872	1891	TGCTCCCTGCGGGCACAGCC	52	33971	33990	164
531062	1877	1896	CAGGTTGCTCCCTGCGGGCA	39	33976	33995	165
531063	1882	1901	GACACCAGGTTGCTCCCTGC	51	33981	34000	166
531064	1887	1906	GTGTAGACACCAGGTTGCTC	56	33986	34005	167
531065	1892	1911	CTTTGGTGTAGACACCAGGT	57	33991	34010	168
531066	1897	1916	AGCGACTTTGGTGTAGACAC	67	33996	34015	169
531067	1902	1921	TACTCAGCGACTTTGGTGTA	31	34001	34020	170
531068	1907	1926	CCATGTACTCAGCGACTTTG	59	34006	34025	171
531069	1912	1931	CCAGTCCATGTACTCAGCGA	56	34011	34030	172
531070	1930	1949	CTGTGTTTTCTCTAAAATCC	68	34029	34048	173
531071	1935	1954	CTGCTCTGTGTTTTCTCTAA	73	34034	34053	174
531072	2026	2045	GCTCAGAATTTGACTTGAAC	64	34125	34144	175
531073	2031	2050	CCCAGGCTCAGAATTTGACT	51	34130	34149	176
531074	2049	2068	CTTTGCAGATGAGGACCCCC	67	34148	34167	177
531075	2054	2073	CCATGCTTTGCAGATGAGGA	64	34153	34172	178

531076	2059	2078	ACTCTCCATGCTTTGCAGAT	68	34158	34177	179
531077	2064	2083	ATGCCACTCTCCATGCTTTG	51	34163	34182	180
531078	2111	2130	AGCAGCTCTGAGTGCACCTGT	77	34210	34229	181
531079	2116	2135	TCCTCAGCAGCTCTGAGTGC	58	34215	34234	182
531080	2121	2140	CATTGTCCTCAGCAGCTCTG	55	34220	34239	183
531081	n/a	n/a	TGGTTTTTGGAAATTCTGAAA	14	31861	31880	184
531082	n/a	n/a	ATATTGGTTTTTTGGAATTCT	31	31865	31884	185

Table 3

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531083	n/a	n/a	TGTACTAGTTTCCTATAACT	60	14738	14757	186
					14809	14828	
					14880	14899	
					14939	14958	
					15071	15090	
					15214	15233	
					15286	15305	
					15345	15364	
					15477	15496	
					15549	15568	
					15607	15626	
					15679	15698	
					15809	15828	
					15881	15900	
					15939	15958	
531084	n/a	n/a	ATAGGGACACAACCAAGGAA	25	16296	16315	187
531085	n/a	n/a	AGGCACAGAGCCAGCACCCA	9	16495	16514	188
531086	n/a	n/a	CCTGCCTCCTGGCAGCCTTC	48	16696	16715	189
531087	n/a	n/a	CCAGGTGTGGACAGCAGCTG	52	16821	16840	190
531088	n/a	n/a	GGTTTTGTTTGTAATAATTAG	27	17159	17178	191
531089	n/a	n/a	AAAACACCATTAATCCATT	45	17306	17325	192
531090	n/a	n/a	ACAGAAACCATGATGTTGCT	59	17644	17663	193
531091	n/a	n/a	TCAGCCCAATGTCCTAACCT	35	17793	17812	194
531092	n/a	n/a	CCTTCACTGACTCTCTTTTC	24	17922	17941	195
531093	n/a	n/a	TTCTCCTGGCTCAGAAGCTC	60	18053	18072	196
					23315	23334	
531094	n/a	n/a	GAATGTCAGGCCTCTGGGCC	48	18181	18200	197
531095	n/a	n/a	CTAACAACCCCAATATCA	20	18390	18409	198

531096	n/a	n/a	CCCAATTCTTAGTCCTTTAA	45	18523	18542	199
531097	n/a	n/a	ACCAAGCTCAGCCTCCAACT	41	18648	18667	200
531098	n/a	n/a	TTATTAGTCAAATCACCCAA	19	18773	18792	201
531099	n/a	n/a	TGGATGGGTAGAGGCCTTTC	64	18898	18917	202
531100	n/a	n/a	CCCCCTCCCTTCCCTACACA	0	19023	19042	203
531101	n/a	n/a	ATGTAAGTTACAAGCCACTA	37	19153	19172	204
531102	n/a	n/a	TGCCTCTTTAATAAAAACTC	42	19484	19503	205
531103	n/a	n/a	ACTCATTGCCTTAACTCAGG	40	19636	19655	206
531104	n/a	n/a	ACTTGACCTTACTGTTTTAG	20	19886	19905	207
531105	n/a	n/a	CTCCTCCCCAGGCTGCTCCT	16	22092	22111	208
531106	n/a	n/a	AAGATCTAGATAATTCTTGT	31	22332	22351	209
531107	n/a	n/a	TCAACTCACACCTGACCTAA	30	22457	22476	210
531108	n/a	n/a	TGAACCCAAAACCTCTGGCAC	50	22771	22790	211
531109	n/a	n/a	AGCCCAAGGAACATCTCACC	52	22959	22978	212
531110	n/a	n/a	GCCTGTTTGGTGGTCTCTTC	86	23110	23129	213
531111	n/a	n/a	CTTCTCCTGGCTCAGAAGCT	68	18054 23316	18073 23335	214
531112	n/a	n/a	ATGTATGATTCTAAGAACTT	14	23479	23498	215
531113	n/a	n/a	AACAGACACATTATTTATAT	0	23604	23623	216
531114	n/a	n/a	AGAGTCAAGTCCACAGACAT	40	24246	24265	217
531115	n/a	n/a	TCCTAAATAGGAACAAAGTA	0	24372	24391	218
531116	n/a	n/a	TTGTTAAGGTTGTAGAGAGA	23	24688	24707	219
531117	n/a	n/a	ACCCAATTATTTTAAATGGC	62	24876	24895	220
531118	n/a	n/a	GCCTAAATGTAAGAGCTAAA	26	25157	25176	221
531119	n/a	n/a	TAAACTCTTACATTTATAGA	0	25293	25312	222
531120	n/a	n/a	AAATAAAAGCACTCAGACTG	0	25418	25437	223
531121	n/a	n/a	TTGGTCTACAGATTCAATGC	72	25550	25569	224
531122	n/a	n/a	TAACAAAAATGCCTTGTGCC	33	25710	25729	225
531123	n/a	n/a	TCCCAGCTCCAGTCACCACC	74	25866	25885	226
531124	n/a	n/a	GTAATAACATCCTAAGTGA	2	25992	26011	227
531125	n/a	n/a	ACTCGCCTTTGTGACTCGAT	23	26264	26283	228
531126	n/a	n/a	TTTTGAATCTTCATTCAAAG	0	26551	26570	229
531127	n/a	n/a	CAGAGCCTTGATCAGAATAA	12	26676	26695	230
531128	n/a	n/a	AAGTTCCACCTTCTAACTGG	18	26831	26850	231
531129	n/a	n/a	AGCAGCTCACACCCAAAAAG	0	27005	27024	232
531130	n/a	n/a	TTCTGTGTCAATTATAAACA	0	27344	27363	233
531131	n/a	n/a	TAGAAAGAGTAAGCCTTCAC	0	27587	27606	234
531132	n/a	n/a	AGTGAGGTTACTCACCAGAG	0	27732	27751	235
531133	n/a	n/a	TTTTGTTGTGCAGACTGAAA	19	27886	27905	236
531134	n/a	n/a	TTACCCATCAAAGCAGTGGG	6	28045	28064	237
531135	n/a	n/a	AATGTTGTGAATACCATCCC	16	28174	28193	238
531136	n/a	n/a	TAACATTTCTATGGGCCTGA	6	28670	28689	239

531137	n/a	n/a	TGTCTACTATTTGACCAATA	19	28795	28814	240
531138	n/a	n/a	TTTAAATGTGTCACTTAATC	0	28987	29006	241
531139	n/a	n/a	TCACTAAAACAAAAATACTT	0	29156	29175	242
531140	n/a	n/a	TCTTCCAGGCCAACACCTT	22	29321	29340	243
531141	n/a	n/a	TGCAAGGCATGTGTGCACAA	47	29532	29551	244
531142	n/a	n/a	TGTTTAAAATATCTCTATAC	8	30008	30027	245
531143	n/a	n/a	CATGGAAAAATTAAGCTCAT	0	30133	30152	246
531144	n/a	n/a	TGAAGATTCTATTTAACAAA	0	30266	30285	247
531145	n/a	n/a	GCCTAGGAGAGAAAAATAAA	0	30445	30464	248
531146	n/a	n/a	CCAGTGTAATTCAAAGGAGC	40	30620	30639	249
531147	n/a	n/a	CCATTATTTCCATCACCTGC	18	30871	30890	250
531148	n/a	n/a	TACCCAAATTATACCTGGAA	8	31015	31034	251
531149	n/a	n/a	AGAGGTAAAGCAACTTGCCC	45	31429	31448	252
531150	n/a	n/a	TCCTTAATAGTCATAGCAGG	48	31558	31577	253
531151	n/a	n/a	TCACCACCATTTTTCACATG	44	31683	31702	254
531152	n/a	n/a	GTTATGGATATAGACTTTAA	0	31808	31827	255
531153	n/a	n/a	CTAGAAGCAATATTTAAAGC	0	31974	31993	256
531154	n/a	n/a	ATGAAGTAAGATGCTTAAAA	16	32162	32181	257
531155	n/a	n/a	CTTCTTGTCTCAGATTACCA	79	32464	32483	258
531156	n/a	n/a	TCTGAAAAGCCCTCCGAGCT	0	32589	32608	259
531157	n/a	n/a	AAGTGAATCAGAGCAGTGTA	46	32961	32980	260
531158	n/a	n/a	ACCTTACAAGCATCTTTTCC	41	33223	33242	261
531159	n/a	n/a	ATTTGTTAAAAGTTGCTTAT	0	33368	33387	262
531160	n/a	n/a	TGATATCATCATCCCAATGA	13	33510	33529	263

Table 4

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531083	n/a	n/a	TGTACTAGTTTCCTATAACT	68	14738	14757	264
					14809	14828	
					14880	14899	
					14939	14958	
					15071	15090	
					15214	15233	
					15286	15305	
					15345	15364	
					15477	15496	
					15549	15568	
					15607	15626	
					15679	15698	

					15809	15828	
					15881	15900	
					15939	15958	
531161	n/a	n/a	CAGACACCTTCTTCACAAGG	40	898	917	264
531162	n/a	n/a	AATTTCCCAGATGTATTAGT	43	1054	1073	265
531163	n/a	n/a	TCAGCAGAAATCATGTAGGC	60	1181	1200	266
531164	n/a	n/a	TTAAATATAAAGAGATCCTC	38	1609	1628	267
531165	n/a	n/a	GTAATAAAAGGAATGATAAA	0	1825	1844	268
531166	n/a	n/a	AGACAGTAAACAAAATCAGG	12	2046	2065	269
531167	n/a	n/a	CAAGAAACCACCAAAGGAAG	37	2176	2195	270
531168	n/a	n/a	ACCCCAACAGACAGCCCACC	55	2314	2333	271
531169	n/a	n/a	TGGGCTCACCCCAGTGGACC	54	2580	2599	272
531170	n/a	n/a	GCCTGGCCCCCAAGACTCTA	54	2743	2762	273
531171	n/a	n/a	AGGCCTGCCACAGGCCAGAC	40	2873	2892	274
531172	n/a	n/a	TTCAAGCCTGGGCAGCACAG	71	3004	3023	275
531173	n/a	n/a	AAAATAACTTCACTAGAGCT	22	3131	3150	276
531174	n/a	n/a	TGTTAAGTATATTAAGTATT	10	3256	3275	277
531175	n/a	n/a	TACTCAGGAAATTAGAATAT	25	3550	3569	278
531176	n/a	n/a	TTATGAAACCTCTTGATTTG	0	3753	3772	279
531177	n/a	n/a	TTCTTGTAATGTCTGAATT	61	3971	3990	280
531178	n/a	n/a	ACCACAGGAACTGTAGCAA	72	4111	4130	281
531179	n/a	n/a	GATTGGACCCAGACACTATA	57	4506	4525	282
531180	n/a	n/a	CCTCTTAAGTCACCATAGAC	45	4785	4804	283
531181	n/a	n/a	GGTTGAGGGACAGACACAGG	36	4940	4959	284
531182	n/a	n/a	ATAATCATGATTTATTTTGC	34	5099	5118	285
531183	n/a	n/a	CATAAGAATGTGCACACAAA	39	5382	5401	286
531184	n/a	n/a	ACTCTTATTAGCTGGTAGAA	74	5538	5557	287
531185	n/a	n/a	GGACCAAACTGAGAGGCAG	63	5663	5682	288
531186	n/a	n/a	CCATTACTCTCAAGCTCCAC	75	5890	5909	289
531187	n/a	n/a	ATCTATTGGTTCAGGAGCCA	72	6015	6034	290
531188	n/a	n/a	GTAAAAACAAGTAGAAGCCA	67	6146	6165	291
531189	n/a	n/a	AGGTGTTCTTGCTTATCCTC	63	6484	6503	292
531190	n/a	n/a	GCAGTCACTCCTCTTCCAGC	59	6659	6678	293
531191	n/a	n/a	AAGTGTATTGCCTAGATTTT	37	6784	6803	294
531192	n/a	n/a	GAGTGCCATCTTCTCTGCAC	61	6968	6987	295
531193	n/a	n/a	TTATTCCCAGCTCTAAAATA	23	7274	7293	296
531194	n/a	n/a	CTCACAATTCTGTAAGGGAA	64	7596	7615	297
531195	n/a	n/a	ATAAAATATATTAAGGCAAC	61	7846	7865	298
531196	n/a	n/a	TTGAGTCAGACATCCTGTGA	38	7996	8015	299
531197	n/a	n/a	TACCTTTTCTCCATGTCATT	42	8148	8167	300
531198	n/a	n/a	GGGATTTTGCTGAAGCTGGT	73	8273	8292	301
531199	n/a	n/a	CTTTGAATAGAAAATGACTA	1	8415	8434	302

531200	n/a	n/a	CAAAATCACAAGTTCTAGAT	51	8617	8636	303
531201	n/a	n/a	TTTCCAATACTTTTACAAAT	52	8760	8779	304
531202	n/a	n/a	ATTAATAAGCATCTCTCTGA	31	9109	9128	305
531203	n/a	n/a	TGACTATCCAATTTCTAGTT	67	9253	9272	306
531204	n/a	n/a	CTTGTAAGTCTGCACTTAATG	60	9418	9437	307
531205	n/a	n/a	ACATTTTTTTAAGTACAGGAA	0	9602	9621	308
531206	n/a	n/a	GAAATGTCTAGCATTTTCTA	28	9755	9774	309
531207	n/a	n/a	CCACTTATTTGATGACCACA	64	9915	9934	310
531208	n/a	n/a	TCCAGAATACTGCCCCATCT	23	10050	10069	311
531209	n/a	n/a	TGGATTCATTTTCTGCAAAT	81	10175	10194	312
531210	n/a	n/a	AGACATTGTCAAATGTCCCC	60	10322	10341	313
531211	n/a	n/a	TTGATGTCAGCACTGTTGAC	77	10480	10499	314
531212	n/a	n/a	ACATCAGTAGCTTCAGATGT	56	10618	10637	315
531213	n/a	n/a	CAAAATTAATTGTGCATAAT	13	10820	10839	316
531214	n/a	n/a	TTTTTCTTTAAATTTTGCTA	37	11120	11139	317
531215	n/a	n/a	TAGAGATTTTATGTACTTGG	63	11245	11264	318
531216	n/a	n/a	AAACACAGGAATTTGCAGAC	33	11408	11427	319
531217	n/a	n/a	GTGGAATAAACCATAATCTA	47	11579	11598	320
531218	n/a	n/a	GATAATTCTTTTCACAGACA	72	12028	12047	321
531219	n/a	n/a	CTTCTCTATCTCCCAGTGTT	61	12227	12246	322
531220	n/a	n/a	CAATACAGGTAAATTTACAG	56	12374	12393	323
531221	n/a	n/a	AAGGGATTTAAAATTTTAT	0	12507	12526	324
531222	n/a	n/a	GGCAAGCTGTACAAGAAAAA	19	12642	12661	325
531223	n/a	n/a	TGTACTCACCGGTACTCTGC	58	12805	12824	326
531224	n/a	n/a	AAGAGAATGCTCAGAAATGG	25	13435	13454	327
531225	n/a	n/a	ACACTTGTACCCCATACATC	45	13560	13579	328
531226	n/a	n/a	GACAGTAGAGACTGGGAAGG	12	13708	13727	329
531227	n/a	n/a	TACCAATTTCTGAAAGGGCA	72	14224	14243	330
531228	n/a	n/a	CAGAGTAAACTCCCCATCTC	33	14387	14406	331
531229	n/a	n/a	CTTCAAAGCCAGCAGTGTA	69	14514	14533	332
531230	n/a	n/a	CTTACTGGGCTAAAATCAAG	46	14639	14658	333
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	94	14744	14763	334
					14815	14834	
					14886	14905	
					14945	14964	
					15005	15024	
					15077	15096	
					15220	15239	
					15292	15311	
					15351	15370	
					15411	15430	
					15483	15502	

					15555	15574	
					15613	15632	
					15685	15704	
					15815	15834	
					15887	15906	
					15945	15964	
531232	n/a	n/a	CTGTACTAGTTTCCTATAAC	85	14739	14758	335
					14810	14829	
					14881	14900	
					14940	14959	
					15000	15019	
					15072	15091	
					15215	15234	
					15287	15306	
					15346	15365	
					15406	15425	
					15478	15497	
					15550	15569	
					15608	15627	
					15680	15699	
					15810	15829	
					15882	15901	
					15940	15959	
531233	n/a	n/a	ACTGTACTAGTTTCCTATAA	86	14740	14759	336
					14811	14830	
					14882	14901	
					14941	14960	
					15001	15020	
					15073	15092	
					15216	15235	
					15288	15307	
					15347	15366	
					15407	15426	
					15479	15498	
					15551	15570	
					15609	15628	
					15681	15700	
					15811	15830	
					15883	15902	
					15941	15960	
531234	n/a	n/a	CACTGTACTAGTTTCCTATA	86	14741	14760	337
					14812	14831	

					14883	14902	
					14942	14961	
					15002	15021	
					15074	15093	
					15217	15236	
					15289	15308	
					15348	15367	
					15408	15427	
					15480	15499	
					15552	15571	
					15610	15629	
					15682	15701	
					15812	15831	
					15884	15903	
					15942	15961	
531235	n/a	n/a	TCACTGTACTAGTTTCCTAT	86	14742	14761	338
					14813	14832	
					14884	14903	
					14943	14962	
					15003	15022	
					15075	15094	
					15218	15237	
					15290	15309	
					15349	15368	
					15409	15428	
					15481	15500	
					15553	15572	
					15611	15630	
					15683	15702	
					15813	15832	
531236	n/a	n/a	ATCACTGTACTAGTTTCCTA	87	14743	14762	339
					14814	14833	
					14885	14904	
					14944	14963	
					15004	15023	
					15076	15095	
					15219	15238	
					15291	15310	
					15350	15369	
					15410	15429	

					15482	15501	
					15554	15573	
					15612	15631	
					15684	15703	
					15814	15833	
					15886	15905	
					15944	15963	
531237	n/a	n/a	GTGGAATGTCATGGCAATTT	56	16399	16418	340

Example 2: Antisense inhibition of human PKK in HepaRG™ cells by antisense oligonucleotides with 2'-MOE sugar modifications

Additional antisense oligonucleotides were designed targeting a PKK nucleic acid and were tested for their effects on PKK mRNA *in vitro*.

The chimeric antisense oligonucleotides in the tables below were designed as 5-10-5 MOE gapmers, 4-9-4 MOE gapmers, 4-10-4 MOE gapmers, 4-10-3 MOE gapmers, 3-10-4 MOE gapmers, or 3-10-3 MOE gapmers. The 5-10-5 MOE gapmers are 20 nucleosides in length, wherein the central gap segment comprises of ten 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising five nucleosides each. The 4-9-4 MOE gapmers are 17 nucleosides in length, wherein the central gap segment comprises of nine 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising four nucleosides each. The 4-10-4 MOE gapmers are 18 nucleosides in length, wherein the central gap segment comprises of ten 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising four nucleosides each. The 4-10-3 MOE gapmers are 17 nucleosides in length, wherein the central gap segment comprises of ten 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising four and three nucleosides respectively. The 3-10-4 MOE gapmers are 17 nucleosides in length, wherein the central gap segment comprises of ten 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising three and four nucleosides respectively. The 3-10-3 MOE gapmers are 16 nucleosides in length, wherein the central gap segment comprises of ten 2'-deoxynucleosides and is flanked by wing segments on the 5' direction and the 3' direction comprising three nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-O-methoxyethyl 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 in the human gene sequence. Each gapmer listed in the tables below is targeted to either SEQ ID NO: 1 or SEQ ID NO: 10. 'n/a' indicates that the antisense oligonucleotide does not target that particular gene sequence.

Cultured HepaRG™ cells at a density of 20,000 cells per well were transfected using electroporation with 5,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and PKK mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3454 was used to measure mRNA levels. PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. The antisense 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. Results are presented as percent inhibition of PKK, relative to untreated control cells.

Table 5

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	98	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546131	4	23	ATGAACGGTCTTCAAGCTGT	5-10-5	75	3396	3415	341
547269	5	24	AATGAACGGTCTTCAAGCTG	5-10-5	56	3397	3416	342
547270	7	26	AAAATGAACGGTCTTCAAGC	5-10-5	68	3399	3418	343
547271	10	29	TTAAAAATGAACGGTCTTCA	5-10-5	60	3402	3421	344
547272	13	32	CACTTAAAAATGAACGGTCT	5-10-5	82	3405	3424	345
547273	25	44	TGAGTCTCTTGTCACCTAAA	5-10-5	93	3417	3436	346
547274	29	48	GAGGTGAGTCTCTTGTCACCT	5-10-5	70	3421	3440	347
546136	30	49	GGAGGTGAGTCTCTTGTCAC	5-10-5	86	3422	3441	348
547275	32	51	TTGGAGGTGAGTCTCTTGTC	5-10-5	87	3424	3443	349
546137	40	59	ATTGCTTCTTGAGGTGAGT	5-10-5	76	3432	3451	350
547276	42	61	CAATTGCTTCTTGAGGTGA	5-10-5	93	3434	3453	351

547277	44	63	CACAATTGCTTCTTGGAGGT	5-10-5	75	3436	3455	352
547278	45	64	ACACAATTGCTTCTTGGAGG	5-10-5	70	3437	3456	353
546138	47	66	AAACACAATTGCTTCTTGA	5-10-5	69	3439	3458	354
547279	48	67	AAAACACAATTGCTTCTTGG	5-10-5	69	3440	3459	355
547280	49	68	GAAAACACAATTGCTTCTTG	5-10-5	47	3441	3460	356
547281	70	89	TTGCTTGAATAAAATCATTC	5-10-5	41	4069	4088	357
546140	72	91	GCTTGCTTGAATAAAATCAT	5-10-5	60	4071	4090	358
547282	74	93	TTGCTTGCTTGAATAAAATC	5-10-5	53	4073	4092	359
547283	76	95	AGTTGCTTGCTTGAATAAAA	5-10-5	67	4075	4094	360
546141	82	101	GAAATAAGTTGCTTGCTTGA	5-10-5	56	4081	4100	361
547284	86	105	AAATGAAATAAGTTGCTTGC	5-10-5	26	4085	4104	362
547285	102	121	ACTGTAGCAAACAAGGAAAT	5-10-5	51	4101	4120	363
546143	106	125	GGAAACTGTAGCAAACAAGG	5-10-5	46	4105	4124	364
546144	110	129	CACAGGAACTGTAGCAAAC	5-10-5	75	4109	4128	365
547286	117	136	AGACATCCACAGGAACTGT	5-10-5	68	n/a	n/a	366
547287	120	139	GTCAGACATCCACAGGAAAC	5-10-5	69	n/a	n/a	367
546146	123	142	TGAGTCAGACATCCACAGGA	5-10-5	72	n/a	n/a	368
547288	131	150	CATAGAGTTGAGTCAGACAT	5-10-5	80	8003	8022	369
546147	132	151	TCATAGAGTTGAGTCAGACA	5-10-5	76	8004	8023	370
547289	133	152	TTCATAGAGTTGAGTCAGAC	5-10-5	74	8005	8024	371
546148	137	156	CGTTTTTCATAGAGTTGAGTC	5-10-5	68	8009	8028	372
546149	155	174	CCCCACCTCTGAAGAAGGCG	5-10-5	83	8027	8046	373
546150	158	177	CATCCCCACCTCTGAAGAAG	5-10-5	58	8030	8049	374
547290	163	182	AGCTACATCCCCACCTCTGA	5-10-5	76	8035	8054	375
546151	166	185	GGAAGCTACATCCCCACCTC	5-10-5	76	8038	8057	376
547291	168	187	ATGGAAGCTACATCCCCACC	5-10-5	74	8040	8059	377
547292	171	190	TACATGGAAGCTACATCCCC	5-10-5	60	8043	8062	378
546152	172	191	GTACATGGAAGCTACATCCC	5-10-5	73	8044	8063	379
546153	176	195	GGGTGTACATGGAAGCTACA	5-10-5	76	8048	8067	380
546154	195	214	TGGCAGTATTGGGCATTG	5-10-5	85	8067	8086	381
547293	199	218	CATCTGGCAGTATTGGGCAT	5-10-5	92	8071	8090	382
547294	201	220	CTCATCTGGCAGTATTGGGC	5-10-5	85	8073	8092	383
546155	202	221	CCTCATCTGGCAGTATTGGG	5-10-5	47	8074	8093	384
547295	203	222	ACCTCATCTGGCAGTATTGG	5-10-5	88	8075	8094	385
547296	206	225	TGCACCTCATCTGGCAGTAT	5-10-5	72	8078	8097	386
546156	211	230	GAATGTGCACCTCATCTGGC	5-10-5	81	8083	8102	387
547297	213	232	TGGAATGTGCACCTCATCTG	5-10-5	84	8085	8104	388
546157	216	235	GGGTGGAATGTGCACCTCAT	5-10-5	85	8088	8107	389
547298	218	237	TTGGGTGGAATGTGCACCTC	5-10-5	90	8090	8109	390
546158	219	238	CTTGGGTGGAATGTGCACCT	5-10-5	95	8091	8110	391
546159	229	248	TAGCAAACACCTTGGGTGGA	5-10-5	76	8101	8120	392
546160	235	254	ACTGAATAGCAAACACCTTG	5-10-5	78	8107	8126	393

547299	237	256	AAACTGAATAGCAAACACCT	5-10-5	76	8109	8128	394
546163	250	269	ACTTGCTGGAAGAAAACCTGA	5-10-5	42	8122	8141	395
547300	252	271	GAACTTGCTGGAAGAAAACCT	5-10-5	37	8124	8143	396
546164	257	276	TGATTGAACTTGCTGGAAGA	5-10-5	33	8129	8148	397
546165	260	279	CATTGATTGAACTTGCTGGA	5-10-5	71	8132	8151	398
547301	261	280	TCATTGATTGAACTTGCTGG	5-10-5	80	8133	8152	399
546166	263	282	TGTCATTGATTGAACTTGCT	5-10-5	70	8135	8154	400
547302	266	285	CCATGTCATTGATTGAACTT	5-10-5	58	8138	8157	401
546167	268	287	CTCCATGTCATTGATTGAAC	5-10-5	73	8140	8159	402
547303	270	289	TTCTCCATGTCATTGATTGA	5-10-5	72	8142	8161	403
547304	273	292	CTTTTCTCCATGTCATTGAT	5-10-5	71	8145	8164	404
547305	280	299	ACCAAACCTTTTCTCCATGT	5-10-5	47	n/a	n/a	405
546170	283	302	GCAACCAAACCTTTTCTCCA	5-10-5	54	n/a	n/a	406
547306	284	303	AGCAACCAAACCTTTTCTCC	5-10-5	62	n/a	n/a	407
547307	286	305	GAAGCAACCAAACCTTTTCT	5-10-5	58	n/a	n/a	408
547308	290	309	TCAAGAAGCAACCAAACCTT	5-10-5	66	n/a	n/a	409
547309	293	312	CTTTCAAGAAGCAACCAAAC	5-10-5	71	9827	9846	410
547310	295	314	ATCTTTCAAGAAGCAACCAA	5-10-5	81	9829	9848	411
546171	297	316	CTATCTTTCAAGAAGCAACC	5-10-5	81	9831	9850	412
547311	299	318	CACTATCTTTCAAGAAGCAA	5-10-5	71	9833	9852	413
546172	301	320	AACACTATCTTTCAAGAAGC	5-10-5	81	9835	9854	414
547312	325	344	ATGTACTTTTGGCAGGGTTC	5-10-5	46	9859	9878	415
546173	327	346	CGATGTACTTTTGGCAGGGT	5-10-5	84	9861	9880	416
547313	330	349	GTTCGATGTACTTTTGGCAG	5-10-5	73	9864	9883	417

Table 6

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	86	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	

						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546174	333	352	CCTGTTCGATGTACTTTTGG	5-10-5	74	9867	9886	418
547314	336	355	GCACCTGTTCGATGTACTTT	5-10-5	73	9870	9889	419
546175	338	357	CTGCACCTGTTCGATGTACT	5-10-5	78	9872	9891	420
547315	340	359	AACTGCACCTGTTCGATGTA	5-10-5	50	9874	9893	421
547316	342	361	GAAACTGCACCTGTTCGATG	5-10-5	75	9876	9895	422
547317	344	363	CAGAAACTGCACCTGTTCGA	5-10-5	75	9878	9897	423
547318	345	364	CCAGAAACTGCACCTGTTCG	5-10-5	74	9879	9898	424
546177	348	367	TGTCCAGAAACTGCACCTGT	5-10-5	75	9882	9901	425
547319	351	370	GAATGTCCAGAAACTGCACC	5-10-5	62	9885	9904	426
547320	353	372	AGGAATGTCCAGAAACTGCA	5-10-5	73	9887	9906	427
547321	356	375	TCAAGGAATGTCCAGAAACT	5-10-5	53	9890	9909	428
547322	358	377	CTTCAAGGAATGTCCAGAAA	5-10-5	65	9892	9911	429
547323	361	380	TTGCTTCAAGGAATGTCCAG	5-10-5	56	9895	9914	430
547324	363	382	CATTGCTTCAAGGAATGTCC	5-10-5	76	9897	9916	431
547325	368	387	GACCACATTGCTTCAAGGAA	5-10-5	67	9902	9921	432
546181	369	388	TGACCACATTGCTTCAAGGA	5-10-5	75	9903	9922	433
547326	370	389	ATGACCACATTGCTTCAAGG	5-10-5	48	9904	9923	434
547327	373	392	TTGATGACCACATTGCTTCA	5-10-5	45	9907	9926	435
547328	375	394	ATTTGATGACCACATTGCTT	5-10-5	40	9909	9928	436
547329	377	396	TTATTTGATGACCACATTGC	5-10-5	24	9911	9930	437
547330	378	397	CTTATTTGATGACCACATTG	5-10-5	60	9912	9931	438
546183	380	399	CACTTATTTGATGACCACAT	5-10-5	69	9914	9933	439
547331	382	401	AGCACTTATTTGATGACCAC	5-10-5	47	n/a	n/a	440
546184	384	403	CAAGCACTTATTTGATGACC	5-10-5	65	n/a	n/a	441
547332	390	409	CGATGGCAAGCACTTATTTG	5-10-5	44	n/a	n/a	442
547333	395	414	TGTCTCGATGGCAAGCACTT	5-10-5	76	n/a	n/a	443
546186	396	415	ATGTCTCGATGGCAAGCACT	5-10-5	84	n/a	n/a	444
547334	397	416	AATGTCTCGATGGCAAGCAC	5-10-5	74	n/a	n/a	445
547335	402	421	TTATAAATGTCTCGATGGCA	5-10-5	93	12658	12677	446
547336	403	422	TTTATAAATGTCTCGATGGC	5-10-5	81	12659	12678	447
546188	407	426	CTCCTTTATAAATGTCTCGA	5-10-5	95	12663	12682	448
547337	409	428	AACTCCTTTATAAATGTCTC	5-10-5	84	12665	12684	449
547338	411	430	TCAACTCCTTTATAAATGTC	5-10-5	71	12667	12686	450
547339	413	432	TATCAACTCCTTTATAAATG	5-10-5	42	12669	12688	451
546190	419	438	CTCTCATATCAACTCCTTTA	5-10-5	92	12675	12694	452
547340	422	441	CTCCTCTCATATCAACTCCT	5-10-5	93	12678	12697	453
547341	424	443	GACTCCTCTCATATCAACTC	5-10-5	87	12680	12699	454

546192	428	447	AATTGACTCCTCTCATATCA	5-10-5	51	12684	12703	455
547342	433	452	ATTAAAATTGACTCCTCTCA	5-10-5	66	12689	12708	456
546193	434	453	CATTAAAATTGACTCCTCTC	5-10-5	57	12690	12709	457
547343	436	455	CACATTAAAATTGACTCCTC	5-10-5	78	12692	12711	458
547344	438	457	GACACATTAAAATTGACTCC	5-10-5	80	12694	12713	459
547345	439	458	AGACACATTAAAATTGACTC	5-10-5	80	12695	12714	460
547346	444	463	ACCTTAGACACATTAAAATT	5-10-5	57	12700	12719	461
546195	448	467	GCTAACCTTAGACACATTAA	5-10-5	83	12704	12723	462
547347	451	470	ACTGCTAACCTTAGACACAT	5-10-5	82	12707	12726	463
546196	452	471	CACTGCTAACCTTAGACACA	5-10-5	83	12708	12727	464
547348	453	472	ACACTGCTAACCTTAGACAC	5-10-5	83	12709	12728	465
547349	458	477	CTTCAACACTGCTAACCTTA	5-10-5	88	12714	12733	466
546198	459	478	TCTTCAACACTGCTAACCTT	5-10-5	85	12715	12734	467
547350	464	483	GGCATTCTTCAACACTGCTA	5-10-5	96	12720	12739	468
546199	465	484	TGGCATTCTTCAACACTGCT	5-10-5	97	12721	12740	469
547351	467	486	TTTGGCATTCTTCAACACTG	5-10-5	92	12723	12742	470
546200	500	519	AAAACTGGCAGCGAATGTTA	5-10-5	91	12756	12775	471
547352	541	560	CCGGTACTCTGCCTTGTGAA	5-10-5	94	12797	12816	472
547354	547	566	ATTGTTCCGGTACTCTGCCT	5-10-5	89	n/a	n/a	473
546203	548	567	AATTGTTCCGGTACTCTGCC	5-10-5	76	n/a	n/a	474
547355	549	568	CAATTGTTCCGGTACTCTGC	5-10-5	77	n/a	n/a	475
546204	555	574	AATAGGCAATTGTTCCGGTA	5-10-5	91	n/a	n/a	476
547356	556	575	TAATAGGCAATTGTTCCGGT	5-10-5	83	n/a	n/a	477
547357	559	578	CTTTAATAGGCAATTGTTCC	5-10-5	78	14130	14149	478
546205	562	581	GTACTIONAATAGGCAATTGT	5-10-5	83	14133	14152	479
547359	569	588	CGGGACTGTACTTTAATAGG	5-10-5	81	14140	14159	480
546208	605	624	CGTTACTCAGCACCTTTATA	5-10-5	92	14176	14195	481
546209	629	648	GCTTCAGTGAGAATCCAGAT	5-10-5	73	14200	14219	482
546210	651	670	CCAATTTCTGAAAGGGCACA	5-10-5	79	14222	14241	483
547360	653	672	AACCAATTTCTGAAAGGGCA	5-10-5	88	n/a	n/a	484
547361	655	674	GCAACCAATTTCTGAAAGGG	5-10-5	46	n/a	n/a	485
546211	656	675	GGCAACCAATTTCTGAAAGG	5-10-5	42	n/a	n/a	486
546212	678	697	AGATGCTGGAAGATGTTTAT	5-10-5	48	26126	26145	487
547362	701	720	CAACATCCACATCTGAGAAC	5-10-5	47	26149	26168	488
547363	703	722	GGCAACATCCACATCTGAGA	5-10-5	84	26151	26170	489
546213	707	726	CCCTGGCAACATCCACATCT	5-10-5	82	26155	26174	490

Table 7

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
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531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	88	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547364	710	729	GAACCCTGGCAACATCCACA	5-10-5	92	26158	26177	491
546214	712	731	GAGAACCCTGGCAACATCCA	5-10-5	88	26160	26179	492
547365	713	732	TGAGAACCCTGGCAACATCC	5-10-5	81	26161	26180	493
547366	717	736	GGAGTGAGAACCCTGGCAAC	5-10-5	86	26165	26184	494
546216	719	738	CTGGAGTGAGAACCCTGGCA	5-10-5	93	26167	26186	495
547367	721	740	ATCTGGAGTGAGAACCCTGG	5-10-5	76	26169	26188	496
547368	723	742	GCATCTGGAGTGAGAACCCT	5-10-5	89	26171	26190	497
547369	725	744	AAGCATCTGGAGTGAGAACC	5-10-5	76	26173	26192	498
547370	728	747	CAAAAGCATCTGGAGTGAGA	5-10-5	73	26176	26195	499
546217	730	749	CACAAAAGCATCTGGAGTGA	5-10-5	83	26178	26197	500
546218	740	759	TGGTCCGACACACAAAAGCA	5-10-5	71	26188	26207	501
547371	741	760	ATGGTCCGACACACAAAAGC	5-10-5	66	26189	26208	502
547372	742	761	GATGGTCCGACACACAAAAG	5-10-5	32	26190	26209	503
547373	745	764	GCAGATGGTCCGACACACAA	5-10-5	90	26193	26212	504
546220	750	769	TAGGTGCAGATGGTCCGACA	5-10-5	71	26198	26217	505
547374	752	771	GATAGGTGCAGATGGTCCGA	5-10-5	81	26200	26219	506
547375	754	773	GTGATAGGTGCAGATGGTCC	5-10-5	72	26202	26221	507
546222	756	775	GGGTGATAGGTGCAGATGGT	5-10-5	12	26204	26223	508
547376	778	797	GAATGTAAAGAAGAGGCAGT	5-10-5	43	26226	26245	509
546224	780	799	TAGAATGTAAAGAAGAGGCA	5-10-5	65	26228	26247	510
547377	788	807	CATTTGTATAGAATGTAAAG	5-10-5	6	26236	26255	511
547378	790	809	TACATTTGTATAGAATGTAA	5-10-5	0	26238	26257	512
546226	793	812	CCATACATTTGTATAGAATG	5-10-5	37	26241	26260	513
547379	802	821	CTCGATTTTCCATACATTTG	5-10-5	37	26250	26269	514
547380	805	824	TGACTCGATTTTCCATACAT	5-10-5	42	26253	26272	515

546228	806	825	GTGACTCGATTTTCCATACA	5-10-5	60	26254	26273	516
547381	807	826	TGTGACTCGATTTTCCATAC	5-10-5	49	26255	26274	517
547382	810	829	CTTTGTGACTCGATTTTCCA	5-10-5	62	26258	26277	518
547383	812	831	TTCTTTGTGACTCGATTTTC	5-10-5	37	n/a	n/a	519
546229	816	835	ACATTTCTTTGTGACTCGAT	5-10-5	19	n/a	n/a	520
547384	818	837	AAACATTTCTTTGTGACTCG	5-10-5	50	n/a	n/a	521
547385	847	866	TGTGCCACTTTCAGATGTTT	5-10-5	80	27111	27130	522
546230	848	867	GTGTGCCACTTTCAGATGTT	5-10-5	70	27112	27131	523
546231	852	871	CTTGGTGTGCCACTTTCAGA	5-10-5	79	27116	27135	524
547386	853	872	ACTTGGTGTGCCACTTTCAG	5-10-5	78	27117	27136	525
546232	857	876	AGGAACCTTGGTGTGCCACTT	5-10-5	86	27121	27140	526
547387	878	897	TGGTGTTTTCTTGAGGAGTA	5-10-5	73	27142	27161	527
546233	879	898	ATGGTGTTTTCTTGAGGAGT	5-10-5	69	27143	27162	528
547388	880	899	TATGGTGTTTTCTTGAGGAG	5-10-5	55	27144	27163	529
547389	884	903	CAGATATGGTGTTTTCTTGA	5-10-5	61	27148	27167	530
546234	885	904	CCAGATATGGTGTTTTCTTG	5-10-5	69	27149	27168	531
547390	887	906	ATCCAGATATGGTGTTTTCT	5-10-5	63	27151	27170	532
547391	889	908	ATATCCAGATATGGTGTTTT	5-10-5	32	27153	27172	533
546235	893	912	GGCTATATCCAGATATGGTG	5-10-5	77	27157	27176	534
547392	895	914	AAGGCTATATCCAGATATGG	5-10-5	81	27159	27178	535
546236	900	919	GTTAAAAGGCTATATCCAGA	5-10-5	50	27164	27183	536
546237	903	922	CAGGTAAAAGGCTATATCC	5-10-5	64	27167	27186	537
547393	905	924	TGCAGGTAAAAGGCTATAT	5-10-5	73	27169	27188	538
547394	907	926	TTTGCAGGTAAAAGGCTAT	5-10-5	29	27171	27190	539
546238	909	928	CTTTTGCAGGTAAAAGGCT	5-10-5	63	27173	27192	540
546239	912	931	GTTCTTTTGCAGGTAAAAG	5-10-5	47	27176	27195	541
547395	914	933	AAGTTCTTTTGCAGGTAAA	5-10-5	15	27178	27197	542
546240	917	936	GTAAAGTTCTTTTGCAGGTT	5-10-5	23	27181	27200	543
546241	920	939	CAGGTAAAGTTCTTTTGCAG	5-10-5	69	27184	27203	544
547396	921	940	TCAGGTAAAGTTCTTTTGCA	5-10-5	49	n/a	n/a	545
547397	923	942	G TTCAGGTAAAGTTCTTTTG	5-10-5	27	n/a	n/a	546
546242	925	944	GGGTT CAGGTAAAGTTCTTT	5-10-5	8	n/a	n/a	547
547398	927	946	CAGGGTTCAGGTAAAGTTCT	5-10-5	16	n/a	n/a	548
547399	928	947	GCAGGGTTCAGGTAAAGTTC	5-10-5	10	n/a	n/a	549
547400	930	949	TGGCAGGGTTCAGGTAAAGT	5-10-5	0	n/a	n/a	550
547401	933	952	GAATGGCAGGGTTCAGGTAA	5-10-5	22	n/a	n/a	551
546243	934	953	AGAATGGCAGGGTTCAGGTA	5-10-5	16	n/a	n/a	552
547402	937	956	TTTAGAATGGCAGGGTTCAG	5-10-5	59	n/a	n/a	553
547403	939	958	ATTTTAGAATGGCAGGGTTC	5-10-5	10	27361	27380	554
546244	942	961	TAAATTTTAGAATGGCAGGG	5-10-5	27	27364	27383	555
547404	956	975	AGTCAACTCCCGGGTAAATT	5-10-5	64	27378	27397	556
547405	959	978	CAAAGTCAACTCCCGGGTAA	5-10-5	47	27381	27400	557

546247	960	979	CCAAAGTCAACTCCCGGGTA	5-10-5	90	27382	27401	558
546248	963	982	CCTCCAAAGTCAACTCCCGG	5-10-5	86	27385	27404	559
547406	965	984	CTCCTCCAAAGTCAACTCCC	5-10-5	81	27387	27406	560
546249	968	987	CTTCTCCTCCAAAGTCAACT	5-10-5	68	27390	27409	561
547407	975	994	TTCAATTCTTCTCCTCCAAA	5-10-5	59	27397	27416	562
546250	977	996	CATTCAATTCTTCTCCTCCA	5-10-5	65	27399	27418	563
547408	980	999	TCACATTCAATTCTTCTCCT	5-10-5	84	27402	27421	564
547409	982	1001	AGTCACATTCAATTCTTCTC	5-10-5	67	27404	27423	565
546251	1007	1026	GGCAAACATTCACTCCTTTA	5-10-5	92	27429	27448	566

Table 8

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	95	14744	14763	344
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546252	1011	1030	TCTTGGCAAACATTCACTCC	5-10-5	73	27433	27452	567
546253	1014	1033	GTCTCTTGGCAAACATTAC	5-10-5	98	27436	27455	568
547410	1017	1036	CAAGTCTCTTGGCAAACATT	5-10-5	88	27439	27458	569
546254	1019	1038	TGCAAGTCTCTTGGCAAACA	5-10-5	95	27441	27460	570
546255	1024	1043	CTTTGTGCAAGTCTCTTGGC	5-10-5	92	27446	27465	571
547411	1027	1046	CATCTTTGTGCAAGTCTCTT	5-10-5	79	27449	27468	572
546256	1028	1047	TCATCTTTGTGCAAGTCTCT	5-10-5	83	27450	27469	573
547412	1029	1048	ATCATCTTTGTGCAAGTCTC	5-10-5	73	27451	27470	574
546258	1036	1055	ACAGCGAATCATCTTTGTGC	5-10-5	74	27458	27477	575
546259	1040	1059	ACTGACAGCGAATCATCTTT	5-10-5	86	27462	27481	576

546260	1045	1064	GAAAAAAGTACAGCGAATCA	5-10-5	84	27467	27486	577
547413	1047	1066	GTGAAAAAAGTACAGCGAAT	5-10-5	94	27469	27488	578
546263	1061	1080	GGAGTAAAGAATAAGTGAAA	5-10-5	0	27483	27502	579
547414	1063	1082	TGGGAGTAAAGAATAAGTGA	5-10-5	76	27485	27504	580
547415	1065	1084	TCTGGGAGTAAAGAATAAGT	5-10-5	71	27487	27506	581
546265	1069	1088	GTCTTCTGGGAGTAAAGAAT	5-10-5	65	27491	27510	582
546266	1072	1091	ACAGTCTTCTGGGAGTAAAG	5-10-5	63	27494	27513	583
547416	1075	1094	CTTACAGTCTTCTGGGAGTA	5-10-5	79	27497	27516	584
546267	1076	1095	CCTTACAGTCTTCTGGGAGT	5-10-5	72	27498	27517	585
547417	1077	1096	TCCTTACAGTCTTCTGGGAG	5-10-5	68	27499	27518	586
546268	1079	1098	CTTCCTTACAGTCTTCTGGG	5-10-5	93	27501	27520	587
547418	1092	1111	CACTTACACTTCTCTTCCTT	5-10-5	0	n/a	n/a	588
546270	1093	1112	ACACTTACACTTCTCTTCCT	5-10-5	32	n/a	n/a	589
546271	1097	1116	AGAAACACTTACACTTCTCT	5-10-5	60	n/a	n/a	590
547419	1101	1120	CTTAAGAAACACTTACACTT	5-10-5	51	n/a	n/a	591
547420	1112	1131	CCATAGATAATCTTAAGAAA	5-10-5	8	27633	27652	592
547421	1115	1134	CATCCATAGATAATCTTAAG	5-10-5	69	27636	27655	593
547422	1117	1136	ACCATCCATAGATAATCTTA	5-10-5	70	27638	27657	594
546275	1119	1138	GAACCATCCATAGATAATCT	5-10-5	87	27640	27659	595
546276	1123	1142	TGGAGAACCATCCATAGATA	5-10-5	74	27644	27663	596
546277	1146	1165	TGTGTCCCATACGCAATCCT	5-10-5	90	27667	27686	597
547423	1150	1169	CCCTTGTGTCCCATACGCAA	5-10-5	95	27671	27690	598
546279	1153	1172	GCTCCCTTGTGTCCCATACG	5-10-5	82	27674	27693	599
547424	1156	1175	AGAGCTCCCTTGTGTCCCAT	5-10-5	90	27677	27696	600
546280	1158	1177	CCAGAGCTCCCTTGTGTCCC	5-10-5	86	27679	27698	601
547425	1161	1180	TAACCAGAGCTCCCTTGTGT	5-10-5	85	27682	27701	602
546281	1162	1181	GTAACCAGAGCTCCCTTGTG	5-10-5	85	27683	27702	603
547426	1164	1183	GAGTAACCAGAGCTCCCTTG	5-10-5	92	27685	27704	604
547427	1166	1185	AAGAGTAACCAGAGCTCCCT	5-10-5	79	27687	27706	605
547428	1169	1188	TCAAAGAGTAACCAGAGCTC	5-10-5	78	27690	27709	606
546283	1171	1190	TCTCAAAGAGTAACCAGAGC	5-10-5	88	27692	27711	607
547429	1173	1192	AATCTCAAAGAGTAACCAGA	5-10-5	81	27694	27713	608
547430	1174	1193	CAATCTCAAAGAGTAACCAG	5-10-5	70	27695	27714	609
546284	1176	1195	CACAATCTCAAAGAGTAACC	5-10-5	89	27697	27716	610
546285	1180	1199	GTTACACAATCTCAAAGAGT	5-10-5	76	27701	27720	611
547431	1184	1203	CAGTGTTACACAATCTCAAA	5-10-5	67	27705	27724	612
547432	1186	1205	CCCAGTGTTACACAATCTCA	5-10-5	90	27707	27726	613
547433	1189	1208	GTCCCCAGTGTTACACAATC	5-10-5	63	27710	27729	614
546287	1192	1211	GTTGTCCCCAGTGTTACACA	5-10-5	82	27713	27732	615
546288	1240	1259	GTTTGTTCCCTCCAACAATGC	5-10-5	78	27916	27935	616
547434	1243	1262	AGAGTTTGTTCCCTCCAACAA	5-10-5	54	27919	27938	617
547435	1248	1267	CAAGAAGAGTTTGTTCTCCTC	5-10-5	85	27924	27943	618

546290	1251	1270	CCCCAAGAAGAGTTTGTTC	5-10-5	86	27927	27946	619
547436	1253	1272	CTCCCCAAGAAGAGTTTGT	5-10-5	0	27929	27948	620
547437	1255	1274	CTCTCCCCAAGAAGAGTTTG	5-10-5	50	27931	27950	621
547438	1261	1280	GGGCCACTCTCCCCAAGAAG	5-10-5	82	27937	27956	622
546291	1263	1282	CAGGGCCACTCTCCCCAAGA	5-10-5	81	27939	27958	623
547439	1298	1317	TCTGAGCTGTCAGCTTCACC	5-10-5	85	27974	27993	624
546293	1301	1320	GCCTCTGAGCTGTCAGCTTC	5-10-5	64	27977	27996	625
547440	1327	1346	TCCTATGAGTGACCCTCCAC	5-10-5	67	28003	28022	626
546294	1328	1347	GTCCTATGAGTGACCCTCCA	5-10-5	72	28004	28023	627
547441	1331	1350	GGTGTCTATGAGTGACCCT	5-10-5	62	28007	28026	628
547442	1332	1351	TGGTGTCTATGAGTGACCC	5-10-5	42	28008	28027	629
547443	1336	1355	CCACTGGTGTCTATGAGTG	5-10-5	70	28012	28031	630
546295	1337	1356	CCCACTGGTGTCTATGAGT	5-10-5	67	28013	28032	631
546296	1370	1389	GAAGCCCATCAAAGCAGTGG	5-10-5	27	n/a	n/a	632
546297	1397	1416	TATAGATGCGCCAAACATCC	5-10-5	82	30475	30494	633
547444	1398	1417	CTATAGATGCGCCAAACATC	5-10-5	71	30476	30495	634
547445	1402	1421	GCCACTATAGATGCGCCAAA	5-10-5	97	30480	30499	635
546299	1404	1423	ATGCCACTATAGATGCGCCA	5-10-5	84	30482	30501	636
546300	1424	1443	TAATGTCTGACAGATTTAAA	5-10-5	58	30502	30521	637
546301	1427	1446	TTGTAATGTCTGACAGATTT	5-10-5	93	30505	30524	638
546302	1444	1463	TGAGAAAGGTGTATCTTTTG	5-10-5	87	30522	30541	639
547446	1447	1466	TTGTGAGAAAGGTGTATCTT	5-10-5	84	30525	30544	640
546303	1448	1467	TTTGTGAGAAAGGTGTATCT	5-10-5	77	30526	30545	641
547447	1449	1468	ATTTGTGAGAAAGGTGTATC	5-10-5	80	30527	30546	642

Table 9

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	96	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	

						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547448	1451	1470	TTATTTGTGAGAAAGGTGTA	5-10-5	75	30529	30548	643
547449	1453	1472	TTTTATTTGTGAGAAAGGTG	5-10-5	71	30531	30550	644
546304	1454	1473	CTTTTATTTGTGAGAAAGGT	5-10-5	94	30532	30551	645
547450	1456	1475	CTCTTTTATTTGTGAGAAAG	5-10-5	71	30534	30553	646
547451	1471	1490	TTGGTGAATAATAATCTCTT	5-10-5	75	30549	30568	647
546306	1472	1491	TTTGGTGAATAATAATCTCT	5-10-5	65	30550	30569	648
547452	1474	1493	GTTTTGGTGAATAATAATCT	5-10-5	47	30552	30571	649
546307	1478	1497	TATAGTTTTGGTGAATAATA	5-10-5	12	30556	30575	650
546308	1482	1501	ACTTTATAGTTTTGGTGAAT	5-10-5	57	30560	30579	651
546309	1492	1511	CCCTTCTGAGACTTTATAGT	5-10-5	88	30570	30589	652
546310	1496	1515	GATTCCTTCTGAGACTTTA	5-10-5	78	30574	30593	653
546311	1499	1518	CATGATTCCTTCTGAGACT	5-10-5	79	30577	30596	654
547453	1500	1519	TCATGATTCCTTCTGAGAC	5-10-5	81	30578	30597	655
547454	1502	1521	TATCATGATTCCTTCTGAG	5-10-5	92	30580	30599	656
547455	1503	1522	ATATCATGATTCCTTCTGA	5-10-5	88	30581	30600	657
547456	1506	1525	GCGATATCATGATTCCTTC	5-10-5	89	30584	30603	658
546313	1507	1526	GGCGATATCATGATTCCTT	5-10-5	60	30585	30604	659
547457	1509	1528	AAGGCGATATCATGATTCCT	5-10-5	89	30587	30606	660
547458	1513	1532	TATCAAGGCGATATCATGAT	5-10-5	84	30591	30610	661
547459	1519	1538	GAGTTTTATCAAGGCGATAT	5-10-5	28	30597	30616	662
547460	1522	1541	CTGGAGTTTTATCAAGGCGA	5-10-5	72	30600	30619	663
546316	1524	1543	GCCTGGAGTTTTATCAAGGC	5-10-5	51	30602	30621	664
546317	1528	1547	AGGAGCCTGGAGTTTTATCA	5-10-5	12	30606	30625	665
546318	1534	1553	ATTCAAAGGAGCCTGGAGTT	5-10-5	47	30612	30631	666
547461	1537	1556	GTAATTCAAAGGAGCCTGGA	5-10-5	49	30615	30634	667
547462	1539	1558	GTGTAATTCAAAGGAGCCTG	5-10-5	59	30617	30636	668
546319	1541	1560	CAGTGTAATTCAAAGGAGCC	5-10-5	50	30619	30638	669
547463	1564	1583	TAGGCATATTGGTTTTTGA	5-10-5	74	31870	31889	670
546320	1566	1585	GGTAGGCATATTGGTTTTTG	5-10-5	72	31872	31891	671
546321	1569	1588	GAAGGTAGGCATATTGGTTT	5-10-5	53	31875	31894	672
546322	1584	1603	CTTGTGTCACCTTTGGAAGG	5-10-5	74	31890	31909	673
547464	1585	1604	GCTTGTGTCACCTTTGGAAG	5-10-5	95	31891	31910	674
546323	1587	1606	GTGCTTGTGTCACCTTTGGA	5-10-5	94	31893	31912	675
547465	1592	1611	AAATTGTGCTTGTGTCACCT	5-10-5	88	31898	31917	676
547466	1596	1615	GTATAAATTGTGCTTGTGTC	5-10-5	82	31902	31921	677
546324	1597	1616	GGTATAAATTGTGCTTGTGT	5-10-5	73	31903	31922	678
547467	1598	1617	TGGTATAAATTGTGCTTGTG	5-10-5	80	31904	31923	679

547468	1600	1619	GTTGGTATAAATTGTGCTTG	5-10-5	61	31906	31925	680
546325	1602	1621	CAGTTGGTATAAATTGTGCT	5-10-5	74	31908	31927	681
546326	1607	1626	CCCAACAGTTGGTATAAATT	5-10-5	62	31913	31932	682
547469	1610	1629	TTACCCAACAGTTGGTATAA	5-10-5	67	31916	31935	683
546327	1612	1631	GGTTACCCAACAGTTGGTAT	5-10-5	95	31918	31937	684
546328	1624	1643	GAAGCCCCATCCGGTTACCC	5-10-5	84	31930	31949	685
547470	1628	1647	TCGAGAAGCCCCATCCGGTT	5-10-5	70	31934	31953	686
546329	1631	1650	CCTTCGAGAAGCCCCATCCG	5-10-5	18	31937	31956	687
546330	1636	1655	TTTCTCCTTCGAGAAGCCCC	5-10-5	55	31942	31961	688
547471	1638	1657	CCTTTCTCCTTCGAGAAGCC	5-10-5	58	31944	31963	689
547472	1641	1660	TCACCTTTCTCCTTCGAGAA	5-10-5	44	n/a	n/a	690
546331	1642	1661	TTCACCTTTCTCCTTCGAGA	5-10-5	59	n/a	n/a	691
547473	1649	1668	TTTGGATTTCACCTTTCTCC	5-10-5	5	n/a	n/a	692
547474	1659	1678	TGTAGAATATTTTGGATTTC	5-10-5	51	33103	33122	693
547475	1686	1705	TTTGTACCAAAGGAATATT	5-10-5	44	33130	33149	694
547476	1688	1707	CATTTGTTACCAAAGGAATA	5-10-5	75	33132	33151	695
546336	1689	1708	TCATTTGTTACCAAAGGAAT	5-10-5	66	33133	33152	696
547477	1692	1711	TCTTCATTTGTTACCAAAGG	5-10-5	74	33136	33155	697
547478	1695	1714	CATTCTTCATTTGTTACCAA	5-10-5	85	33139	33158	698
546339	1712	1731	CTTGATATCTTTTCTGGCAT	5-10-5	65	33156	33175	699
546340	1716	1735	TAATCTTGATATCTTTTCTG	5-10-5	30	33160	33179	700
547479	1718	1737	TATAATCTTGATATCTTTTC	5-10-5	48	33162	33181	701
547480	1756	1775	TTCTTTATAGCCAGCACAGA	5-10-5	60	33200	33219	702
547481	1758	1777	CCTTCTTTATAGCCAGCACA	5-10-5	71	33202	33221	703
547482	1760	1779	CCCCTTCTTTATAGCCAGCA	5-10-5	90	33204	33223	704
546343	1761	1780	CCCCCTTCTTTATAGCCAGC	5-10-5	97	33205	33224	705
547483	1762	1781	TCCCCCTTCTTTATAGCCAG	5-10-5	71	33206	33225	706
546345	1773	1792	CAAGCATCTTTTCCCCCTTC	5-10-5	86	33217	33236	707
546346	1796	1815	AGGGACCACCTGAATCTCCC	5-10-5	83	33895	33914	708
547484	1799	1818	CTAAGGGACCACCTGAATCT	5-10-5	69	33898	33917	709
546347	1800	1819	ACTAAGGGACCACCTGAATC	5-10-5	28	33899	33918	710
547485	1803	1822	CAAACCTAAGGGACCACCTGA	5-10-5	49	33902	33921	711
546348	1804	1823	GCAAACCTAAGGGACCACCTG	5-10-5	79	33903	33922	712
547486	1805	1824	TGCAAACCTAAGGGACCACCT	5-10-5	89	33904	33923	713
546349	1810	1829	GTGTTTGCAAACCTAAGGGAC	5-10-5	48	33909	33928	714
547487	1811	1830	TGTGTTTGCAAACCTAAGGGA	5-10-5	72	33910	33929	715
546350	1868	1887	CCCTGCGGGCACAGCCTTCA	5-10-5	88	33967	33986	716
546351	1873	1892	TTGCTCCCTGCGGGCACAGC	5-10-5	82	33972	33991	717
546352	1880	1899	CACCAGGTTGCTCCCTGCGG	5-10-5	75	33979	33998	718
547488	1881	1900	ACACCAGGTTGCTCCCTGCG	5-10-5	71	33980	33999	719

Table 10

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	72	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547448	1451	1470	TTATTTGTGAGAAAGGTGTA	5-10-5	83	30529	30548	643
547449	1453	1472	TTTTATTTGTGAGAAAGGTG	5-10-5	73	30531	30550	644
546304	1454	1473	CTTTTATTTGTGAGAAAGGT	5-10-5	86	30532	30551	645
547450	1456	1475	CTCTTTTATTTGTGAGAAAG	5-10-5	67	30534	30553	646
547451	1471	1490	TTGGTGAATAATAATCTCTT	5-10-5	64	30549	30568	647
546306	1472	1491	TTTGGTGAATAATAATCTCT	5-10-5	71	30550	30569	648
547452	1474	1493	GTTTTGGTGAATAATAATCT	5-10-5	62	30552	30571	649
546307	1478	1497	TATAGTTTTGGTGAATAATA	5-10-5	0	30556	30575	650
546308	1482	1501	ACTTTATAGTTTTGGTGAAT	5-10-5	43	30560	30579	651
546309	1492	1511	CCCTTCTGAGACTTTATAGT	5-10-5	81	30570	30589	652
546310	1496	1515	GATTCCCTTCTGAGACTTTA	5-10-5	67	30574	30593	653
546311	1499	1518	CATGATTCCCTTCTGAGACT	5-10-5	76	30577	30596	654
547453	1500	1519	TCATGATTCCCTTCTGAGAC	5-10-5	81	30578	30597	655
547454	1502	1521	TATCATGATTCCCTTCTGAG	5-10-5	78	30580	30599	656
547455	1503	1522	ATATCATGATTCCCTTCTGA	5-10-5	66	30581	30600	657
547456	1506	1525	GCGATATCATGATTCCCTTC	5-10-5	96	30584	30603	658
546313	1507	1526	GGCGATATCATGATTCCCTT	5-10-5	75	30585	30604	659
547457	1509	1528	AAGGCGATATCATGATTCCC	5-10-5	92	30587	30606	660
547458	1513	1532	TATCAAGGCGATATCATGAT	5-10-5	64	30591	30610	661
547459	1519	1538	GAGTTTTATCAAGGCGATAT	5-10-5	51	30597	30616	662
547460	1522	1541	CTGGAGTTTTATCAAGGCGA	5-10-5	75	30600	30619	663

546316	1524	1543	GCCTGGAGTTTTATCAAGGC	5-10-5	60	30602	30621	664
546317	1528	1547	AGGAGCCTGGAGTTTTATCA	5-10-5	31	30606	30625	665
546318	1534	1553	ATTCAAAGGAGCCTGGAGTT	5-10-5	46	30612	30631	666
547461	1537	1556	GTAATTCAAAGGAGCCTGGA	5-10-5	55	30615	30634	667
547462	1539	1558	GTGTAATTCAAAGGAGCCTG	5-10-5	54	30617	30636	668
546319	1541	1560	CAGTGTAATTCAAAGGAGCC	5-10-5	61	30619	30638	669
547463	1564	1583	TAGGCATATTGGTTTTTGA	5-10-5	84	31870	31889	670
546320	1566	1585	GGTAGGCATATTGGTTTTTG	5-10-5	69	31872	31891	671
546321	1569	1588	GAAGGTAGGCATATTGGTTT	5-10-5	56	31875	31894	672
546322	1584	1603	CTTGTGTCACCTTTGGAAGG	5-10-5	68	31890	31909	673
547464	1585	1604	GCTTGTGTCACCTTTGGAAG	5-10-5	84	31891	31910	674
546323	1587	1606	GTGCTTGTGTCACCTTTGGA	5-10-5	80	31893	31912	675
547465	1592	1611	AAATTGTGCTTGTGTCACCT	5-10-5	85	31898	31917	676
547466	1596	1615	GTATAAATTGTGCTTGTGTC	5-10-5	43	31902	31921	677
546324	1597	1616	GGTATAAATTGTGCTTGTGT	5-10-5	82	31903	31922	678
547467	1598	1617	TGGTATAAATTGTGCTTGTG	5-10-5	65	31904	31923	679
547468	1600	1619	GTTGGTATAAATTGTGCTTG	5-10-5	46	31906	31925	680
546325	1602	1621	CAGTTGGTATAAATTGTGCT	5-10-5	79	31908	31927	681
546326	1607	1626	CCCAACAGTTGGTATAAATT	5-10-5	64	31913	31932	682
547469	1610	1629	TTACCCAACAGTTGGTATAA	5-10-5	50	31916	31935	683
546327	1612	1631	GGTTACCCAACAGTTGGTAT	5-10-5	84	31918	31937	684
546328	1624	1643	GAAGCCCCATCCGGTTACCC	5-10-5	81	31930	31949	685
547470	1628	1647	TCGAGAAGCCCCATCCGGTT	5-10-5	68	31934	31953	686
546329	1631	1650	CCTTCGAGAAGCCCCATCCG	5-10-5	8	31937	31956	687
546330	1636	1655	TTTCTCCTTCGAGAAGCCCC	5-10-5	67	31942	31961	688
547471	1638	1657	CCTTTCTCCTTCGAGAAGCC	5-10-5	43	31944	31963	689
547472	1641	1660	TCACCTTTCTCCTTCGAGAA	5-10-5	42	n/a	n/a	690
546331	1642	1661	TTCACCTTTCTCCTTCGAGA	5-10-5	44	n/a	n/a	691
547473	1649	1668	TTTGGATTTACACCTTTCTCC	5-10-5	26	n/a	n/a	692
547474	1659	1678	TGTAGAATATTTTGGATTTTC	5-10-5	34	33103	33122	693
547475	1686	1705	TTTGTTACCAAAGGAATATT	5-10-5	42	33130	33149	694
547476	1688	1707	CATTTGTTACCAAAGGAATA	5-10-5	71	33132	33151	695
546336	1689	1708	TCATTTGTTACCAAAGGAAT	5-10-5	73	33133	33152	696
547477	1692	1711	TCTTCATTTGTTACCAAAGG	5-10-5	68	33136	33155	697
547478	1695	1714	CATTCTTCATTTGTTACCAA	5-10-5	55	33139	33158	698
546339	1712	1731	CTTGATATCTTTTCTGGCAT	5-10-5	64	33156	33175	699
546340	1716	1735	TAATCTTGATATCTTTTCTG	5-10-5	56	33160	33179	700
547479	1718	1737	TATAATCTTGATATCTTTTTC	5-10-5	9	33162	33181	701
547480	1756	1775	TTCTTTATAGCCAGCACAGA	5-10-5	49	33200	33219	702
547481	1758	1777	CCTTCTTTATAGCCAGCACA	5-10-5	77	33202	33221	703
547482	1760	1779	CCCCTTCTTTATAGCCAGCA	5-10-5	65	33204	33223	704
546343	1761	1780	CCCCCTTCTTTATAGCCAGC	5-10-5	91	33205	33224	705

547483	1762	1781	TCCCCCTTCTTTATAGCCAG	5-10-5	77	33206	33225	706
546345	1773	1792	CAAGCATCTTTTCCCCCTTC	5-10-5	80	33217	33236	707
546346	1796	1815	AGGGACCACCTGAATCTCCC	5-10-5	70	33895	33914	708
547484	1799	1818	CTAAGGGACCACCTGAATCT	5-10-5	64	33898	33917	709
546347	1800	1819	ACTAAGGGACCACCTGAATC	5-10-5	22	33899	33918	710
547485	1803	1822	CAAACCTAAGGGACCACCTGA	5-10-5	66	33902	33921	711
546348	1804	1823	GCAAACCTAAGGGACCACCTG	5-10-5	76	33903	33922	712
547486	1805	1824	TGCAAACCTAAGGGACCACCT	5-10-5	78	33904	33923	713
546349	1810	1829	GTGTTTGCAAACCTAAGGGAC	5-10-5	35	33909	33928	714
547487	1811	1830	TGTGTTTGCAAACCTAAGGGA	5-10-5	61	33910	33929	715
546350	1868	1887	CCCTGCGGGCACAGCCTTCA	5-10-5	74	33967	33986	716
546351	1873	1892	TTGCTCCCTGCGGGCACAGC	5-10-5	60	33972	33991	717
546352	1880	1899	CACCAGGTTGCTCCCTGCGG	5-10-5	74	33979	33998	718
547488	1881	1900	ACACCAGGTTGCTCCCTGCG	5-10-5	72	33980	33999	719

Table 11

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	90	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547489	1883	1902	AGACACCAGGTTGCTCCCTG	5-10-5	34	33982	34001	720
547490	1885	1904	GTAGACACCAGGTTGCTCCC	5-10-5	55	33984	34003	721
546353	1900	1919	CTCAGCGACTTTGGTGTAGA	5-10-5	55	33999	34018	722
546354	1903	1922	GTA CTCAGCGACTTTGGTGT	5-10-5	47	34002	34021	723
547491	1906	1925	CATGTA CTCAGCGACTTTGG	5-10-5	47	34005	34024	724

547492	1911	1930	CAGTCCATGTACTCAGCGAC	5-10-5	62	34010	34029	725
546356	1913	1932	TCCAGTCCATGTACTCAGCG	5-10-5	60	34012	34031	726
546357	1947	1966	GCTTTTCCATCACTGCTCTG	5-10-5	79	34046	34065	727
546358	1951	1970	CTGAGCTTTTCCATCACTGC	5-10-5	83	34050	34069	728
547493	1952	1971	TCTGAGCTTTTCCATCACTG	5-10-5	72	34051	34070	729
546359	1955	1974	GCATCTGAGCTTTTCCATCA	5-10-5	79	34054	34073	730
546360	1958	1977	ACTGCATCTGAGCTTTTCCA	5-10-5	13	34057	34076	731
547494	1963	1982	TGGTGACTGCATCTGAGCTT	5-10-5	70	34062	34081	732
547495	1965	1984	GCTGGTGACTGCATCTGAGC	5-10-5	61	34064	34083	733
547496	1967	1986	ATGCTGGTGACTGCATCTGA	5-10-5	80	34066	34085	734
546362	1969	1988	TCATGCTGGTGACTGCATCT	5-10-5	71	34068	34087	735
546363	1973	1992	CTTCTCATGCTGGTGACTGC	5-10-5	81	34072	34091	736
547497	1977	1996	ACTGCTTCTCATGCTGGTGA	5-10-5	68	34076	34095	737
546364	1979	1998	GGACTGCTTCTCATGCTGGT	5-10-5	61	34078	34097	738
547498	1981	2000	CTGGACTGCTTCTCATGCTG	5-10-5	44	34080	34099	739
547499	1983	2002	CTCTGGACTGCTTCTCATGC	5-10-5	65	34082	34101	740
546365	1986	2005	AGACTCTGGACTGCTTCTCA	5-10-5	64	34085	34104	741
547500	1989	2008	CCTAGACTCTGGACTGCTTC	5-10-5	65	34088	34107	742
546366	1991	2010	TGCCTAGACTCTGGACTGCT	5-10-5	79	34090	34109	743
547501	1993	2012	ATTGCCTAGACTCTGGACTG	5-10-5	55	34092	34111	744
546367	1997	2016	AAAAATTGCCTAGACTCTGG	5-10-5	61	34096	34115	745
546368	2003	2022	GGTTGTAAAAATTGCCTAGA	5-10-5	44	34102	34121	746
547502	2006	2025	TCAGGTTGTAAAAATTGCCT	5-10-5	64	34105	34124	747
546369	2007	2026	CTCAGGTTGTAAAAATTGCC	5-10-5	51	34106	34125	748
547503	2008	2027	ACTCAGGTTGTAAAAATTGC	5-10-5	66	34107	34126	749
547504	2010	2029	GAACTCAGGTTGTAAAAATT	5-10-5	37	34109	34128	750
546370	2014	2033	ACTTGAACCTCAGGTTGTAAA	5-10-5	34	34113	34132	751
547505	2015	2034	GACTTGAACCTCAGGTTGTAA	5-10-5	69	34114	34133	752
546372	2021	2040	GAATTTGACTTGAACCTCAGG	5-10-5	49	34120	34139	753
546373	2025	2044	CTCAGAATTTGACTTGAACCT	5-10-5	59	34124	34143	754
547506	2028	2047	AGGCTCAGAATTTGACTTGA	5-10-5	78	34127	34146	755
547507	2029	2048	CAGGCTCAGAATTTGACTTG	5-10-5	56	34128	34147	756
546374	2030	2049	CCAGGCTCAGAATTTGACTT	5-10-5	50	34129	34148	757
547508	2032	2051	CCCCAGGCTCAGAATTTGAC	5-10-5	69	34131	34150	758
547509	2034	2053	CCCCCAGGCTCAGAATTTG	5-10-5	58	34133	34152	759
546375	2036	2055	GACCCCCAGGCTCAGAATT	5-10-5	48	34135	34154	760
547510	2041	2060	ATGAGGACCCCCCAGGCTCA	5-10-5	40	34140	34159	761
547511	2042	2061	GATGAGGACCCCCCAGGCTC	5-10-5	53	34141	34160	762
547512	2045	2064	GCAGATGAGGACCCCCCAGG	5-10-5	74	34144	34163	763
547513	2046	2065	TGCAGATGAGGACCCCCCAG	5-10-5	72	34145	34164	764
546378	2048	2067	TTTGCAGATGAGGACCCCCC	5-10-5	79	34147	34166	765
546379	2056	2075	CTCCATGCTTTGCAGATGAG	5-10-5	69	34155	34174	766

546380	2062	2081	GCCACTCTCCATGCTTTGCA	5-10-5	81	34161	34180	767
547514	2066	2085	AGATGCCACTCTCCATGCTT	5-10-5	85	34165	34184	768
546381	2068	2087	GAAGATGCCACTCTCCATGC	5-10-5	73	34167	34186	769
547515	2069	2088	AGAAGATGCCACTCTCCATG	5-10-5	58	34168	34187	770
546382	2072	2091	CAAAGAAGATGCCACTCTCC	5-10-5	58	34171	34190	771
547516	2076	2095	GATGCAAAGAAGATGCCACT	5-10-5	48	34175	34194	772
546383	2077	2096	GGATGCAAAGAAGATGCCAC	5-10-5	57	34176	34195	773
547517	2079	2098	TAGGATGCAAAGAAGATGCC	5-10-5	57	34178	34197	774
547518	2083	2102	TCCTTAGGATGCAAAGAAGA	5-10-5	51	34182	34201	775
546384	2085	2104	CGTCCTTAGGATGCAAAGAA	5-10-5	81	34184	34203	776
546385	2120	2139	ATTGTCCTCAGCAGCTCTGA	5-10-5	67	34219	34238	777
547519	n/a	n/a	CCAGACATTGTCCTCAGCAG	5-10-5	76	34225	34244	778
546386	n/a	n/a	AGCCAGACATTGTCCTCAGC	5-10-5	78	34227	34246	779
547520	n/a	n/a	TCAGCCAGACATTGTCCTCA	5-10-5	76	34229	34248	780
547521	n/a	n/a	CTTCAGCCAGACATTGTCCT	5-10-5	58	34231	34250	781
546387	n/a	n/a	AGCGGGCTTCAGCCAGACAT	5-10-5	77	34237	34256	782
547522	n/a	n/a	GAAAGCGGGCTTCAGCCAGA	5-10-5	73	34240	34259	783
546388	n/a	n/a	CTGAAAGCGGGCTTCAGCCA	5-10-5	71	34242	34261	784
546389	2147	2166	CGTGCTGAAAGCGGGCTTCA	5-10-5	71	34246	34265	785
546390	2165	2184	GTCAGCCCCTGGTTACGGCG	5-10-5	70	34264	34283	786
547523	2167	2186	TTGTCAGCCCCTGGTTACGG	5-10-5	69	34266	34285	787
547524	2169	2188	CATTGTCAGCCCCTGGTTAC	5-10-5	58	34268	34287	788
546391	2170	2189	GCATTGTCAGCCCCTGGTTA	5-10-5	54	34269	34288	789
547525	2174	2193	CCTCGCATTGTCAGCCCCTG	5-10-5	78	34273	34292	790
546392	2176	2195	GACCTCGCATTGTCAGCCCC	5-10-5	72	34275	34294	791
547526	2178	2197	GCGACCTCGCATTGTCAGCC	5-10-5	59	34277	34296	792
547527	2185	2204	CTCAGTTGCGACCTCGCATT	5-10-5	58	34284	34303	793
546393	2186	2205	TCTCAGTTGCGACCTCGCAT	5-10-5	77	34285	34304	794
546394	2196	2215	GTCATGGAGATCTCAGTTGC	5-10-5	71	34295	34314	795
547528	2200	2219	CACAGTCATGGAGATCTCAG	5-10-5	78	34299	34318	796

Table 12

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	90	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	

						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546403	n/a	n/a	CCATGAACATCCTATCCGTG	5-10-5	83	3282	3301	797
546406	n/a	n/a	TGTCCTGTCAACATATTCCA	5-10-5	80	3299	3318	798
546409	n/a	n/a	GGGTTTCTGCCAACAGTTTC	5-10-5	77	3326	3345	799
546410	n/a	n/a	GACTTTGGGTTTCTGCCAAC	5-10-5	83	3332	3351	800
546411	n/a	n/a	ATATTGACTTTGGGTTTCTG	5-10-5	56	3337	3356	801
546412	n/a	n/a	GGCTTCAATATTGACTTTGG	5-10-5	84	3344	3363	802
546416	n/a	n/a	CTGCAGGCAATATTTTGCTT	5-10-5	62	3364	3383	803
546418	n/a	n/a	ATGTGGCACTGCAGGCAATA	5-10-5	72	3372	3391	804
546419	n/a	n/a	TTCTAATGTGGCACTGCAGG	5-10-5	65	3377	3396	805
546421	n/a	n/a	TCAAGCTGTTCTAATGTGGC	5-10-5	71	3385	3404	806
546422	n/a	n/a	ACGGTCTTCAAGCTGTTCTA	5-10-5	72	3392	3411	807
546425	n/a	n/a	GGTCAATCTGACTAGTGAAT	5-10-5	69	2284	2303	808
546426	n/a	n/a	TCTCTGGTCAATCTGACTAG	5-10-5	49	2289	2308	809
546429	n/a	n/a	GCCCACCAACAATCTCTGGT	5-10-5	84	2301	2320	810
546432	n/a	n/a	GACCCCAACAGACAGCCAC	5-10-5	62	2315	2334	811
546444	n/a	n/a	CCAGAATCATGCCTTGTGGG	5-10-5	61	4765	4784	812
546447	n/a	n/a	GTCACCATAGACCCAGAATC	5-10-5	68	4777	4796	813
546450	n/a	n/a	GTGGCCCTCTTAAGTCACCA	5-10-5	73	4790	4809	814
546453	n/a	n/a	CTCATTGTTGTGTGGCCCTC	5-10-5	82	4801	4820	815
546459	n/a	n/a	GTAGCCATACATCTGAGGAA	5-10-5	46	4830	4849	816
546461	n/a	n/a	ATGTTTATTGTAGCCATACA	5-10-5	53	4839	4858	817
546492	n/a	n/a	CTCGCCTTTGTGACTCGATT	5-10-5	61	26263	26282	818
546493	n/a	n/a	CATACTCGCCTTTGTGACTC	5-10-5	35	26267	26286	819
546494	n/a	n/a	GCATACTCGCCTTTGTGACT	5-10-5	67	26268	26287	820
546495	n/a	n/a	TGCATACTCGCCTTTGTGAC	5-10-5	65	26269	26288	821
546395	2209	2228	TTCACAACACACAGTCATGG	5-10-5	72	34308	34327	822
546397	2233	2252	TTTTTTGATCTTTCACCATT	5-10-5	55	n/a	n/a	823
546496	n/a	n/a	ATGCATACTCGCCTTTGTGA	5-10-5	54	26270	26289	824
						26301	26320	
546497	n/a	n/a	CATGCATACTCGCCTTTGTG	5-10-5	56	26271	26290	825
						26302	26321	

546498	n/a	n/a	CCATGCATACTCGCCTTTGT	5-10-5	65	26272 26303	26291 26322	826
547529	2203	2222	ACACACAGTCATGGAGATCT	5-10-5	49	34302	34321	827
547530	2206	2225	ACAACACACAGTCATGGAGA	5-10-5	63	34305	34324	828
547531	2213	2232	TTATTTACAAACACACAGTC	5-10-5	69	34312	34331	829
546499	n/a	n/a	TCCATGCATACTCGCCTTTG	5-10-5	20	26273	26292	830
546500	n/a	n/a	TTCCATGCATACTCGCCTTT	5-10-5	46	26274	26293	831
546501	n/a	n/a	TTTCCATGCATACTCGCCTT	5-10-5	53	26275	26294	832
546502	n/a	n/a	GATTTTCCATGCATACTCGC	5-10-5	37	26278	26297	833
546503	n/a	n/a	GTGATGCGATTTTCCATGCA	5-10-5	53	26285	26304	834
546508	n/a	n/a	GCAGCAAGTGCTCCCCATGC	5-10-5	43	26317	26336	835
546511	n/a	n/a	GTGATGAAAGTACAGCAGCA	5-10-5	50	26331	26350	836
546683	n/a	n/a	TCCTATCCGTGTTTACAGCTGT	5-10-5	69	3273	3292	837
546684	n/a	n/a	TACTCTCTACATACTCAGGA	5-10-5	71	3561	3580	838
546687	n/a	n/a	TGAGACCTCCAGACTACTGT	5-10-5	76	3847	3866	839
546690	n/a	n/a	CTCTGCTGGTTTTAGACCAC	5-10-5	44	4027	4046	840
546695	n/a	n/a	GGGACAATCTCCACCCCGA	5-10-5	36	4225	4244	841
546698	n/a	n/a	TGCAGAGTGTCATCTGCGAA	5-10-5	59	4387	4406	842
546700	n/a	n/a	TGGTTCCCTAGCGGTCCAGA	5-10-5	78	4561	4580	843
546705	n/a	n/a	CCCCTGTAGTTGGCTGTGGT	5-10-5	66	5046	5065	844
546707	n/a	n/a	GCAAGTCAAAGAGTGTCAC	5-10-5	73	5283	5302	845
546710	n/a	n/a	GAAGCCTGTTAGAGTTGGCC	5-10-5	73	5576	5595	846
546719	n/a	n/a	CCCCCATGTCCATGGACTTT	5-10-5	55	6329	6348	847
547532	n/a	n/a	CTGCCAACAGTTTCAACTTT	5-10-5	65	3320	3339	848
547533	n/a	n/a	TTTTGCTTGGCTTCAATATT	5-10-5	23	3352	3371	849
547534	n/a	n/a	ATCTGACTAGTGAATGGCTT	5-10-5	72	2279	2298	850
547535	n/a	n/a	AGACAGCCCACCAACAATCT	5-10-5	28	2306	2325	851
547536	n/a	n/a	TGCATAGACCCCAACAGACA	5-10-5	48	2321	2340	852
547537	n/a	n/a	CCTGTGCATAGACCCCAACA	5-10-5	65	2325	2344	853
547538	n/a	n/a	CCAGCAGAAATCCTGTGCAT	5-10-5	77	2336	2355	854
547539	n/a	n/a	AGAACTCCAGCAGAAATCCT	5-10-5	43	2342	2361	855
547540	n/a	n/a	TTGTGTGGCCCTCTTAAGTC	5-10-5	44	4794	4813	856
547541	n/a	n/a	TATAGATGTTTATTGTAGCC	5-10-5	36	4844	4863	857
547542	n/a	n/a	ATACTCGCCTTTGTGACTCG	5-10-5	35	26266	26285	858
547543	n/a	n/a	TTTTCCATGCATACTCGCCT	5-10-5	54	26276	26295	859
547544	n/a	n/a	TCGCCTTTGTGATGCGATTT	5-10-5	15	26293	26312	860
547545	n/a	n/a	ATACTCGCCTTTGTGATGCG	5-10-5	43	26297	26316	861
547546	n/a	n/a	CATACTCGCCTTTGTGATGC	5-10-5	11	26298	26317	862
547547	n/a	n/a	GCATACTCGCCTTTGTGATG	5-10-5	42	26299	26318	863
547548	n/a	n/a	TGCATACTCGCCTTTGTGAT	5-10-5	61	26300	26319	864
547549	n/a	n/a	CCCATGCATACTCGCCTTTG	5-10-5	36	26304	26323	865
547550	n/a	n/a	CCCCATGCATACTCGCCTTT	5-10-5	53	26305	26324	866

547551	n/a	n/a	TCCCCATGCATACTCGCCTT	5-10-5	38	26306	26325	867
547552	n/a	n/a	CTCCCCATGCATACTCGCCT	5-10-5	53	26307	26326	868
547553	n/a	n/a	TGCTCCCCATGCATACTCGC	5-10-5	64	26309	26328	869
547554	n/a	n/a	GCTCTGATTGGGTCACCACA	5-10-5	50	5743	5762	870
547555	n/a	n/a	TGTCTCCTTCCACTTGCTCC	5-10-5	58	5923	5942	871
547556	n/a	n/a	GCCATTTTATCCCTGAGATT	5-10-5	55	6130	6149	872
547557	n/a	n/a	CTGTGCTGTATTTTGGAGCC	5-10-5	59	6413	6432	873

Table 13

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	85	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546732	n/a	n/a	GGATTTGGCCCTGAGCCCCA	5-10-5	14	6933	6952	874
546735	n/a	n/a	CAACCTGTCCATTCCCTGGG	5-10-5	46	7082	7101	875
546739	n/a	n/a	ATTCGGTGTCTTTACTGGCT	5-10-5	89	7228	7247	876
546746	n/a	n/a	TCCTGTTGCCTGACATGCTA	5-10-5	65	7694	7713	877
546747	n/a	n/a	CTCCCACTGACTGACTACTC	5-10-5	64	7904	7923	878
546749	n/a	n/a	GCTGGTCCTTGAACCCCGTG	5-10-5	53	8259	8278	879
546753	n/a	n/a	CTGGCTCACTATAGGCCCCA	5-10-5	91	8655	8674	880
546756	n/a	n/a	ATAAGCATCTCTCTGACCTA	5-10-5	47	9105	9124	881
546763	n/a	n/a	GCTTCCCCAATACTTGCTGG	5-10-5	84	9695	9714	882
546765	n/a	n/a	GTGTCCAGAATACTGCCCCA	5-10-5	82	10053	10072	883
546770	n/a	n/a	GTGGACGACTGCCCTGTGCC	5-10-5	74	10435	10454	884
546773	n/a	n/a	TCTCTAGCATCCTAGTCCTC	5-10-5	67	10586	10605	885

546780	n/a	n/a	ATACTGGCTAAGTCAGGCC	5-10-5	83	10982	11001	886
546784	n/a	n/a	GGCAGGGAGGTGGATTATTC	5-10-5	58	11440	11459	887
546789	n/a	n/a	GCTTCTCTATCTCCCAGTGT	5-10-5	79	12228	12247	888
546791	n/a	n/a	GATGCATGCAGCAATACAGG	5-10-5	52	12385	12404	889
546795	n/a	n/a	GTCTCGATGGCAAGCTGTAC	5-10-5	72	12650	12669	890
546796	n/a	n/a	GTACTCACCGGTACTCTGCC	5-10-5	82	12804	12823	891
546799	n/a	n/a	ATGAAGGGCGAGGCGCAGTG	5-10-5	5	13258	13277	892
546803	n/a	n/a	CCCCATACATCTATGCAAAT	5-10-5	40	13551	13570	893
546804	n/a	n/a	ACATGACTCCAGTGATGGAT	5-10-5	57	13632	13651	894
546808	n/a	n/a	AAAATGACACCAAATTCGC	5-10-5	0	13841	13860	895
546811	n/a	n/a	TGGACATCCTTCCCCTCGCA	5-10-5	49	13967	13986	896
546817	n/a	n/a	GCTCTGAGCCTTCGCCTCT	5-10-5	77	14472	14491	897
546822	n/a	n/a	ACTAGTTTCCTATAACTGCT	5-10-5	32	14735	14754	898
546823	n/a	n/a	TACTAGTTTCCTATAACTGC	5-10-5	44	14736	14755	899
546824	n/a	n/a	GTACTAGTTTCCTATAACTG	5-10-5	79	14737	14756	900
546825	n/a	n/a	GTATCACTGTACTAGTTTCC	5-10-5	96	14745	14764	901
						14816	14835	
						14887	14906	
						14946	14965	
						15006	15025	
						15078	15097	
						15221	15240	
						15293	15312	
						15352	15371	
						15412	15431	
						15484	15503	
						15556	15575	
						15614	15633	
						15686	15705	
546826	n/a	n/a	AGTATCACTGTACTAGTTTC	5-10-5	90	15816	15835	902
						15888	15907	
						15946	15965	
						14746	14765	
						14817	14836	
						14888	14907	
						14947	14966	
						15007	15026	
						15079	15098	
						15222	15241	
						15294	15313	
						15353	15372	
						15413	15432	

						15485	15504	
						15557	15576	
						15615	15634	
						15687	15706	
						15817	15836	
						15889	15908	
						15947	15966	
546827	n/a	n/a	CAGTATCACTGTACTAGTTT	5-10-5	98	14747	14766	903
						14818	14837	
						14889	14908	
						14948	14967	
						15008	15027	
						15080	15099	
						15152	15171	
						15223	15242	
						15295	15314	
						15354	15373	
						15414	15433	
						15486	15505	
						15558	15577	
						15616	15635	
						15688	15707	
						15818	15837	
546828	n/a	n/a	ACAGTATCACTGTACTAGTT	5-10-5	95	15890	15909	904
						15948	15967	
						14748	14767	
						14819	14838	
						14890	14909	
						14949	14968	
						15009	15028	
						15081	15100	
						15153	15172	
						15224	15243	
						15296	15315	
						15355	15374	
						15415	15434	
						15487	15506	
						15559	15578	
						15617	15636	
						15689	15708	
						15819	15838	
						15891	15910	

						15949	15968	
546829	n/a	n/a	AACAGTATCACTGTACTAGT	5-10-5	94	14749	14768	905
						14820	14839	
						14891	14910	
						14950	14969	
						15010	15029	
						15082	15101	
						15154	15173	
						15225	15244	
						15297	15316	
						15356	15375	
						15416	15435	
						15488	15507	
						15560	15579	
						15618	15637	
						15690	15709	
						15820	15839	
						15892	15911	
						15950	15969	
546830	n/a	n/a	TAACAGTATCACTGTACTAG	5-10-5	78	14750	14769	906
						14821	14840	
						14892	14911	
						14951	14970	
						15011	15030	
						15083	15102	
						15155	15174	
						15226	15245	
						15298	15317	
						15357	15376	
						15417	15436	
						15489	15508	
						15561	15580	
						15619	15638	
						15691	15710	
						15821	15840	
						15893	15912	
						15951	15970	
546831	n/a	n/a	TCTAACAGTATCACTGTACT	5-10-5	79	14752	14771	907
						14823	14842	
						14894	14913	
						15013	15032	
						15085	15104	

						15228	15247	
						15300	15319	
						15419	15438	
						15491	15510	
						15621	15640	
						15823	15842	
						15953	15972	
546832	n/a	n/a	CTCTAACAGTATCACTGTAC	5-10-5	88	14753	14772	908
						14824	14843	
						14895	14914	
						15014	15033	
						15086	15105	
						15229	15248	
						15301	15320	
						15420	15439	
						15492	15511	
						15622	15641	
						15824	15843	
						15954	15973	
546833	n/a	n/a	ACTCTAACAGTATCACTGTA	5-10-5	90	14754	14773	909
						14825	14844	
						14896	14915	
						15015	15034	
						15087	15106	
						15230	15249	
						15302	15321	
						15421	15440	
						15493	15512	
						15623	15642	
						15825	15844	
						15955	15974	
546834	n/a	n/a	AACTCTAACAGTATCACTGT	5-10-5	86	14755	14774	910
						14826	14845	
						14897	14916	
						15016	15035	
						15088	15107	
						15231	15250	
						15303	15322	
						15422	15441	
						15494	15513	
						15624	15643	
						15826	15845	

						15956	15975	
546835	n/a	n/a	TAACTCTAACAGTATCACTG	5-10-5	86	14756	14775	911
						14827	14846	
						14898	14917	
						15017	15036	
						15089	15108	
						15232	15251	
						15304	15323	
						15423	15442	
						15495	15514	
						15625	15644	
						15827	15846	
						15957	15976	
546836	n/a	n/a	ATAACTCTAACAGTATCACT	5-10-5	30	14757	14776	912
						14828	14847	
						14899	14918	
						15018	15037	
						15090	15109	
						15233	15252	
						15305	15324	
						15424	15443	
						15496	15515	
						15626	15645	
						15828	15847	
						15958	15977	
546837	n/a	n/a	TATAACTCTAACAGTATCAC	5-10-5	0	14758	14777	913
						14829	14848	
						14900	14919	
						15019	15038	
						15091	15110	
						15234	15253	
						15306	15325	
						15425	15444	
						15497	15516	
						15627	15646	
						15829	15848	
						15959	15978	
546838	n/a	n/a	CTATAACTCTAACAGTATCA	5-10-5	43	14759	14778	914
						14830	14849	
						14901	14920	
						15020	15039	
						15092	15111	

						15235	15254	
						15307	15326	
						15426	15445	
						15498	15517	
						15628	15647	
						15830	15849	
						15960	15979	
546839	n/a	n/a	CCTATAACTCTAACAGTATC	5-10-5	47	14760	14779	915
						14831	14850	
						14902	14921	
						15021	15040	
						15093	15112	
						15236	15255	
						15308	15327	
						15427	15446	
						15499	15518	
						15629	15648	
						15831	15850	
						15961	15980	
546840	n/a	n/a	CTGTCCTATAACTCTAACAG	5-10-5	53	14764	14783	916
						14835	14854	
546841	n/a	n/a	CACTGTCCTATAACTCTAAC	5-10-5	38	14766	14785	917
						14837	14856	
546842	n/a	n/a	TCACTGTCCTATAACTCTAA	5-10-5	54	14767	14786	918
						14838	14857	
546843	n/a	n/a	TATCACTGTCCTATAACTCT	5-10-5	52	14769	14788	919
						14840	14859	
546844	n/a	n/a	GTCCTATATCACTGTCCTAT	5-10-5	75	14775	14794	920
						14846	14865	
						15180	15199	
						15716	15735	
546845	n/a	n/a	TGTCTATATCACTGTCCTA	5-10-5	75	14776	14795	921
						14847	14866	
						15181	15200	
						15717	15736	
546846	n/a	n/a	CTGTCCTATATCACTGTCCT	5-10-5	95	14777	14796	922
						14848	14867	
						15182	15201	
						15718	15737	
546847	n/a	n/a	ACTGTCCTATATCACTGTCC	5-10-5	88	14778	14797	923
						14849	14868	
						15183	15202	

						15719	15738	
546848	n/a	n/a	TCACTGTCCTATATCACTGT	5-10-5	86	14780	14799	924
						14851	14870	
						14976	14995	
						15185	15204	
						15257	15276	
						15382	15401	
						15520	15539	
						15650	15669	
						15721	15740	
						15852	15871	
						15982	16001	
547558	n/a	n/a	CCCCCAGTTCCCATGCAAGG	5-10-5	52	6640	6659	925
547559	n/a	n/a	GAGCACAGATCTCTCAAGT	5-10-5	69	6822	6841	926
547560	n/a	n/a	GACGGTCACCCAGCCCTGAC	5-10-5	42	7459	7478	927
547561	n/a	n/a	AAGGGAAATTAGAGGCAGGC	5-10-5	57	7583	7602	928
547562	n/a	n/a	CTTTCTTGAGACAATCCCTT	5-10-5	59	8463	8482	929
547563	n/a	n/a	GTGGGATCAGAGAATGACTA	5-10-5	48	9267	9286	930
547564	n/a	n/a	CCCTCTGTCTTAGATGTCCA	5-10-5	94	9390	9409	931
547565	n/a	n/a	CTTATCAGTCCCAGTCATGT	5-10-5	63	10698	10717	932
547566	n/a	n/a	AAGAGTTGGGATGCGACTCT	5-10-5	76	11335	11354	933
547567	n/a	n/a	TCCACTCCTAAGAAGTATGG	5-10-5	60	11546	11565	934
547568	n/a	n/a	GCACCCTTTTCATTGAGATT	5-10-5	70	12070	12089	935
547569	n/a	n/a	ACTACCATTTGGGTTGGTAG	5-10-5	9	12571	12590	936
547570	n/a	n/a	AAGCCCTGTTTGGTTTTTAG	5-10-5	18	12900	12919	937
547571	n/a	n/a	AAATGACACCAAAATTGAGT	5-10-5	14	13744	13763	938
547572	n/a	n/a	AAATGACACCAAAATTCGCT	5-10-5	40	13840	13859	939
547573	n/a	n/a	TAAGCAAGGCCTATGTGTGG	5-10-5	2	13880	13899	940
547574	n/a	n/a	ACACGCACAGGTCCCAGGGC	5-10-5	51	14314	14333	941
547575	n/a	n/a	GGGAAACTCTTTCCTCGCCC	5-10-5	89	14583	14602	942
547576	n/a	n/a	CTAGTTTCCTATAACTGCTG	5-10-5	29	14734	14753	943
547577	n/a	n/a	CTAACAGTATCACTGTACTA	5-10-5	79	14751	14770	944
						14822	14841	
						14893	14912	
						15012	15031	
						15084	15103	
						15227	15246	
						15299	15318	
						15418	15437	
						15490	15509	
						15620	15639	
						15822	15841	

						15952	15971	
547578	n/a	n/a	GTCCTATAACTCTAACAGTA	5-10-5	30	14762	14781	945
						14833	14852	
547579	n/a	n/a	TGTCCTATAACTCTAACAGT	5-10-5	0	14763	14782	946
						14834	14853	
547580	n/a	n/a	ATCACTGTCCTATAACTCTA	5-10-5	61	14768	14787	947
						14839	14858	
547581	n/a	n/a	ATATCACTGTCCTATAACTC	5-10-5	60	14770	14789	948
						14841	14860	
547582	n/a	n/a	TATATCACTGTCCTATAACT	5-10-5	22	14771	14790	949
						14842	14861	
						15176	15195	
						15712	15731	
547583	n/a	n/a	CACTGTCCTATATCACTGTC	5-10-5	80	16160	16179	950
						14779	14798	
						14850	14869	
						15184	15203	
						15720	15739	

Table 14

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	85	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546849	n/a	n/a	ATCACTGTCCTATATCACTG	5-10-5	93	14781	14800	951

						14852	14871	
						14977	14996	
						15186	15205	
						15258	15277	
						15383	15402	
						15521	15540	
						15651	15670	
						15722	15741	
						15853	15872	
						15983	16002	
546850	n/a	n/a	TATCACTGTCCTATATCACT	5-10-5	80	14782	14801	952
						14853	14872	
						14978	14997	
						15116	15135	
						15187	15206	
						15259	15278	
						15384	15403	
						15522	15541	
						15652	15671	
						15723	15742	
						15854	15873	
						15984	16003	
546851	n/a	n/a	AGTATCACTGTCCTATATCA	5-10-5	81	14784	14803	953
						14980	14999	
						15118	15137	
						15386	15405	
						15524	15543	
						15986	16005	
546852	n/a	n/a	CAGTATCACTGTCCTATATC	5-10-5	94	14785	14804	954
						14981	15000	
						15119	15138	
						15387	15406	
						15525	15544	
						15987	16006	
546853	n/a	n/a	ACAGTATCACTGTCCTATAT	5-10-5	86	14786	14805	955
						14982	15001	
						15120	15139	
						15388	15407	
						15526	15545	
						15988	16007	
546854	n/a	n/a	TAACAGTATCACTGTCCTAT	5-10-5	90	14788	14807	956
						14984	15003	

						15050	15069	
						15122	15141	
						15390	15409	
						15456	15475	
						15528	15547	
						15990	16009	
546855	n/a	n/a	ATAACAGTATCACTGTCCTA	5-10-5	87	14789	14808	957
						14985	15004	
						15051	15070	
						15123	15142	
						15391	15410	
						15457	15476	
						15529	15548	
						15991	16010	
546856	n/a	n/a	AACTATAACAGTATCACTGT	5-10-5	54	14793	14812	958
						15055	15074	
						15127	15146	
						15160	15179	
						15461	15480	
						15533	15552	
						15566	15585	
						15696	15715	
						15898	15917	
						15995	16014	
546857	n/a	n/a	TATAACTATAACAGTATCAC	5-10-5	7	14796	14815	959
						15058	15077	
						15130	15149	
						15163	15182	
						15464	15483	
						15536	15555	
						15569	15588	
						15699	15718	
						15770	15789	
						15998	16017	
546858	n/a	n/a	CTATAACTATAACAGTATCA	5-10-5	21	14797	14816	960
						15059	15078	
						15131	15150	
						15164	15183	
						15465	15484	
						15537	15556	
						15570	15589	
						15700	15719	

						15771	15790	
						15999	16018	
546859	n/a	n/a	TTTCCTATAACTATAACAGT	5-10-5	7	14801	14820	961
						15063	15082	
						15469	15488	
						15541	15560	
546860	n/a	n/a	CTAGTTTCCTATAACTATAA	5-10-5	36	14805	14824	962
						14876	14895	
						14935	14954	
						15067	15086	
						15210	15229	
						15282	15301	
						15341	15360	
						15473	15492	
						15545	15564	
						15603	15622	
						15675	15694	
						15746	15765	
						15805	15824	
						15877	15896	
						15935	15954	
546861	n/a	n/a	TAACAATATCACTGTCCTAT	5-10-5	68	14859	14878	963
						15193	15212	
						15265	15284	
						15586	15605	
						15658	15677	
						15729	15748	
						15860	15879	
						16086	16105	
						16183	16202	
						16234	16253	
546862	n/a	n/a	AACTATAACAATATCACTGT	5-10-5	0	14864	14883	964
						14923	14942	
						15198	15217	
						15270	15289	
						15329	15348	
						15591	15610	
						15663	15682	
						15734	15753	
						15793	15812	
						15865	15884	
						15923	15942	

						16066	16085	
						16091	16110	
						16144	16163	
						16239	16258	
546863	n/a	n/a	TAACTATAACAATATCACTG	5-10-5	21	14865	14884	965
						14924	14943	
						15199	15218	
						15271	15290	
						15330	15349	
						15592	15611	
						15664	15683	
						15735	15754	
						15794	15813	
						15866	15885	
						15924	15943	
						16067	16086	
						16092	16111	
						16145	16164	
						16240	16259	
546864	n/a	n/a	ATAACTATAACAATATCACT	5-10-5	0	14866	14885	966
						14925	14944	
						15200	15219	
						15272	15291	
						15331	15350	
						15593	15612	
						15665	15684	
						15736	15755	
						15795	15814	
						15867	15886	
						15925	15944	
						16068	16087	
						16093	16112	
						16146	16165	
						16241	16260	
546865	n/a	n/a	TATAACTATAACAATATCAC	5-10-5	0	14867	14886	967
						14926	14945	
						15201	15220	
						15273	15292	
						15332	15351	
						15594	15613	
						15666	15685	
						15737	15756	

						15796	15815	
						15868	15887	
						15926	15945	
						16069	16088	
						16094	16113	
						16147	16166	
						16242	16261	
546866	n/a	n/a	GTTTCCTATAACTATAACAA	5-10-5	35	14873	14892	968
						14932	14951	
						15207	15226	
						15279	15298	
						15338	15357	
						15600	15619	
						15672	15691	
						15743	15762	
						15802	15821	
						15874	15893	
546867	n/a	n/a	ACCTATAACTCTAACAGTAT	5-10-5	40	15932	15951	969
						14903	14922	
						15022	15041	
						15094	15113	
						15237	15256	
						15309	15328	
						15428	15447	
						15500	15519	
						15630	15649	
						15832	15851	
546868	n/a	n/a	TACCTATAACTCTAACAGTA	5-10-5	51	15962	15981	970
						14904	14923	
						15023	15042	
						15095	15114	
						15238	15257	
						15310	15329	
						15429	15448	
						15501	15520	
						15631	15650	
						15833	15852	
546869	n/a	n/a	TGTACCTATAACTCTAACAG	5-10-5	53	15963	15982	971
						14906	14925	
						15025	15044	
						15240	15259	
						15312	15331	

						15431	15450	
						15503	15522	
						15633	15652	
						15835	15854	
						15965	15984	
546870	n/a	n/a	CTGTACCTATAACTCTAACA	5-10-5	87	14907	14926	972
						15026	15045	
						15241	15260	
						15313	15332	
						15432	15451	
						15504	15523	
						15634	15653	
						15836	15855	
						15966	15985	
546871	n/a	n/a	ACTGTACCTATAACTCTAAC	5-10-5	73	14908	14927	973
						15027	15046	
						15242	15261	
						15314	15333	
						15433	15452	
						15505	15524	
						15635	15654	
						15837	15856	
						15967	15986	
546872	n/a	n/a	CACTGTACCTATAACTCTAA	5-10-5	87	14909	14928	974
						15028	15047	
						15243	15262	
						15315	15334	
						15434	15453	
						15506	15525	
						15636	15655	
						15838	15857	
						15968	15987	
546873	n/a	n/a	CAATATCACTGTACCTATAA	5-10-5	34	14915	14934	975
						15321	15340	
						15785	15804	
546874	n/a	n/a	ATAACAATATCACTGTACCT	5-10-5	68	14919	14938	976
						15325	15344	
						15789	15808	
						16062	16081	
						16140	16159	
546875	n/a	n/a	ACTATAACAATATCACTGTA	5-10-5	33	14922	14941	977
						15328	15347	

						15792	15811	
						16065	16084	
						16143	16162	
546876	n/a	n/a	GTCCTATATCACTGTACCTG	5-10-5	87	14971	14990	978
546877	n/a	n/a	CACTGTCCTATATCACTGTA	5-10-5	88	14975	14994	979
						15256	15275	
						15381	15400	
						15519	15538	
						15649	15668	
						15851	15870	
						15981	16000	
546878	n/a	n/a	CCTATAACAGTATCACTGTC	5-10-5	81	14988	15007	980
						15394	15413	
546879	n/a	n/a	TTTCCTATAACAGTATCACT	5-10-5	42	14991	15010	981
						15397	15416	
546880	n/a	n/a	GTTTCCTATAACAGTATCAC	5-10-5	41	14992	15011	982
						15398	15417	
546881	n/a	n/a	AGTTTCCTATAACAGTATCA	5-10-5	49	14993	15012	983
						15399	15418	
546882	n/a	n/a	TAGTTTCCTATAACAGTATC	5-10-5	24	14994	15013	984
						15400	15419	
546883	n/a	n/a	CTAGTTTCCTATAACAGTAT	5-10-5	19	14995	15014	985
						15401	15420	
546884	n/a	n/a	ACTAGTTTCCTATAACAGTA	5-10-5	6	14996	15015	986
						15402	15421	
547584	n/a	n/a	GTATCACTGTCCTATATCAC	5-10-5	85	14783	14802	987
						14979	14998	
						15117	15136	
						15385	15404	
						15523	15542	
						15985	16004	
547585	n/a	n/a	AACAGTATCACTGTCCTATA	5-10-5	85	14787	14806	988
						14983	15002	
						15121	15140	
						15389	15408	
						15527	15546	
						15989	16008	
547586	n/a	n/a	TATAACAGTATCACTGTCCT	5-10-5	82	14790	14809	989
						14986	15005	
						15052	15071	
						15124	15143	
						15392	15411	

						15458	15477	
						15530	15549	
						15992	16011	
547587	n/a	n/a	CTATAACAGTATCACTGTCC	5-10-5	96	14791	14810	990
						14987	15006	
						15053	15072	
						15125	15144	
						15393	15412	
						15459	15478	
						15531	15550	
						15993	16012	
547588	n/a	n/a	ACTATAACAGTATCACTGTC	5-10-5	83	14792	14811	991
						15054	15073	
						15126	15145	
						15460	15479	
						15532	15551	
						15994	16013	
547589	n/a	n/a	TAACTATAACAGTATCACTG	5-10-5	36	14794	14813	992
						15056	15075	
						15128	15147	
						15161	15180	
						15462	15481	
						15534	15553	
						15567	15586	
						15697	15716	
						15996	16015	
547590	n/a	n/a	ATAACTATAACAGTATCACT	5-10-5	0	14795	14814	993
						15057	15076	
						15129	15148	
						15162	15181	
						15463	15482	
						15535	15554	
						15568	15587	
						15698	15717	
						15997	16016	
547591	n/a	n/a	CCTATAACTATAACAGTATC	5-10-5	23	14798	14817	994
						15060	15079	
						15165	15184	
						15466	15485	
						15538	15557	
						15571	15590	
						15701	15720	

						15772	15791	
						16000	16019	
547592	n/a	n/a	TCCTATAACTATAACAGTAT	5-10-5	27	14799	14818	995
						15061	15080	
						15166	15185	
						15467	15486	
						15539	15558	
						15572	15591	
						15702	15721	
						16001	16020	
547593	n/a	n/a	TTCCTATAACTATAACAGTA	5-10-5	29	14800	14819	996
						15062	15081	
						15468	15487	
						15540	15559	
547594	n/a	n/a	GTTTCCTATAACTATAACAG	5-10-5	19	14802	14821	997
						15064	15083	
						15470	15489	
						15542	15561	
547595	n/a	n/a	ACTAGTTTCCTATAACTATA	5-10-5	21	14806	14825	998
						14877	14896	
						14936	14955	
						15068	15087	
						15211	15230	
						15283	15302	
						15342	15361	
						15474	15493	
						15546	15565	
						15604	15623	
						15676	15695	
						15747	15766	
						15806	15825	
						15878	15897	
						15936	15955	
547596	n/a	n/a	TACTAGTTTCCTATAACTAT	5-10-5	14	14807	14826	999
						14878	14897	
						14937	14956	
						15069	15088	
						15212	15231	
						15284	15303	
						15343	15362	
						15475	15494	
						15547	15566	

						15605	15624	
						15677	15696	
						15748	15767	
						15807	15826	
						15879	15898	
						15937	15956	
547597	n/a	n/a	CAATATCACTGTCCTATATC	5-10-5	29	14856	14875	1000
						15190	15209	
						15262	15281	
						15655	15674	
						15726	15745	
						15857	15876	
547598	n/a	n/a	ACTATAACAATATCACTGTC	5-10-5	59	14863	14882	1001
						15197	15216	
						15269	15288	
						15590	15609	
						15662	15681	
						15733	15752	
						15864	15883	
						15922	15941	
						16090	16109	
						16238	16257	
547599	n/a	n/a	TTCCTATAACTATAACAATA	5-10-5	4	14871	14890	1002
						14930	14949	
						15205	15224	
						15277	15296	
						15336	15355	
						15598	15617	
						15670	15689	
						15741	15760	
						15800	15819	
						15872	15891	
						15930	15949	
547600	n/a	n/a	TTTCCTATAACTATAACAAT	5-10-5	26	14872	14891	1003
						14931	14950	
						15206	15225	
						15278	15297	
						15337	15356	
						15599	15618	
						15671	15690	
						15742	15761	
						15801	15820	

						15873	15892	
						15931	15950	
547601	n/a	n/a	GTACCTATAACTCTAACAGT	5-10-5	75	14905	14924	1004
						15024	15043	
						15239	15258	
						15311	15330	
						15430	15449	
						15502	15521	
						15632	15651	
						15834	15853	
						15964	15983	
547602	n/a	n/a	TCACTGTACCTATAACTCTA	5-10-5	93	14910	14929	1005
						15029	15048	
						15244	15263	
						15316	15335	
						15435	15454	
						15507	15526	
						15637	15656	
						15839	15858	
						15969	15988	
547603	n/a	n/a	TATCACTGTACCTATAACTC	5-10-5	41	14912	14931	1006
						15246	15265	
						15318	15337	
						15509	15528	
						15639	15658	
						15841	15860	
						15971	15990	
547604	n/a	n/a	ATATCACTGTACCTATAACT	5-10-5	0	14913	14932	1007
						15247	15266	
						15319	15338	
						15510	15529	
						15640	15659	
						15783	15802	
						15842	15861	
						15972	15991	
547605	n/a	n/a	ACAATATCACTGTACCTATA	5-10-5	43	14916	14935	1008
						15322	15341	
						15786	15805	
						16137	16156	
547606	n/a	n/a	AACAATATCACTGTACCTAT	5-10-5	43	14917	14936	1009
						15323	15342	
						15787	15806	

						16138	16157	
547607	n/a	n/a	TAACAATATCACTGTACCTA	5-10-5	49	14918	14937	1010
						15324	15343	
						15788	15807	
						16139	16158	
547608	n/a	n/a	TATAACAATATCACTGTACC	5-10-5	35	14920	14939	1011
						15326	15345	
						15790	15809	
						16063	16082	
547609	n/a	n/a	CTATAACAATATCACTGTAC	5-10-5	23	16141	16160	1012
						14921	14940	
						15327	15346	
						15791	15810	
547610	n/a	n/a	TGTAACAGTATCACTGTACT	5-10-5	45	16064	16083	1013
547611	n/a	n/a	CTGTAACAGTATCACTGTAC	5-10-5	71	16142	16161	1014
547612	n/a	n/a	CCTGTAACAGTATCACTGTA	5-10-5	68	14953	14972	1015
547613	n/a	n/a	CTATATCACTGTACCTGTAA	5-10-5	39	14954	14973	1016
547614	n/a	n/a	CCTATATCACTGTACCTGTA	5-10-5	81	14955	14974	1017
547615	n/a	n/a	TCCTATATCACTGTACCTGT	5-10-5	84	14968	14987	1018
547616	n/a	n/a	TGTCCTATATCACTGTACCT	5-10-5	86	14970	14989	1019
						14972	14991	
						15253	15272	
						15378	15397	
						15516	15535	
						15646	15665	
547617	n/a	n/a	CTGTCCTATATCACTGTACC	5-10-5	91	15848	15867	1020
						15978	15997	
						14973	14992	
						15254	15273	
						15379	15398	
						15517	15536	
547618	n/a	n/a	ACTGTCCTATATCACTGTAC	5-10-5	87	15647	15666	1021
						15849	15868	
						15979	15998	
						14974	14993	
						15255	15274	
						15380	15399	
547618	n/a	n/a	ACTGTCCTATATCACTGTAC	5-10-5	87	15518	15537	1021
						15648	15667	
						15850	15869	
						15980	15999	

547619	n/a	n/a	TCCTATAACAGTATCACTGT	5-10-5	70	14989	15008	1022
						15395	15414	
547620	n/a	n/a	TTCCTATAACAGTATCACTG	5-10-5	65	14990	15009	1023
						15396	15415	
547621	n/a	n/a	TACTAGTTTCCTATAACAGT	5-10-5	12	14997	15016	1024
						15403	15422	
547622	n/a	n/a	GTCACGTGTACCTATAACTCT	5-10-5	88	15030	15049	1025
						15436	15455	
547623	n/a	n/a	TGTCACGTGTACCTATAACTC	5-10-5	81	15031	15050	1026
						15437	15456	
547624	n/a	n/a	ATGTCACGTGTACCTATAACT	5-10-5	64	15032	15051	1027
						15438	15457	

Table 15

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	% inhibition	Motif	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	93	5-10-5	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546885	n/a	n/a	TATGTCACGTGTACCTATAAC	46	5-10-5	15033	15052	1028
						15439	15458	
546886	n/a	n/a	CTATGTCACGTGTACCTATAA	80	5-10-5	15034	15053	1029
						15440	15459	
546887	n/a	n/a	CCTATGTCACGTGTACCTATA	82	5-10-5	15035	15054	1030
						15441	15460	
546888	n/a	n/a	TCCTATGTCACGTGTACCTAT	78	5-10-5	15036	15055	1031

						15442	15461	
546889	n/a	n/a	GTCCTATGTCACGTGTACCTA	93	5-10-5	15037	15056	1032
						15443	15462	
546890	n/a	n/a	TGTCCTATGTCACGTGTACCT	78	5-10-5	15038	15057	1033
						15444	15463	
546891	n/a	n/a	CTGTCCTATGTCACGTGTACC	81	5-10-5	15039	15058	1034
						15445	15464	
546892	n/a	n/a	ACTGTCCTATGTCACGTGTAC	82	5-10-5	15040	15059	1035
						15446	15465	
546893	n/a	n/a	CACTGTCCTATGTCACGTGTA	70	5-10-5	15041	15060	1036
						15447	15466	
546894	n/a	n/a	TCACTGTCCTATGTCACGTGT	91	5-10-5	15042	15061	1037
						15448	15467	
546895	n/a	n/a	TATCACTGTCCTATGTCACGT	77	5-10-5	15044	15063	1038
						15450	15469	
546896	n/a	n/a	GTATCACTGTCCTATGTCAC	75	5-10-5	15045	15064	1039
						15451	15470	
546897	n/a	n/a	AGTATCACTGTCCTATGTCA	90	5-10-5	15046	15065	1040
						15452	15471	
546898	n/a	n/a	AACAGTATCACTGTCCTATG	91	5-10-5	15049	15068	1041
						15455	15474	
546899	n/a	n/a	CTACCTATAACTCTAACAGT	27	5-10-5	15096	15115	1042
546901	n/a	n/a	ACTGTCCTATAACTATAACA	56	5-10-5	15170	15189	1043
						15576	15595	
						15706	15725	
						16005	16024	
						16076	16095	
						16101	16120	
546902	n/a	n/a	CACTGTCCTATAACTATAAC	71	5-10-5	16154	16173	1044
						15171	15190	
						15577	15596	
						15707	15726	
						16006	16025	
						16077	16096	
546903	n/a	n/a	CCTATATCACTGTACCTATA	91	5-10-5	16102	16121	1045
						16155	16174	
						15250	15269	
						15375	15394	
						15513	15532	
						15643	15662	
						15845	15864	
						15975	15994	

546904	n/a	n/a	TCCTATATCACTGTACCTAT	80	5-10-5	15251	15270	1046
						15376	15395	
						15514	15533	
						15644	15663	
						15846	15865	
						15976	15995	
546905	n/a	n/a	TACCTATAACAGTATCACTG	65	5-10-5	15363	15382	1047
546907	n/a	n/a	ATAACTATAACAGTATCACC	37	5-10-5	15769	15788	1048
546908	n/a	n/a	TCACTGTACCTATAACTATA	77	5-10-5	15780	15799	1049
						16252	16271	
546909	n/a	n/a	AACAATATCACTGTACCTTT	44	5-10-5	16060	16079	1050
546910	n/a	n/a	TAACAATATCACTGTACCTT	82	5-10-5	16061	16080	1051
546911	n/a	n/a	GTCCTATAACTATAACAATA	52	5-10-5	16073	16092	1052
						16098	16117	
						16151	16170	
547625	n/a	n/a	CAGTATCACTGTCCTATGTC	79	5-10-5	15047	15066	1053
						15453	15472	
547626	n/a	n/a	ACAGTATCACTGTCCTATGT	91	5-10-5	15048	15067	1054
						15454	15473	
547627	n/a	n/a	TCTACCTATAACTCTAACAG	71	5-10-5	15097	15116	1055
547628	n/a	n/a	CTCTACCTATAACTCTAACA	34	5-10-5	15098	15117	1056
547629	n/a	n/a	ACTCTACCTATAACTCTAAC	0	5-10-5	15099	15118	1057
547630	n/a	n/a	ACTGTCCTATATCACTCTAC	76	5-10-5	15112	15131	1058
547631	n/a	n/a	CACTGTCCTATATCACTCTA	85	5-10-5	15113	15132	1059
547632	n/a	n/a	TCACTGTCCTATATCACTCT	87	5-10-5	15114	15133	1060
547633	n/a	n/a	ATCACTGTCCTATATCACTC	87	5-10-5	15115	15134	1061
547634	n/a	n/a	ATCACTGTACTAGTTTTCTA	72	5-10-5	15148	15167	1062
547635	n/a	n/a	TATCACTGTACTAGTTTTCT	53	5-10-5	15149	15168	1063
547636	n/a	n/a	GTATCACTGTACTAGTTTTCT	86	5-10-5	15150	15169	1064
547637	n/a	n/a	AGTATCACTGTACTAGTTTT	88	5-10-5	15151	15170	1065
547638	n/a	n/a	ATAACAGTATCACTGTACTA	87	5-10-5	15156	15175	1066
						15358	15377	
						15562	15581	
						15692	15711	
						15894	15913	
547639	n/a	n/a	GTCCTATAACTATAACAGTA	72	5-10-5	15167	15186	1067
						15573	15592	
						15703	15722	
						16002	16021	
547640	n/a	n/a	TGTCCTATAACTATAACAGT	13	5-10-5	15168	15187	1068
						15574	15593	
						15704	15723	

						16003	16022	
547641	n/a	n/a	CTGTCCTATAACTATAACAG	43	5-10-5	15169	15188	1069
						15575	15594	
						15705	15724	
						16004	16023	
547642	n/a	n/a	TCACTGTCCTATAACTATAA	72	5-10-5	15172	15191	1070
						15578	15597	
						15708	15727	
						16007	16026	
						16078	16097	
						16103	16122	
547643	n/a	n/a	ATCACTGTCCTATAACTATA	72	5-10-5	16156	16175	1071
						15173	15192	
						15579	15598	
						15709	15728	
						16008	16027	
						16079	16098	
						16104	16123	
547644	n/a	n/a	TATCACTGTCCTATAACTAT	51	5-10-5	16157	16176	1072
						16176	16195	
						15174	15193	
						15580	15599	
						15710	15729	
						16009	16028	
						16080	16099	
						16158	16177	
547645	n/a	n/a	ATATCACTGTCCTATAACTA	60	5-10-5	16177	16196	1073
						16228	16247	
						15175	15194	
						15581	15600	
						15711	15730	
						16010	16029	
						16081	16100	
						16159	16178	
547646	n/a	n/a	CTATATCACTGTACCTATAA	23	5-10-5	16178	16197	1074
						16229	16248	
						15249	15268	
						15374	15393	
						15512	15531	
						15642	15661	
						15844	15863	
						15974	15993	

547647	n/a	n/a	GTCCTATATCACTGTACCTA	92	5-10-5	15252	15271	1075
						15377	15396	
						15515	15534	
						15645	15664	
						15847	15866	
						15977	15996	
547648	n/a	n/a	CCTATAACAGTATCACTGTA	83	5-10-5	15361	15380	1076
547649	n/a	n/a	ACCTATAACAGTATCACTGT	73	5-10-5	15362	15381	1077
547650	n/a	n/a	GTACCTATAACAGTATCACT	32	5-10-5	15364	15383	1078
547651	n/a	n/a	TGTACCTATAACAGTATCAC	48	5-10-5	15365	15384	1079
547652	n/a	n/a	TCACTGTACCTATAACAGTA	59	5-10-5	15369	15388	1080
547653	n/a	n/a	ATCACTGTACCTATAACAGT	57	5-10-5	15370	15389	1081
547654	n/a	n/a	TATCACTGTACCTATAACAG	53	5-10-5	15371	15390	1082
547655	n/a	n/a	AATATCACTGTCCTATAACT	37	5-10-5	15582	15601	1083
						16011	16030	
						16082	16101	
						16179	16198	
						16230	16249	
547656	n/a	n/a	CAATATCACTGTCCTATAAC	42	5-10-5	15583	15602	1084
						16083	16102	
						16180	16199	
						16231	16250	
547657	n/a	n/a	ACAATATCACTGTCCTATAA	43	5-10-5	15584	15603	1085
						16084	16103	
						16181	16200	
						16232	16251	
547658	n/a	n/a	CGTACTAGTTTCCTATAACT	68	5-10-5	15750	15769	1086
547659	n/a	n/a	ACTATAACAGTATCACCGTA	80	5-10-5	15766	15785	1087
547660	n/a	n/a	AACTATAACAGTATCACCGT	68	5-10-5	15767	15786	1088
547661	n/a	n/a	TAACTATAACAGTATCACCG	80	5-10-5	15768	15787	1089
547662	n/a	n/a	ACCTATAACTATAACAGTAT	0	5-10-5	15773	15792	1090
547663	n/a	n/a	TACCTATAACTATAACAGTA	10	5-10-5	15774	15793	1091
547664	n/a	n/a	GTACCTATAACTATAACAGT	2	5-10-5	15775	15794	1092
547665	n/a	n/a	TGTACCTATAACTATAACAG	10	5-10-5	15776	15795	1093
547666	n/a	n/a	ATCACTGTACCTATAACTAT	71	5-10-5	15781	15800	1094
						16253	16272	
547667	n/a	n/a	TATCACTGTACCTATAACTA	55	5-10-5	15782	15801	1095
547668	n/a	n/a	CAACTATAACAGTATCACTG	44	5-10-5	15899	15918	1096
547669	n/a	n/a	ACAACCTATAACAGTATCACT	0	5-10-5	15900	15919	1097
547670	n/a	n/a	TACAACCTATAACAGTATCAC	0	5-10-5	15901	15920	1098
547671	n/a	n/a	CTACAACCTATAACAGTATCA	0	5-10-5	15902	15921	1099
547672	n/a	n/a	CAATATCACTGTCCTACAAC	36	5-10-5	15915	15934	1100

547673	n/a	n/a	GAATATCACTGTCCTATAAC	21	5-10-5	16012	16031	1101
547674	n/a	n/a	ACAATATCACTGTACCTTTA	53	5-10-5	16059	16078	1102
547675	n/a	n/a	TGTCCTATAACTATAACAAT	10	5-10-5	16074	16093	1103
						16099	16118	
						16152	16171	
547676	n/a	n/a	CTGTCCTATAACTATAACAA	41	5-10-5	16075	16094	1104
						16100	16119	
						16153	16172	

Table 16

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	93	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546529	n/a	n/a	GCACCTGGCAGAACAGTACC	5-10-5	65	26419	26438	1105
546578	n/a	n/a	GACAGTGGGCCAGAGCCTTG	5-10-5	73	26686	26705	1106
546912	n/a	n/a	ACATCACTGTCCTATAACTA	5-10-5	26	16106	16125	1107
546913	n/a	n/a	GTACCTATATCACTGTAAC	5-10-5	38	16126	16145	1108
546914	n/a	n/a	ATATCACTGTACCTATATCA	5-10-5	52	16134	16153	1109
546915	n/a	n/a	TCACTGTCCTATAACTATAT	5-10-5	39	16175	16194	1110
546916	n/a	n/a	CGTCACTGTACCTATAACTG	5-10-5	92	16203	16222	1111
546917	n/a	n/a	ATCACTGTCCTATAACTATT	5-10-5	63	16227	16246	1112
546918	n/a	n/a	AACATCACTGTACCTATAAC	5-10-5	14	16256	16275	1113
546926	n/a	n/a	GCCATCCAGGGTGCTCTCCC	5-10-5	81	16839	16858	1114
546931	n/a	n/a	GCCCCCGGAGCACCTTCACT	5-10-5	58	17205	17224	1115

546935	n/a	n/a	CGTGGTTAGCCTGACATCTC	5-10-5	86	17412	17431	1116
546939	n/a	n/a	GCCATCTGGTTAGCCTCCGA	5-10-5	89	17664	17683	1117
546942	n/a	n/a	TACACTGAACCCCCTTAGGC	5-10-5	56	18570	18589	1118
546943	n/a	n/a	CAGTTTGGCCTTTCCATCTC	5-10-5	54	18819	18838	1119
546944	n/a	n/a	GCCACTAACCACCTCTTAA	5-10-5	42	19140	19159	1120
546946	n/a	n/a	ACTCCCATCTACTCCCCAT	5-10-5	41	19291	19310	1121
546954	n/a	n/a	CTGCTGATTGTGTCTGGCTC	5-10-5	71	20235	20254	1122
546955	n/a	n/a	ACAAGGCTTCGAGGACAGCC	5-10-5	49	20339	20358	1123
546964	n/a	n/a	GCGATTCCCTGCCTCTGCTG	5-10-5	53	21550	21569	1124
546967	n/a	n/a	CACCGCGCGAATGCCTGCCT	5-10-5	93	22657	22676	1125
546969	n/a	n/a	ATCCAACCTCTCTCCCTATC	5-10-5	53	22901	22920	1126
546970	n/a	n/a	GCCCAAGCCTACATGCATAC	5-10-5	61	23426	23445	1127
546975	n/a	n/a	GGCCTGGATACAGCCTTTCT	5-10-5	70	23825	23844	1128
546977	n/a	n/a	GTCCCGAAGAGTCAAGTCCA	5-10-5	76	24253	24272	1129
546979	n/a	n/a	ACTGTTGTCCATAGCAGCAT	5-10-5	71	24504	24523	1130
546980	n/a	n/a	AGCCCTCAATTGTTGCTGGT	5-10-5	79	24664	24683	1131
546983	n/a	n/a	GATGACCTGCAGATGCACAG	5-10-5	74	24978	24997	1132
546986	n/a	n/a	CAGGATAGAACTGATGGTCC	5-10-5	91	25318	25337	1133
546990	n/a	n/a	AGAACAGGAGACAATCCACT	5-10-5	49	25680	25699	1134
546994	n/a	n/a	GTTTCATGTGGCAACCTGTGA	5-10-5	58	26112	26131	1135
547677	n/a	n/a	CATCACTGTCCTATAACTAT	5-10-5	62	16105	16124	1136
547678	n/a	n/a	TACCTATATCACTGTAACTA	5-10-5	21	16125	16144	1137
547679	n/a	n/a	TGTACCTATATCACTGTAAC	5-10-5	28	16127	16146	1138
547680	n/a	n/a	TATCACTGTACCTATATCAC	5-10-5	41	16133	16152	1139
547681	n/a	n/a	AATATCACTGTACCTATATC	5-10-5	6	16135	16154	1140
547682	n/a	n/a	CAATATCACTGTACCTATAT	5-10-5	20	16136	16155	1141
547683	n/a	n/a	ACTATATCACTGTCCTATAA	5-10-5	33	16162	16181	1142
547684	n/a	n/a	TAACCTATATCACTGTCCTAT	5-10-5	43	16164	16183	1143
547685	n/a	n/a	ATAACTATATCACTGTCCTA	5-10-5	35	16165	16184	1144
547686	n/a	n/a	CTGTCCTATAACTATATCAC	5-10-5	36	16172	16191	1145
547687	n/a	n/a	ACTGTCCTATAACTATATCA	5-10-5	41	16173	16192	1146
547688	n/a	n/a	CACTGTCCTATAACTATATC	5-10-5	47	16174	16193	1147
547689	n/a	n/a	GTAACAATATCACTGTCCTA	5-10-5	73	16184	16203	1148
547690	n/a	n/a	CTGTAACAATATCACTGTCC	5-10-5	76	16186	16205	1149
547691	n/a	n/a	ACTGTAACAATATCACTGTC	5-10-5	36	16187	16206	1150
547692	n/a	n/a	CACTGTACCTATAACTGTAA	5-10-5	47	16200	16219	1151
547693	n/a	n/a	TCACCTGTACCTATAACTGTA	5-10-5	61	16201	16220	1152
547694	n/a	n/a	GTCACCTGTACCTATAACTGT	5-10-5	92	16202	16221	1153
547695	n/a	n/a	ACTGTCCTATAACTATTACA	5-10-5	31	16224	16243	1154
547696	n/a	n/a	CACTGTCCTATAACTATTAC	5-10-5	26	16225	16244	1155
547697	n/a	n/a	TCACCTGTACCTATAACTATTA	5-10-5	63	16226	16245	1156
547698	n/a	n/a	ACCTATAACTATAACAATAT	5-10-5	0	16245	16264	1157

547699	n/a	n/a	TACCTATAACTATAACAATA	5-10-5	10	16246	16265	1158
547700	n/a	n/a	GTACCTATAACTATAACAAT	5-10-5	0	16247	16266	1159
547701	n/a	n/a	CATCACTGTACCTATAACTA	5-10-5	49	16254	16273	1160
547702	n/a	n/a	ACATCACTGTACCTATAACT	5-10-5	44	16255	16274	1161
547703	n/a	n/a	CAACATCACTGTACCTATAA	5-10-5	25	16257	16276	1162
547704	n/a	n/a	ACATCTTGTCATTAACATCC	5-10-5	61	16435	16454	1163
547705	n/a	n/a	GCACCCAATACAGGGCCAGG	5-10-5	69	16512	16531	1164
547706	n/a	n/a	TGCCTCCTGGCAGCCTTCAA	5-10-5	73	16694	16713	1165
547707	n/a	n/a	TGAAAAGCCACGCCCTTAGC	5-10-5	32	16975	16994	1166
547708	n/a	n/a	GCCAGGAGACAGCCCTACTC	5-10-5	67	17055	17074	1167
547709	n/a	n/a	AGCCCAATGTCCTAACCTGT	5-10-5	76	17791	17810	1168
547710	n/a	n/a	TGCGGTTATATGGGCTGAAG	5-10-5	85	19540	19559	1169
547711	n/a	n/a	CCTTTAGCCACTCCTCTTGC	5-10-5	45	20061	20080	1170
547712	n/a	n/a	CCCCATGGTACCAAAGCCAT	5-10-5	79	20528	20547	1171
547713	n/a	n/a	CTCAATGCCACCCTTTCCCC	5-10-5	37	20880	20899	1172
547714	n/a	n/a	CTGTCTAACTGGCCTGGCTG	5-10-5	19	21326	21345	1173
547715	n/a	n/a	GGTCAGAAGGCCTCTTATTC	5-10-5	21	21750	21769	1174
547716	n/a	n/a	CCATCTGTCCCCTCAATCCC	5-10-5	9	22197	22216	1175
547717	n/a	n/a	ACTCTGGCACTGGTCATGGA	5-10-5	54	22761	22780	1176
547718	n/a	n/a	ATAAAGTGCGATTAAGCCCC	5-10-5	86	23515	23534	1177
547719	n/a	n/a	TACCAAGCTTGTAAGAAGGGA	5-10-5	69	23633	23652	1178
547720	n/a	n/a	GAAAGACGGCCAATGGGAAA	5-10-5	8	24177	24196	1179
547721	n/a	n/a	CTCTATCAAAATCCTGCTGC	5-10-5	68	25527	25546	1180
547722	n/a	n/a	CTCCAGTCACCACCATTGCC	5-10-5	80	25860	25879	1181

Table 17

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	91	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	

						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
546599	n/a	n/a	AAGAGTAAGCCTTCACAGGG	5-10-5	82	27583	27602	1182
546606	n/a	n/a	CTCACCAGAGTTGTCCCAG	5-10-5	0	27722	27741	1183
546999	n/a	n/a	GCAGCTCACACCCAAAAAGC	5-10-5	29	27004	27023	1184
547000	n/a	n/a	TCTGTTACCTTGAGGATTGT	5-10-5	63	27276	27295	1185
547006	n/a	n/a	CGCCATCTGCCCTGTACAGA	5-10-5	39	28248	28267	1186
547008	n/a	n/a	TTGGTGGTGGGATTGGTGGT	5-10-5	81	28333	28352	1187
						28388	28407	
						28443	28462	
						28608	28627	
						28620	28639	
547009	n/a	n/a	AATTGGTGGTGGGATTGGTG	5-10-5	73	28335	28354	1188
547010	n/a	n/a	GAATTGGTGGTGGGATTGGT	5-10-5	39	28336	28355	1189
547011	n/a	n/a	GGCAGGATTGGTGGTGGAAT	5-10-5	22	28352	28371	1190
547013	n/a	n/a	TGAGATTGGTGGTGGGTGGC	5-10-5	0	28369	28388	1191
547015	n/a	n/a	GGTGGTGGGATTGGTGCTGA	5-10-5	55	28429	28448	1192
547016	n/a	n/a	GTAGGTGGTGGGATTGGTGG	5-10-5	62	28456	28475	1193
						28535	28554	
547017	n/a	n/a	GGTAGGTGGTGGGATTGGTG	5-10-5	61	28457	28476	1194
						28536	28555	
547018	n/a	n/a	GGTGCGGGATTGGTGGTGG	5-10-5	58	28477	28496	1195
						28556	28575	
547019	n/a	n/a	GATCGGTGGTGGGATTGGTC	5-10-5	83	28500	28519	1196
						28579	28598	
547020	n/a	n/a	GGATCGGTGGTGGGATTGGT	5-10-5	47	28501	28520	1197
						28580	28599	
547021	n/a	n/a	TTGGTGGCGGGATCGGTGGT	5-10-5	57	28510	28529	1198
						28589	28608	
547022	n/a	n/a	ATTGGTGGCGGGATCGGTGG	5-10-5	69	28511	28530	1199
547023	n/a	n/a	GATTGGTGGCGGGATCGGTG	5-10-5	91	28512	28531	1200
547024	n/a	n/a	GGATTGGTGGCGGGATCGGT	5-10-5	56	28513	28532	1201
547025	n/a	n/a	TGGTGGTGGGATTGGTGGTT	5-10-5	72	28607	28626	1202
547029	n/a	n/a	TCTTCTAGGGCCACACCTCT	5-10-5	50	28891	28910	1203
547035	n/a	n/a	TGGTCCCAAATTGGAGTGCA	5-10-5	40	29383	29402	1204
547039	n/a	n/a	TCTCTATACAGCTGGGCACA	5-10-5	0	29997	30016	1205
547049	n/a	n/a	CACTTCCCAGCAACCCTCAC	5-10-5	20	30765	30784	1206
547055	n/a	n/a	GCTCCTGGCAGCAATGACCC	5-10-5	70	31104	31123	1207
547059	n/a	n/a	GGGTATCTTCACTGTTCCAG	5-10-5	12	31540	31559	1208

547063	n/a	n/a	CGTCATGCTTACCTTTCTCC	5-10-5	23	31955	31974	1209
547069	n/a	n/a	GCCCTCCGAGCTTTGGCAAC	5-10-5	35	32581	32600	1210
547071	n/a	n/a	GCAGCCCCCAGAAATCCCA	5-10-5	27	32708	32727	1211
547076	n/a	n/a	TCTCAAGCAGCCTATTGTGT	5-10-5	14	33263	33282	1212
547080	n/a	n/a	GTGCAAGACCTTGCTTGCCA	5-10-5	54	33657	33676	1213
547081	n/a	n/a	CTGTAGTCCACTACACAGCA	5-10-5	83	33801	33820	1214
547082	n/a	n/a	TCTCCCTGAGTCACAGTGGA	5-10-5	64	33881	33900	1215
547085	n/a	n/a	CCAGGTGCAGCACGGAGAGG	5-10-5	44	34479	34498	1216
547723	n/a	n/a	TAGAATGGCAGGGTTCTGTG	5-10-5	53	27357	27376	1217
547724	n/a	n/a	GATGCATCCAACACTTACCC	5-10-5	16	28059	28078	1218
547725	n/a	n/a	ATTGGTGGTGGGATTGGTGG	5-10-5	26	28334	28353	1219
						28389	28408	
						28444	28463	
						28523	28542	
						28609	28628	
						28621	28640	
547726	n/a	n/a	GCAGGATTGGTGGTGGGAATT	5-10-5	0	28351	28370	1220
547727	n/a	n/a	TGGCAGGATTGGTGGTGGAA	5-10-5	0	28353	28372	1221
547728	n/a	n/a	GAGATTGGTGGTGGGTGGCA	5-10-5	88	28368	28387	1222
547729	n/a	n/a	GTGAGATTGGTGGTGGGTGG	5-10-5	45	28370	28389	1223
547730	n/a	n/a	GATTGGTGGTGGGATTGGTG	5-10-5	60	28390	28409	1224
						28433	28452	
						28445	28464	
						28524	28543	
						28610	28629	
						28622	28641	
547731	n/a	n/a	GGATTGGTGGTGGGATTGGT	5-10-5	49	28391	28410	1225
						28434	28453	
						28446	28465	
						28525	28544	
						28611	28630	
						28623	28642	
547732	n/a	n/a	AGGATTGGTGGTGGGATTGG	5-10-5	0	28392	28411	1226
547733	n/a	n/a	TAGGATTGGTGGTGGGATTG	5-10-5	0	28393	28412	1227
547734	n/a	n/a	GTAGGATTGGTGGTGGGATT	5-10-5	14	28394	28413	1228
547735	n/a	n/a	GGTAGGATTGGTGGTGGGAT	5-10-5	39	28395	28414	1229
547736	n/a	n/a	TGGTAGGATTGGTGGTGGGA	5-10-5	54	28396	28415	1230
547737	n/a	n/a	TGGTGGTGGGATTGGTGCTG	5-10-5	59	28430	28449	1231
547738	n/a	n/a	TTGGTGGTGGGATTGGTGCT	5-10-5	41	28431	28450	1232
547739	n/a	n/a	ATTGGTGGTGGGATTGGTGC	5-10-5	12	28432	28451	1233
547740	n/a	n/a	AGGTGGTGGGATTGGTGGTG	5-10-5	30	28454	28473	1234
						28533	28552	

547741	n/a	n/a	TAGGTGGTGGGATTGGTGGT	5-10-5	47	28455 28534	28474 28553	1235
547742	n/a	n/a	ATCGGTGGTGGGATTGGTCG	5-10-5	57	28499 28578	28518 28597	1236
547743	n/a	n/a	GGTGGTGGGATTGGTGGCGG	5-10-5	61	28520	28539	1237
547744	n/a	n/a	TGGTGGTGGGATTGGTGGCG	5-10-5	65	28521	28540	1238
547745	n/a	n/a	TTGGTGGTGGGATTGGTGGC	5-10-5	55	28522	28541	1239
547746	n/a	n/a	GTTGGTGGCGGGATCGGTGG	5-10-5	0	28590	28609	1240
547748	n/a	n/a	GGTTGGTGGCGGGATCGGTG	5-10-5	78	28591	28610	1241
547750	n/a	n/a	TGGTTGGTGGCGGGATCGGT	5-10-5	41	28592	28611	1242
547752	n/a	n/a	GTGGTTGGTGGCGGGATCGG	5-10-5	41	28593	28612	1243
547754	n/a	n/a	GGGATTGGTGGTTGGTGGCG	5-10-5	47	28600	28619	1244
547756	n/a	n/a	GGGTCTTGCTCCACCCACAT	5-10-5	49	29244	29263	1245
547758	n/a	n/a	CCAAGTAGTGCAAGGCATGT	5-10-5	24	29540	29559	1246
547760	n/a	n/a	ATCATGCTTACTGCAAGTGA	5-10-5	19	30219	30238	1247
547762	n/a	n/a	TGAAACTGGGCAGTCCTTCC	5-10-5	0	30417	30436	1248
547764	n/a	n/a	CCACCTTCTTACATATGCTA	5-10-5	24	30644	30663	1249
547766	n/a	n/a	GCCTCTCAGACGGCACAGAC	5-10-5	0	30902	30921	1250
547768	n/a	n/a	TTGCCCTCACACATTTCGAAT	5-10-5	0	30977	30996	1251
547770	n/a	n/a	TGCTTTCTGCCCAACCTCTA	5-10-5	48	31727	31746	1252
547772	n/a	n/a	CTGTGCTCCCGGCCATTAGC	5-10-5	0	32312	32331	1253
547774	n/a	n/a	GAGACAGTTTGGCAAGCTAC	5-10-5	46	32389	32408	1254
547776	n/a	n/a	GGAGAGAGACGGCACCCCTGT	5-10-5	48	32828	32847	1255
547778	n/a	n/a	TCACCTGTGAGTAACCAATA	5-10-5	53	33085	33104	1256
547780	n/a	n/a	CCCCTCTTAAATAGCACATG	5-10-5	67	33441	33460	1257
547782	n/a	n/a	CCAAGTATCTCATGTGCCTG	5-10-5	67	33580	33599	1258

Table 18

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Motif	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	5-10-5	90	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	

						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
548706	n/a	n/a	CTAGTTTCCTATAACT	3-10-3	0	14738	14753	1259
						14809	14824	
						14880	14895	
						14939	14954	
						15071	15086	
						15214	15229	
						15286	15301	
						15345	15360	
						15477	15492	
						15549	15564	
						15607	15622	
						15679	15694	
						15750	15765	
						15809	15824	
						15881	15896	
						15939	15954	
548707	n/a	n/a	ACTAGTTTCCTATAAC	3-10-3	10	14739	14754	1260
						14810	14825	
						14881	14896	
						14940	14955	
						15000	15015	
						15072	15087	
						15215	15230	
						15287	15302	
						15346	15361	
						15406	15421	
						15478	15493	
						15550	15565	
						15608	15623	
						15680	15695	
						15751	15766	
						15810	15825	
						15882	15897	
						15940	15955	
548708	n/a	n/a	TACTAGTTTCCTATAA	3-10-3	0	14740	14755	1261

						14811	14826	
						14882	14897	
						14941	14956	
						15001	15016	
						15073	15088	
						15216	15231	
						15288	15303	
						15347	15362	
						15407	15422	
						15479	15494	
						15551	15566	
						15609	15624	
						15681	15696	
						15752	15767	
						15811	15826	
						15883	15898	
						15941	15956	
548709	n/a	n/a	GTACTAGTTTCCTATA	3-10-3	0	14741	14756	1262
						14812	14827	
						14883	14898	
						14942	14957	
						15002	15017	
						15074	15089	
						15217	15232	
						15289	15304	
						15348	15363	
						15408	15423	
						15480	15495	
						15552	15567	
						15610	15625	
						15682	15697	
						15753	15768	
						15812	15827	
						15884	15899	
						15942	15957	
548710	n/a	n/a	TGTACTAGTTTCCTAT	3-10-3	0	14742	14757	1263
						14813	14828	
						14884	14899	
						14943	14958	
						15003	15018	
						15075	15090	
						15218	15233	

						15290	15305	
						15349	15364	
						15409	15424	
						15481	15496	
						15553	15568	
						15611	15626	
						15683	15698	
						15813	15828	
						15885	15900	
						15943	15958	
548711	n/a	n/a	CTGTACTAGTTTCCTA	3-10-3	21	14743	14758	1264
						14814	14829	
						14885	14900	
						14944	14959	
						15004	15019	
						15076	15091	
						15219	15234	
						15291	15306	
						15350	15365	
						15410	15425	
						15482	15497	
						15554	15569	
						15612	15627	
						15684	15699	
						15814	15829	
						15886	15901	
						15944	15959	
548712	n/a	n/a	ACTGTACTAGTTTCCT	3-10-3	9	14744	14759	1265
						14815	14830	
						14886	14901	
						14945	14960	
						15005	15020	
						15077	15092	
						15220	15235	
						15292	15307	
						15351	15366	
						15411	15426	
						15483	15498	
						15555	15570	
						15613	15628	
						15685	15700	
						15815	15830	

						15887	15902	
						15945	15960	
548713	n/a	n/a	CACTGTACTAGTTTCC	3-10-3	33	14745	14760	1266
						14816	14831	
						14887	14902	
						14946	14961	
						15006	15021	
						15078	15093	
						15221	15236	
						15293	15308	
						15352	15367	
						15412	15427	
						15484	15499	
						15556	15571	
						15614	15629	
						15686	15701	
						15816	15831	
						15888	15903	
						15946	15961	
548714	n/a	n/a	TCACTGTACTAGTTTC	3-10-3	15	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548715	n/a	n/a	ATCACTGTACTAGTTT	3-10-3	0	14747	14762	1268
						14818	14833	
						14889	14904	
						14948	14963	
						15008	15023	
						15080	15095	

						15152	15167	
						15223	15238	
						15295	15310	
						15354	15369	
						15414	15429	
						15486	15501	
						15558	15573	
						15616	15631	
						15688	15703	
						15818	15833	
						15890	15905	
						15948	15963	
548716	n/a	n/a	TATCACTGTACTAGTT	3-10-3	10	14748	14763	1269
						14819	14834	
						14890	14905	
						14949	14964	
						15009	15024	
						15081	15096	
						15153	15168	
						15224	15239	
						15296	15311	
						15355	15370	
						15415	15430	
						15487	15502	
						15559	15574	
						15617	15632	
						15689	15704	
						15819	15834	
548717	n/a	n/a	ACTAGTTTCCTATAACT	3-10-4	0	14738	14754	1270
						14809	14825	
						14880	14896	
						14939	14955	
						15071	15087	
						15214	15230	
						15286	15302	
						15345	15361	
						15477	15493	
						15549	15565	
						15607	15623	
						15679	15695	

						15750	15766	
						15809	15825	
						15881	15897	
						15939	15955	
548718	n/a	n/a	TACTAGTTTCCTATAAC	3-10-4	0	14739	14755	1271
						14810	14826	
						14881	14897	
						14940	14956	
						15000	15016	
						15072	15088	
						15215	15231	
						15287	15303	
						15346	15362	
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						15550	15566	
						15608	15624	
						15680	15696	
						15751	15767	
						15810	15826	
						15882	15898	
						15940	15956	
548719	n/a	n/a	GTACTAGTTTCCTATAA	3-10-4	0	14740	14756	1272
						14811	14827	
						14882	14898	
						14941	14957	
						15001	15017	
						15073	15089	
						15216	15232	
						15288	15304	
						15347	15363	
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						15479	15495	
						15551	15567	
						15609	15625	
						15681	15697	
						15752	15768	
						15811	15827	
						15883	15899	
						15941	15957	
548720	n/a	n/a	TGTACTAGTTTCCTATA	3-10-4	0	14741	14757	1273
						14812	14828	

						14883	14899	
						14942	14958	
						15002	15018	
						15074	15090	
						15217	15233	
						15289	15305	
						15348	15364	
						15408	15424	
						15480	15496	
						15552	15568	
						15610	15626	
						15682	15698	
						15812	15828	
						15884	15900	
						15942	15958	
548721	n/a	n/a	CTGTACTAGTTTCCTAT	3-10-4	27	14742	14758	1274
						14813	14829	
						14884	14900	
						14943	14959	
						15003	15019	
						15075	15091	
						15218	15234	
						15290	15306	
						15349	15365	
						15409	15425	
						15481	15497	
						15553	15569	
						15611	15627	
						15683	15699	
						15813	15829	
548722	n/a	n/a	ACTGTACTAGTTTCCTA	3-10-4	26	15885	15901	1275
						15943	15959	
						14743	14759	
						14814	14830	
						14885	14901	
						14944	14960	
						15004	15020	
						15076	15092	
						15219	15235	
						15291	15307	
						15350	15366	
						15410	15426	

						15482	15498	
						15554	15570	
						15612	15628	
						15684	15700	
						15814	15830	
						15886	15902	
						15944	15960	
548723	n/a	n/a	CACTGTACTAGTTTCCT	3-10-4	62	14744	14760	1276
						14815	14831	
						14886	14902	
						14945	14961	
						15005	15021	
						15077	15093	
						15220	15236	
						15292	15308	
						15351	15367	
						15411	15427	
						15483	15499	
						15555	15571	
						15613	15629	
						15685	15701	
548724	n/a	n/a	TCACTGTACTAGTTTCC	3-10-4	61	14745	14761	1277
						14816	14832	
						14887	14903	
						14946	14962	
						15006	15022	
						15078	15094	
						15221	15237	
						15293	15309	
						15352	15368	
						15412	15428	
						15484	15500	
						15556	15572	
						15614	15630	
						15686	15702	
548725	n/a	n/a	ATCACTGTACTAGTTTC	3-10-4	32	15816	15832	1278
						15888	15904	
						15946	15962	

						14817	14833	
						14888	14904	
						14947	14963	
						15007	15023	
						15079	15095	
						15222	15238	
						15294	15310	
						15353	15369	
						15413	15429	
						15485	15501	
						15557	15573	
						15615	15631	
						15687	15703	
						15817	15833	
						15889	15905	
						15947	15963	
548726	n/a	n/a	TATCACTGTACTAGTTT	3-10-4	21	14747	14763	1279
						14818	14834	
						14889	14905	
						14948	14964	
						15008	15024	
						15080	15096	
						15152	15168	
						15223	15239	
						15295	15311	
						15354	15370	
						15414	15430	
						15486	15502	
						15558	15574	
						15616	15632	
						15688	15704	
						15818	15834	
						15890	15906	
						15948	15964	
548727	n/a	n/a	ACTAGTTTCCTATAACT	4-10-3	0	14738	14754	1270
						14809	14825	
						14880	14896	
						14939	14955	
						15071	15087	
						15214	15230	
						15286	15302	
						15345	15361	

						15477	15493	
						15549	15565	
						15607	15623	
						15679	15695	
						15750	15766	
						15809	15825	
						15881	15897	
						15939	15955	
548728	n/a	n/a	TACTAGTTTCCTATAAC	4-10-3	0	14739	14755	1271
						14810	14826	
						14881	14897	
						14940	14956	
						15000	15016	
						15072	15088	
						15215	15231	
						15287	15303	
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						15550	15566	
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						15680	15696	
						15751	15767	
						15810	15826	
						15882	15898	
						15940	15956	
548729	n/a	n/a	GTACTAGTTTCCTATAA	4-10-3	13	14740	14756	1272
						14811	14827	
						14882	14898	
						14941	14957	
						15001	15017	
						15073	15089	
						15216	15232	
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						15551	15567	
						15609	15625	
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						15883	15899	
						15941	15957	
548730	n/a	n/a	TGTACTAGTTTCCTATA	4-10-3	0	14741	14757	1273
						14812	14828	
						14883	14899	
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						15217	15233	
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						15812	15828	
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						15942	15958	
548731	n/a	n/a	CTGTACTAGTTTCCTAT	4-10-3	49	14742	14758	1274
						14813	14829	
						14884	14900	
						14943	14959	
						15003	15019	
						15075	15091	
						15218	15234	
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						15813	15829	
						15885	15901	
						15943	15959	
548732	n/a	n/a	ACTGTACTAGTTTCCTA	4-10-3	36	14743	14759	1275
						14814	14830	
						14885	14901	
						14944	14960	
						15004	15020	
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						15219	15235	
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						15554	15570	
						15612	15628	
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						15814	15830	
						15886	15902	
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548733	n/a	n/a	CACTGTACTAGTTTCCT	4-10-3	84	14744	14760	1276
						14815	14831	
						14886	14902	
						14945	14961	
						15005	15021	
						15077	15093	
						15220	15236	
						15292	15308	
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						15555	15571	
						15613	15629	
						15685	15701	
548734	n/a	n/a	TCACTGTACTAGTTTCC	4-10-3	51	14745	14761	1277
						14816	14832	
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						15293	15309	
						15352	15368	
						15412	15428	
						15484	15500	
						15556	15572	
						15614	15630	
						15686	15702	

						15816	15832	
						15888	15904	
						15946	15962	
548735	n/a	n/a	ATCACTGTACTAGTTTC	4-10-3	48	14746	14762	1278
						14817	14833	
						14888	14904	
						14947	14963	
						15007	15023	
						15079	15095	
						15222	15238	
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						15353	15369	
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						15485	15501	
						15557	15573	
						15615	15631	
						15687	15703	
						15817	15833	
						15889	15905	
						15947	15963	
548736	n/a	n/a	TATCACTGTACTAGTTT	4-10-3	21	14747	14763	1279
						14818	14834	
						14889	14905	
						14948	14964	
						15008	15024	
						15080	15096	
						15152	15168	
						15223	15239	
						15295	15311	
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						15414	15430	
						15486	15502	
						15558	15574	
						15616	15632	
						15688	15704	
						15818	15834	
						15890	15906	
						15948	15964	
548737	n/a	n/a	ACTAGTTTCCTATAACT	4-9-4	11	14738	14754	1270
						14809	14825	
						14880	14896	
						14939	14955	

						15071	15087	
						15214	15230	
						15286	15302	
						15345	15361	
						15477	15493	
						15549	15565	
						15607	15623	
						15679	15695	
						15750	15766	
						15809	15825	
						15881	15897	
						15939	15955	
548738	n/a	n/a	TACTAGTTTCCTATAAC	4-9-4	0	14739	14755	1271
						14810	14826	
						14881	14897	
						14940	14956	
						15000	15016	
						15072	15088	
						15215	15231	
						15287	15303	
						15346	15362	
						15406	15422	
						15478	15494	
						15550	15566	
						15608	15624	
						15680	15696	
						15751	15767	
548739	n/a	n/a	GTACTAGTTTCCTATAA	4-9-4	0	15810	15826	1272
						15882	15898	
						15940	15956	
						14740	14756	
						14811	14827	
						14882	14898	
						14941	14957	
						15001	15017	
						15073	15089	
						15216	15232	
						15288	15304	
						15347	15363	
						15407	15423	
						15479	15495	
						15551	15567	

						15609	15625	
						15681	15697	
						15752	15768	
						15811	15827	
						15883	15899	
						15941	15957	
548740	n/a	n/a	TGTACTAGTTTCCTATA	4-9-4	0	14741	14757	1273
						14812	14828	
						14883	14899	
						14942	14958	
						15002	15018	
						15074	15090	
						15217	15233	
						15289	15305	
						15348	15364	
						15408	15424	
						15480	15496	
						15552	15568	
						15610	15626	
						15682	15698	
						15812	15828	
						15884	15900	
						15942	15958	
548741	n/a	n/a	CTGTACTAGTTTCCTAT	4-9-4	69	14742	14758	1274
						14813	14829	
						14884	14900	
						14943	14959	
						15003	15019	
						15075	15091	
						15218	15234	
						15290	15306	
						15349	15365	
						15409	15425	
						15481	15497	
						15553	15569	
						15611	15627	
						15683	15699	
						15813	15829	
						15885	15901	
						15943	15959	
548742	n/a	n/a	ACTGTACTAGTTTCCTA	4-9-4	50	14743	14759	1275
						14814	14830	

						14885	14901	
						14944	14960	
						15004	15020	
						15076	15092	
						15219	15235	
						15291	15307	
						15350	15366	
						15410	15426	
						15482	15498	
						15554	15570	
						15612	15628	
						15684	15700	
						15814	15830	
						15886	15902	
						15944	15960	
548743	n/a	n/a	CACTGTACTAGTTTCCT	4-9-4	80	14744	14760	1276
						14815	14831	
						14886	14902	
						14945	14961	
						15005	15021	
						15077	15093	
						15220	15236	
						15292	15308	
						15351	15367	
						15411	15427	
						15483	15499	
						15555	15571	
						15613	15629	
						15685	15701	
						15815	15831	
548744	n/a	n/a	TCACTGTACTAGTTTCC	4-9-4	83	15887	15903	1277
						15945	15961	
						14745	14761	
						14816	14832	
						14887	14903	
						14946	14962	
						15006	15022	
						15078	15094	
						15221	15237	
						15293	15309	
						15352	15368	
						15412	15428	

						15484	15500	
						15556	15572	
						15614	15630	
						15686	15702	
						15816	15832	
						15888	15904	
						15946	15962	
548745	n/a	n/a	ATCACTGTACTAGTTTC	4-9-4	71	14746	14762	1278
						14817	14833	
						14888	14904	
						14947	14963	
						15007	15023	
						15079	15095	
						15222	15238	
						15294	15310	
						15353	15369	
						15413	15429	
						15485	15501	
						15557	15573	
						15615	15631	
						15687	15703	
						15817	15833	
548746	n/a	n/a	TATCACTGTACTAGTTT	4-9-4	40	15889	15905	1279
						15947	15963	
						14747	14763	
						14818	14834	
						14889	14905	
						14948	14964	
						15008	15024	
						15080	15096	
						15152	15168	
						15223	15239	
						15295	15311	
						15354	15370	
						15414	15430	
						15486	15502	
						15558	15574	
						15616	15632	
						15688	15704	
						15818	15834	
						15890	15906	
						15948	15964	

548747	n/a	n/a	TACTAGTTTCCTATAACT	4-10-4	2	14738	14755	1280
						14809	14826	
						14880	14897	
						14939	14956	
						15071	15088	
						15214	15231	
						15286	15303	
						15345	15362	
						15477	15494	
						15549	15566	
						15607	15624	
						15679	15696	
						15750	15767	
						15809	15826	
						15881	15898	
						15939	15956	
548748	n/a	n/a	GTACTAGTTTCCTATAAC	4-10-4	0	14739	14756	1281
						14810	14827	
						14881	14898	
						14940	14957	
						15000	15017	
						15072	15089	
						15215	15232	
						15287	15304	
						15346	15363	
						15406	15423	
						15478	15495	
						15550	15567	
						15608	15625	
						15680	15697	
						15751	15768	
						15810	15827	
						15882	15899	
						15940	15957	
548749	n/a	n/a	TGTACTAGTTTCCTATAA	4-10-4	0	14740	14757	1282
						14811	14828	
						14882	14899	
						14941	14958	
						15001	15018	
						15073	15090	
						15216	15233	
						15288	15305	

						15347	15364	
						15407	15424	
						15479	15496	
						15551	15568	
						15609	15626	
						15681	15698	
						15811	15828	
						15883	15900	
						15941	15958	
548750	n/a	n/a	CTGTACTAGTTTCCTATA	4-10-4	62	14741	14758	1283
						14812	14829	
						14883	14900	
						14942	14959	
						15002	15019	
						15074	15091	
						15217	15234	
						15289	15306	
						15348	15365	
						15408	15425	
						15480	15497	
						15552	15569	
						15610	15627	
						15682	15699	
						15812	15829	
						15884	15901	
						15942	15959	
548751	n/a	n/a	ACTGTACTAGTTTCCTAT	4-10-4	53	14742	14759	1284
						14813	14830	
						14884	14901	
						14943	14960	
						15003	15020	
						15075	15092	
						15218	15235	
						15290	15307	
						15349	15366	
						15409	15426	
						15481	15498	
						15553	15570	
						15611	15628	
						15683	15700	
						15813	15830	
						15885	15902	

						15943	15960	
548752	n/a	n/a	CACTGTACTAGTTTCCTA	4-10-4	89	14743	14760	1285
						14814	14831	
						14885	14902	
						14944	14961	
						15004	15021	
						15076	15093	
						15219	15236	
						15291	15308	
						15350	15367	
						15410	15427	
						15482	15499	
						15554	15571	
						15612	15629	
						15684	15701	
						15814	15831	
						15886	15903	
						15944	15961	
548753	n/a	n/a	TCACTGTACTAGTTTCCT	4-10-4	82	14744	14761	1286
						14815	14832	
						14886	14903	
						14945	14962	
						15005	15022	
						15077	15094	
						15220	15237	
						15292	15309	
						15351	15368	
						15411	15428	
						15483	15500	
						15555	15572	
						15613	15630	
						15685	15702	
						15815	15832	
						15887	15904	
						15945	15962	
548754	n/a	n/a	ATCACTGTACTAGTTTCC	4-10-4	77	14745	14762	1287
						14816	14833	
						14887	14904	
						14946	14963	
						15006	15023	
						15078	15095	
						15221	15238	

						15293	15310	
						15352	15369	
						15412	15429	
						15484	15501	
						15556	15573	
						15614	15631	
						15686	15703	
						15816	15833	
						15888	15905	
						15946	15963	
548755	n/a	n/a	TATCACTGTACTAGTTTC	4-10-4	20	14746	14763	1288
						14817	14834	
						14888	14905	
						14947	14964	
						15007	15024	
						15079	15096	
						15222	15239	
						15294	15311	
						15353	15370	
						15413	15430	
						15485	15502	
						15557	15574	
						15615	15632	
						15687	15704	
548756	n/a	n/a	GTATCACTGTACTAGTT	4-9-4	81	14748	14764	1289
						14819	14835	
						14890	14906	
						14949	14965	
						15009	15025	
						15081	15097	
						15153	15169	
						15224	15240	
						15296	15312	
						15355	15371	
						15415	15431	
						15487	15503	
						15559	15575	
						15617	15633	
						15689	15705	

						15819	15835	
						15891	15907	
						15949	15965	
548757	n/a	n/a	AGTATCACTGTACTAGT	4-9-4	87	14749	14765	1290
						14820	14836	
						14891	14907	
						14950	14966	
						15010	15026	
						15082	15098	
						15154	15170	
						15225	15241	
						15297	15313	
						15356	15372	
						15416	15432	
						15488	15504	
						15560	15576	
						15618	15634	
						15690	15706	
						15820	15836	
						15892	15908	
						15950	15966	
548758	n/a	n/a	CAGTATCACTGTACTAG	4-9-4	97	14750	14766	1291
						14821	14837	
						14892	14908	
						14951	14967	
						15011	15027	
						15083	15099	
						15155	15171	
						15226	15242	
						15298	15314	
						15357	15373	
						15417	15433	
						15489	15505	
						15561	15577	
						15619	15635	
						15691	15707	
						15821	15837	
						15893	15909	
						15951	15967	
548759	n/a	n/a	AACAGTATCACTGTACT	4-9-4	68	14752	14768	1292
						14823	14839	
						14894	14910	

						14953	14969	
						15013	15029	
						15085	15101	
						15157	15173	
						15228	15244	
						15300	15316	
						15359	15375	
						15419	15435	
						15491	15507	
						15563	15579	
						15621	15637	
						15693	15709	
						15823	15839	
						15895	15911	
						15953	15969	
548760	n/a	n/a	TAACAGTATCACTGTAC	4-9-4	53	14753	14769	1293
						14824	14840	
						14895	14911	
						14954	14970	
						15014	15030	
						15086	15102	
						15158	15174	
						15229	15245	
						15301	15317	
						15360	15376	
						15420	15436	
						15492	15508	
						15564	15580	
						15622	15638	
						15694	15710	
						15824	15840	
						15896	15912	
						15954	15970	
548761	n/a	n/a	CTAACAGTATCACTGTA	4-9-4	49	14754	14770	1294
						14825	14841	
						14896	14912	
						15015	15031	
						15087	15103	
						15230	15246	
						15302	15318	
						15421	15437	
						15493	15509	

						15623	15639	
						15825	15841	
						15955	15971	
548762	n/a	n/a	TCTAACAGTATCACTGT	4-9-4	16	14755	14771	1295
						14826	14842	
						14897	14913	
						15016	15032	
						15088	15104	
						15231	15247	
						15303	15319	
						15422	15438	
						15494	15510	
						15624	15640	
						15826	15842	
						15956	15972	
548763	n/a	n/a	CTCTAACAGTATCACTG	4-9-4	44	14756	14772	1296
						14827	14843	
						14898	14914	
						15017	15033	
						15089	15105	
						15232	15248	
						15304	15320	
						15423	15439	
						15495	15511	
						15625	15641	
						15827	15843	
						15957	15973	
548764	n/a	n/a	TATCACTGTCCTATAAC	4-9-4	31	14772	14788	1297
						14843	14859	
						15177	15193	
						15583	15599	
						15713	15729	
						16012	16028	
						16083	16099	
						16161	16177	
						16180	16196	
						16231	16247	
548765	n/a	n/a	ATATCACTGTCCTATAA	4-9-4	0	14773	14789	1298
						14844	14860	
						15178	15194	
						15584	15600	
						15714	15730	

						16013	16029	
						16084	16100	
						16162	16178	
						16181	16197	
						16232	16248	
548766	n/a	n/a	TATATCACTGTCCTATA	4-9-4	36	14774	14790	1299
						14845	14861	
						15179	15195	
						15715	15731	
						16163	16179	
548767	n/a	n/a	TATCACTGTCCTATATC	4-9-4	59	14785	14801	1300
						14856	14872	
						14981	14997	
						15119	15135	
						15190	15206	
						15262	15278	
						15387	15403	
						15525	15541	
						15655	15671	
						15726	15742	
						15857	15873	
						15987	16003	
548768	n/a	n/a	GTATCACTGTCCTATAT	4-9-4	56	14786	14802	1301
						14982	14998	
						15120	15136	
						15388	15404	
						15526	15542	
						15988	16004	
548769	n/a	n/a	AGTATCACTGTCCTATA	4-9-4	64	14787	14803	1302
						14983	14999	
						15121	15137	
						15389	15405	
						15527	15543	
						15989	16005	
548770	n/a	n/a	TAACAGTATCACTGTCC	4-9-4	92	14791	14807	1303
						14987	15003	
						15053	15069	
						15125	15141	
						15393	15409	
						15459	15475	
						15531	15547	
						15993	16009	

548771	n/a	n/a	ATAACAGTATCACTGTC	4-9-4	62	14792	14808	1304
						14988	15004	
						15054	15070	
						15126	15142	
						15394	15410	
						15460	15476	
						15532	15548	
						15994	16010	
548772	n/a	n/a	TATAACAGTATCACTGT	4-9-4	0	14793	14809	1305
						14989	15005	
						15055	15071	
						15127	15143	
						15160	15176	
						15362	15378	
						15395	15411	
						15461	15477	
						15533	15549	
						15566	15582	
						15696	15712	
						15898	15914	
548773	n/a	n/a	CTATAACAGTATCACTG	4-9-4	0	14794	14810	1306
						14990	15006	
						15056	15072	
						15128	15144	
						15161	15177	
						15363	15379	
						15396	15412	
						15462	15478	
						15534	15550	
						15567	15583	
						15697	15713	
						15899	15915	
548774	n/a	n/a	CCTATAACTATAACAGT	4-9-4	0	14801	14817	1307
						15063	15079	
						15168	15184	
						15469	15485	
						15541	15557	
						15574	15590	
						15704	15720	
						15775	15791	

						16003	16019	
548775	n/a	n/a	TCCTATAACTATAACAG	4-9-4	0	14802	14818	1308
						15064	15080	
						15169	15185	
						15470	15486	
						15542	15558	
						15575	15591	
						15705	15721	
						16004	16020	
548776	n/a	n/a	CCTATAACTATAACAAT	4-9-4	0	14872	14888	1309
						14931	14947	
						15206	15222	
						15278	15294	
						15337	15353	
						15599	15615	
						15671	15687	
						15742	15758	
						15801	15817	
						15873	15889	
						15931	15947	
						16074	16090	
						16099	16115	
						16152	16168	
						16247	16263	
548777	n/a	n/a	GTAACAGTATCACTGTA	4-9-4	41	14955	14971	1310
548778	n/a	n/a	ATAACAGTATCACTGTA	4-9-4	20	15159	15175	1311
						15361	15377	
						15565	15581	
						15695	15711	
548779	n/a	n/a	GTCCTATAACTATAACA	4-9-4	0	15897	15913	1312
						15170	15186	
						15576	15592	
						15706	15722	
						16005	16021	
						16076	16092	
548780	n/a	n/a	TGTCCTATAACTATAAC	4-9-4	22	16101	16117	1313
						16154	16170	
						15171	15187	
						15577	15593	
						15707	15723	
						16006	16022	
						16077	16093	

						16102	16118	
						16155	16171	
548781	n/a	n/a	ACCTATAACTATAACAG	4-9-4	0	15776	15792	1314
548782	n/a	n/a	TACCTATAACTATAACA	4-9-4	0	15777	15793	1315
						16249	16265	
548783	n/a	n/a	ACCTATAACTATAACAA	4-9-4	0	16248	16264	1316

Example 3: Antisense inhibition of human PKK in HepaRG™ cells by antisense oligonucleotides with MOE, deoxy and cEt sugar modifications

Additional antisense oligonucleotides were designed targeting a PKK nucleic acid and were tested for their effects on PKK mRNA *in vitro*.

The chimeric antisense oligonucleotides in the tables below were designed as deoxy, MOE and cEt gapmers. The gapmers are 16 nucleosides in length wherein the nucleoside have either a MOE sugar modification, a cEt sugar modification, or a deoxy modification. The ‘Chemistry’ column describes the sugar modifications of each oligonucleotide. ‘k’ indicates an cEt sugar modification; the number indicates the number of deoxynucleosides; otherwise, ‘d’ indicates a deoxynucleoside; and ‘e’ indicates a 2’-O-methoxyethyl modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. 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 in the human gene sequence. Each gapmer listed in the tables below is targeted to either the human PKK mRNA, designated herein as SEQ ID NO: 1 or the human PKK genomic sequence, designated herein as SEQ ID NO: 10. ‘n/a’ indicates that the antisense oligonucleotide does not target that particular gene sequence.

Cultured HepaRG™ cells at a density of 20,000 cells per well were transfected using electroporation with 1,000 nM antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and PKK mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS3454 was used to measure mRNA levels. ISIS 531231 was also included in this assay. PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. The antisense 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. Results are presented as percent inhibition of PKK, relative to untreated control cells.

Table 19

ISIS NO	SEQ ID NO: 1 Start	SEQ ID NO: 1 Stop	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start	SEQ ID NO: 10 Stop	SEQ ID NO
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	Site	Site				Site	Site	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	95	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548074	1642	1657	CCTTTCTCCTTCGAGA	eekd ₁₀ kke	0	31948	31963	1317
548075	1643	1658	ACCTTTCTCCTTCGAG	eekd ₁₀ kke	0	31949	31964	1318
548076	1644	1659	CACCTTTCTCCTTCGA	eekd ₁₀ kke	26	n/a	n/a	1319
548077	1691	1706	ATTTGTTACCAAAGGA	eekd ₁₀ kke	51	33135	33150	1320
548078	1696	1711	TCTTCATTTGTTACCA	eekd ₁₀ kke	36	33140	33155	1321
548079	1762	1777	CCTTCTTTATAGCCAG	eekd ₁₀ kke	39	33206	33221	1322
548080	1763	1778	CCCTTCTTTATAGCCA	eekd ₁₀ kke	0	33207	33222	1323
548081	1764	1779	CCCCTTCTTTATAGCC	eekd ₁₀ kke	64	33208	33223	1324
548082	1776	1791	AAGCATCTTTTCCCCC	eekd ₁₀ kke	42	33220	33235	1325
548083	1800	1815	AGGGACCACCTGAATC	eekd ₁₀ kke	0	33899	33914	1326
548084	1801	1816	AAGGGACCACCTGAAT	eekd ₁₀ kke	0	33900	33915	1327
548085	1802	1817	TAAGGGACCACCTGAA	eekd ₁₀ kke	8	33901	33916	1328
548086	1803	1818	CTAAGGGACCACCTGA	eekd ₁₀ kke	36	33902	33917	1329
548087	1804	1819	ACTAAGGGACCACCTG	eekd ₁₀ kke	24	33903	33918	1330
548088	1805	1820	AACTAAGGGACCACCT	eekd ₁₀ kke	27	33904	33919	1331
548089	1806	1821	AAACTAAGGGACCACC	eekd ₁₀ kke	34	33905	33920	1332
548090	1807	1822	CAAACCTAAGGGACCAC	eekd ₁₀ kke	46	33906	33921	1333
548091	1809	1824	TGCAAACCTAAGGGACC	eekd ₁₀ kke	62	33908	33923	1334
548092	1810	1825	TTGCAAACCTAAGGGAC	eekd ₁₀ kke	30	33909	33924	1335
548093	1811	1826	TTTGCAAACCTAAGGGA	eekd ₁₀ kke	0	33910	33925	1336
548094	1812	1827	GTTTGCAAACCTAAGGG	eekd ₁₀ kke	74	33911	33926	1337
548095	1813	1828	TGTTTGCAAACCTAAGG	eekd ₁₀ kke	35	33912	33927	1338
548096	1814	1829	GTGTTTGCAAACCTAAG	eekd ₁₀ kke	23	33913	33928	1339

548097	1876	1891	TGCTCCCTGCGGGCAC	eekd ₁₀ kke	2	33975	33990	1340
548098	1887	1902	AGACACCAGGTTGCTC	eekd ₁₀ kke	0	33986	34001	1341
548099	1904	1919	CTCAGCGACTTTGGTG	eekd ₁₀ kke	55	34003	34018	1342
548100	1905	1920	ACTCAGCGACTTTGGT	eekd ₁₀ kke	25	34004	34019	1343
548101	1906	1921	TACTCAGCGACTTTGG	eekd ₁₀ kke	47	34005	34020	1344
548102	1907	1922	GTA CT CAGCGACTTTG	eekd ₁₀ kke	58	34006	34021	1345
548103	1908	1923	TGTACTCAGCGACTTT	eekd ₁₀ kke	66	34007	34022	1346
548104	1909	1924	ATGTACTCAGCGACTT	eekd ₁₀ kke	59	34008	34023	1347
548105	1910	1925	CATGTACTCAGCGACT	eekd ₁₀ kke	49	34009	34024	1348
548106	1911	1926	CCATGTACTCAGCGAC	eekd ₁₀ kke	79	34010	34025	1349
548107	1912	1927	TCCATGTACTCAGCGA	eekd ₁₀ kke	76	34011	34026	1350
548108	1953	1968	GAGCTTTTCCATCACT	eekd ₁₀ kke	61	34052	34067	1351
548109	1959	1974	GCATCTGAGCTTTTCC	eekd ₁₀ kke	77	34058	34073	1352
548110	1960	1975	TGCATCTGAGCTTTTC	eekd ₁₀ kke	62	34059	34074	1353
548111	1963	1978	GACTGCATCTGAGCTT	eekd ₁₀ kke	53	34062	34077	1354
548112	1965	1980	GTGACTGCATCTGAGC	eekd ₁₀ kke	23	34064	34079	1355
548113	1966	1981	GGT GACTGCATCTGAG	eekd ₁₀ kke	56	34065	34080	1356
548114	1967	1982	TGGT GACTGCATCTGA	eekd ₁₀ kke	70	34066	34081	1357
548115	1972	1987	CATGCTGGTGACTGCA	eekd ₁₀ kke	76	34071	34086	1358
548116	1973	1988	TCATGCTGGTGACTGC	eekd ₁₀ kke	3	34072	34087	1359
548117	1974	1989	CTCATGCTGGTGACTG	eekd ₁₀ kke	73	34073	34088	1360
548118	1975	1990	TCTCATGCTGGTGACT	eekd ₁₀ kke	47	34074	34089	1361
548119	1984	1999	TGGACTGCTTCTCATG	eekd ₁₀ kke	25	34083	34098	1362
548121	1986	2001	TCTGGACTGCTTCTCA	eekd ₁₀ kke	64	34085	34100	1363
548122	1987	2002	CTCTGGACTGCTTCTC	eekd ₁₀ kke	55	34086	34101	1364
548123	1990	2005	AGACTCTGGACTGCTT	eekd ₁₀ kke	49	34089	34104	1365
548124	1991	2006	TAGACTCTGGACTGCT	eekd ₁₀ kke	51	34090	34105	1366
548125	1992	2007	CTAGACTCTGGACTGC	eekd ₁₀ kke	89	34091	34106	1367
548126	1995	2010	TGCCTAGACTCTGGAC	eekd ₁₀ kke	19	34094	34109	1368
548127	1996	2011	TTGCCTAGACTCTGGA	eekd ₁₀ kke	60	34095	34110	1369
548128	1997	2012	ATTGCCTAGACTCTGG	eekd ₁₀ kke	55	34096	34111	1370
548129	2022	2037	TTTGACTTGA ACTCAG	eekd ₁₀ kke	35	34121	34136	1371
548130	2023	2038	ATTTGACTTGA ACTCA	eekd ₁₀ kke	27	34122	34137	1372
548131	2024	2039	AATTTGACTTGA ACTC	eekd ₁₀ kke	45	34123	34138	1373
548132	2025	2040	GAATTTGACTTGA ACT	eekd ₁₀ kke	0	34124	34139	1374
548133	2026	2041	AGAATTTGACTTGA AC	eekd ₁₀ kke	23	34125	34140	1375
548134	2027	2042	CAGAATTTGACTTGAA	eekd ₁₀ kke	17	34126	34141	1376
548135	2028	2043	TCAGAATTTGACTTGAA	eekd ₁₀ kke	46	34127	34142	1377
548136	2031	2046	GGCTCAGAATTTGACT	eekd ₁₀ kke	39	34130	34145	1378
548137	2032	2047	AGGCTCAGAATTTGAC	eekd ₁₀ kke	62	34131	34146	1379
548138	2036	2051	CCCCAGGCTCAGAATT	eekd ₁₀ kke	52	34135	34150	1380
548139	2047	2062	AGATGAGGACCCCCCA	eekd ₁₀ kke	56	34146	34161	1381

548140	2048	2063	CAGATGAGGACCCCCC	eekd ₁₀ kke	74	34147	34162	1382
548141	2049	2064	GCAGATGAGGACCCCCC	eekd ₁₀ kke	66	34148	34163	1383
548142	2063	2078	ACTCTCCATGCTTTGC	eekd ₁₀ kke	44	34162	34177	1384
548143	2064	2079	CACTCTCCATGCTTTG	eekd ₁₀ kke	39	34163	34178	1385
548144	2068	2083	ATGCCACTCTCCATGC	eekd ₁₀ kke	52	34167	34182	1386
548145	2079	2094	ATGCAAAGAAGATGCC	eekd ₁₀ kke	63	34178	34193	1387
548146	2088	2103	GTCCTTAGGATGCAAA	eekd ₁₀ kke	68	34187	34202	1388
548147	2089	2104	CGTCCTTAGGATGCAA	eekd ₁₀ kke	81	34188	34203	1389
548148	2114	2129	GCAGCTCTGAGTGCAC	eekd ₁₀ kke	66	34213	34228	1390
548149	2127	2142	GACATTGTCCTCAGCA	eekd ₁₀ kke	39	34226	34241	1391
548150	2129	2144	CAGACATTGTCCTCAG	eekd ₁₀ kke	60	34228	34243	1392

Table 20

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	84	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
547843	384	399	CACTTATTTGATGACC	eekd ₁₀ kke	83	9918	9933	1393
547844	385	400	GCACTTATTTGATGAC	eekd ₁₀ kke	13	n/a	n/a	1394
547845	394	409	CGATGGCAAGCACTTA	eekd ₁₀ kke	0	n/a	n/a	1395
547846	395	410	TCGATGGCAAGCACTT	eekd ₁₀ kke	0	n/a	n/a	1396
547847	396	411	CTCGATGGCAAGCACT	eekd ₁₀ kke	46	n/a	n/a	1397
547848	400	415	ATGTCTCGATGGCAAG	eekd ₁₀ kke	93	12656	12671	1398
547849	401	416	AATGTCTCGATGGCAA	eekd ₁₀ kke	79	12657	12672	1399

547850	402	417	AAATGTCTCGATGGCA	eekd ₁₀ kke	51	12658	12673	1400
547851	403	418	TAAATGTCTCGATGGC	eekd ₁₀ kke	93	12659	12674	1401
547852	404	419	ATAAATGTCTCGATGG	eekd ₁₀ kke	67	12660	12675	1402
547853	405	420	TATAAATGTCTCGATG	eekd ₁₀ kke	0	12661	12676	1403
547854	416	431	ATCAACTCCTTTATAA	eekd ₁₀ kke	10	12672	12687	1404
547855	417	432	TATCAACTCCTTTATA	eekd ₁₀ kke	59	12673	12688	1405
547856	419	434	CATATCAACTCCTTTA	eekd ₁₀ kke	93	12675	12690	1406
547858	423	438	CTCTCATATCAACTCC	eekd ₁₀ kke	82	12679	12694	1407
547859	424	439	CCTCTCATATCAACTC	eekd ₁₀ kke	77	12680	12695	1408
547860	425	440	TCCTCTCATATCAACT	eekd ₁₀ kke	71	12681	12696	1409
547861	427	442	ACTCCTCTCATATCAA	eekd ₁₀ kke	0	12683	12698	1410
547862	428	443	GACTCCTCTCATATCA	eekd ₁₀ kke	22	12684	12699	1411
547863	429	444	TGACTCCTCTCATATC	eekd ₁₀ kke	73	12685	12700	1412
547864	430	445	TTGACTCCTCTCATAT	eekd ₁₀ kke	53	12686	12701	1413
547865	434	449	AAAATTGACTCCTCTC	eekd ₁₀ kke	3	12690	12705	1414
547866	436	451	TTAAAATTGACTCCTC	eekd ₁₀ kke	46	12692	12707	1415
547867	447	462	CCTTAGACACATTAAA	eekd ₁₀ kke	34	12703	12718	1416
547868	448	463	ACCTTAGACACATTAA	eekd ₁₀ kke	47	12704	12719	1417
547869	449	464	AACCTTAGACACATTA	eekd ₁₀ kke	45	12705	12720	1418
547870	451	466	CTAACCTTAGACACAT	eekd ₁₀ kke	89	12707	12722	1419
547871	452	467	GCTAACCTTAGACACA	eekd ₁₀ kke	96	12708	12723	1420
547872	453	468	TGCTAACCTTAGACAC	eekd ₁₀ kke	85	12709	12724	1421
547873	454	469	CTGCTAACCTTAGACA	eekd ₁₀ kke	77	12710	12725	1422
547874	455	470	ACTGCTAACCTTAGAC	eekd ₁₀ kke	70	12711	12726	1423
547875	456	471	CACTGCTAACCTTAGA	eekd ₁₀ kke	73	12712	12727	1424
547876	457	472	ACACTGCTAACCTTAG	eekd ₁₀ kke	78	12713	12728	1425
547877	458	473	AACACTGCTAACCTTA	eekd ₁₀ kke	81	12714	12729	1426
547879	460	475	TCAACACTGCTAACCT	eekd ₁₀ kke	69	12716	12731	1427
547880	461	476	TTCAACACTGCTAACCC	eekd ₁₀ kke	69	12717	12732	1428
547881	465	480	ATTCTTCAACACTGCT	eekd ₁₀ kke	0	12721	12736	1429
547882	500	515	CTGGCAGCGAATGTTA	eekd ₁₀ kke	91	12756	12771	1430
547883	501	516	ACTGGCAGCGAATGTT	eekd ₁₀ kke	99	12757	12772	1431
547884	518	533	CGTGGCATATGAAAAA	eekd ₁₀ kke	87	12774	12789	1432
547885	539	554	CTCTGCCTTGTGAAAT	eekd ₁₀ kke	45	12795	12810	1433
547886	544	559	CGGTACTCTGCCTTGT	eekd ₁₀ kke	97	12800	12815	1434
547889	547	562	TTCCGGTACTCTGCCT	eekd ₁₀ kke	91	n/a	n/a	1435
547890	550	565	TTGTTCCGGTACTCTG	eekd ₁₀ kke	97	n/a	n/a	1436
547891	551	566	ATTGTTCCGGTACTCT	eekd ₁₀ kke	84	n/a	n/a	1437
547892	553	568	CAATTGTTCCGGTACT	eekd ₁₀ kke	29	n/a	n/a	1438

547893	554	569	GCAATTGTTCCGGTAC	eekd ₁₀ kke	81	n/a	n/a	1439
547894	555	570	GGCAATTGTTCCGGTA	eekd ₁₀ kke	92	n/a	n/a	1440
547898	563	578	CTTTAATAGGCAATTG	eekd ₁₀ kke	0	14134	14149	1441
547899	566	581	GTACTTTAATAGGCAA	eekd ₁₀ kke	49	14137	14152	1442
547900	567	582	TGTACTTTAATAGGCA	eekd ₁₀ kke	93	14138	14153	1443
547901	568	583	CTGTACTTTAATAGGC	eekd ₁₀ kke	77	14139	14154	1444
547902	569	584	ACTGTACTTTAATAGG	eekd ₁₀ kke	20	14140	14155	1445
547903	604	619	CTCAGCACCTTTATAG	eekd ₁₀ kke	62	14175	14190	1446
547904	605	620	ACTCAGCACCTTTATA	eekd ₁₀ kke	56	14176	14191	1447
547905	606	621	TACTCAGCACCTTTAT	eekd ₁₀ kke	20	14177	14192	1448
547906	607	622	TTACTCAGCACCTTTA	eekd ₁₀ kke	59	14178	14193	1449
547907	652	667	ATTTCTGAAAGGGCAC	eekd ₁₀ kke	27	14223	14238	1450
547908	654	669	CAATTTCTGAAAGGGC	eekd ₁₀ kke	94	14225	14240	1451
547909	655	670	CCAATTTCTGAAAGGG	eekd ₁₀ kke	82	14226	14241	1452
547910	656	671	ACCAATTTCTGAAAGG	eekd ₁₀ kke	26	14227	14242	1453
547911	661	676	TGGCAACCAATTTCTG	eekd ₁₀ kke	0	n/a	n/a	1454
547912	701	716	ATCCACATCTGAGAAC	eekd ₁₀ kke	23	26149	26164	1455
547913	706	721	GCAACATCCACATCTG	eekd ₁₀ kke	71	26154	26169	1456
547914	707	722	GGCAACATCCACATCT	eekd ₁₀ kke	74	26155	26170	1457
547915	708	723	TGGCAACATCCACATC	eekd ₁₀ kke	0	26156	26171	1458
547916	710	725	CCTGGCAACATCCACA	eekd ₁₀ kke	70	26158	26173	1459
547917	712	727	ACCCTGGCAACATCCA	eekd ₁₀ kke	33	26160	26175	1460
547918	713	728	AACCCTGGCAACATCC	eekd ₁₀ kke	1	26161	26176	1461
547919	714	729	GAACCCTGGCAACATC	eekd ₁₀ kke	41	26162	26177	1462

Table 21

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	62	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	

						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	88	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
547751	7	22	TGAACGGTCTTCAAGC	eekd ₁₀ kke	0	3399	3414	1463
547753	8	23	ATGAACGGTCTTCAAG	eekd ₁₀ kke	3	3400	3415	1464
547755	13	28	TAAAAATGAACGGTCT	eekd ₁₀ kke	0	3405	3420	1465
547757	28	43	GAGTCTCTTGTCACCT	eekd ₁₀ kke	69	3420	3435	1466
547759	29	44	TGAGTCTCTTGTCACCT	eekd ₁₀ kke	73	3421	3436	1467
547763	31	46	GGTGAGTCTCTTGTCAC	eekd ₁₀ kke	66	3423	3438	1468
547765	32	47	AGGTGAGTCTCTTGTC	eekd ₁₀ kke	20	3424	3439	1469
547767	35	50	TGGAGGTGAGTCTCTT	eekd ₁₀ kke	74	3427	3442	1470
547769	36	51	TTGGAGGTGAGTCTCT	eekd ₁₀ kke	81	3428	3443	1471
547771	37	52	CTTGGAGGTGAGTCTC	eekd ₁₀ kke	60	3429	3444	1472
547773	38	53	TCTTGGAGGTGAGTCT	eekd ₁₀ kke	47	3430	3445	1473
547777	43	58	TTGCTTCTTGGAGGTG	eekd ₁₀ kke	69	3435	3450	1474
547779	44	59	ATTGCTTCTTGGAGGT	eekd ₁₀ kke	41	3436	3451	1475
547781	46	61	CAATTGCTTCTTGGAG	eekd ₁₀ kke	49	3438	3453	1476
547783	48	63	CACAATTGCTTCTTGG	eekd ₁₀ kke	48	3440	3455	1477
547784	72	87	GCTTGAATAAAAATCAT	eekd ₁₀ kke	46	4071	4086	1478
547785	79	94	GTTGCTTGTGTAATA	eekd ₁₀ kke	48	4078	4093	1479

547786	80	95	AGTTGCTTGCTTGAAT	eekd ₁₀ kke	44	4079	4094	1480
547787	81	96	AAGTTGCTTGCTTGAA	eekd ₁₀ kke	22	4080	4095	1481
547788	82	97	TAAGTTGCTTGCTTGA	eekd ₁₀ kke	49	4081	4096	1482
547789	86	101	GAAATAAGTTGCTTGC	eekd ₁₀ kke	20	4085	4100	1483
547790	87	102	TGAAATAAGTTGCTTG	eekd ₁₀ kke	23	4086	4101	1484
547791	106	121	ACTGTAGCAAACAAGG	eekd ₁₀ kke	49	4105	4120	1485
547792	116	131	TCCACAGGAAACTGTA	eekd ₁₀ kke	31	n/a	n/a	1486
547793	117	132	ATCCACAGGAAACTGT	eekd ₁₀ kke	16	n/a	n/a	1487
547794	136	151	TCATAGAGTTGAGTCA	eekd ₁₀ kke	49	8008	8023	1488
547795	155	170	ACCTCTGAAGAAGGCG	eekd ₁₀ kke	66	8027	8042	1489
547796	161	176	ATCCCCACCTCTGAAG	eekd ₁₀ kke	35	8033	8048	1490
547797	167	182	AGCTACATCCCCACCT	eekd ₁₀ kke	33	8039	8054	1491
547799	169	184	GAAGCTACATCCCCAC	eekd ₁₀ kke	41	8041	8056	1492
547800	174	189	ACATGGAAGCTACATC	eekd ₁₀ kke	20	8046	8061	1493
547801	175	190	TACATGGAAGCTACAT	eekd ₁₀ kke	11	8047	8062	1494
547802	176	191	GTACATGGAAGCTACA	eekd ₁₀ kke	41	8048	8063	1495
547803	177	192	TGTACATGGAAGCTAC	eekd ₁₀ kke	0	8049	8064	1496
547804	178	193	GTGTACATGGAAGCTA	eekd ₁₀ kke	22	8050	8065	1497
547805	180	195	GGGTGTACATGGAAGC	eekd ₁₀ kke	54	8052	8067	1498
547807	197	212	GCAGTATTGGGCATTT	eekd ₁₀ kke	75	8069	8084	1499
547808	203	218	CATCTGGCAGTATTGG	eekd ₁₀ kke	56	8075	8090	1500
547809	204	219	TCATCTGGCAGTATTG	eekd ₁₀ kke	33	8076	8091	1501
547810	206	221	CCTCATCTGGCAGTAT	eekd ₁₀ kke	60	8078	8093	1502
547811	207	222	ACCTCATCTGGCAGTA	eekd ₁₀ kke	49	8079	8094	1503
547812	211	226	GTGCACCTCATCTGGC	eekd ₁₀ kke	51	8083	8098	1504
547813	219	234	GGTGGAATGTGCACCT	eekd ₁₀ kke	34	8091	8106	1505
547814	220	235	GGGTGGAATGTGCACC	eekd ₁₀ kke	60	8092	8107	1506
547815	255	270	AACTTGCTGGAAGAAA	eekd ₁₀ kke	3	8127	8142	1507
547816	256	271	GAACTTGCTGGAAGAA	eekd ₁₀ kke	45	8128	8143	1508
547817	257	272	TGAACTTGCTGGAAGA	eekd ₁₀ kke	18	8129	8144	1509
547818	260	275	GATTGAACTTGCTGGA	eekd ₁₀ kke	4	8132	8147	1510
547819	264	279	CATTGATTGAACTTGC	eekd ₁₀ kke	11	8136	8151	1511
547820	265	280	TCATTGATTGAACTTG	eekd ₁₀ kke	0	8137	8152	1512
547821	282	297	CAAACCTTTTCTCCAT	eekd ₁₀ kke	44	n/a	n/a	1513
547822	287	302	GCAACCAAACCTTTTC	eekd ₁₀ kke	71	n/a	n/a	1514
547823	288	303	AGCAACCAAACCTTTT	eekd ₁₀ kke	51	n/a	n/a	1515
547824	331	346	CGATGTACTTTTGGCA	eekd ₁₀ kke	82	9865	9880	1516
547825	332	347	TCGATGTACTTTTGGC	eekd ₁₀ kke	59	9866	9881	1517
547826	333	348	TTCGATGTACTTTTGG	eekd ₁₀ kke	31	9867	9882	1518
547827	334	349	GTTCGATGTACTTTTG	eekd ₁₀ kke	47	9868	9883	1519
547828	337	352	CCTGTTCGATGTACTT	eekd ₁₀ kke	63	9871	9886	1520
547829	338	353	ACCTGTTCGATGTACT	eekd ₁₀ kke	59	9872	9887	1521

547830	340	355	GCACCTGTTTCGATGTA	eekd ₁₀ kke	74	9874	9889	1522
547831	342	357	CTGCACCTGTTTCGATG	eekd ₁₀ kke	49	9876	9891	1523
547832	343	358	ACTGCACCTGTTTCGAT	eekd ₁₀ kke	59	9877	9892	1524
547833	344	359	AACTGCACCTGTTTCGA	eekd ₁₀ kke	40	9878	9893	1525
547834	345	360	AAACTGCACCTGTTTCG	eekd ₁₀ kke	63	9879	9894	1526
547835	349	364	CCAGAAACTGCACCTG	eekd ₁₀ kke	81	9883	9898	1527
547836	350	365	TCCAGAAACTGCACCT	eekd ₁₀ kke	50	9884	9899	1528
547837	352	367	TGTCCAGAAACTGCAC	eekd ₁₀ kke	51	9886	9901	1529
547838	362	377	CTTCAAGGAATGTCCA	eekd ₁₀ kke	45	9896	9911	1530
547839	363	378	GCTTCAAGGAATGTCC	eekd ₁₀ kke	35	9897	9912	1531
547840	365	380	TTGCTTCAAGGAATGT	eekd ₁₀ kke	36	9899	9914	1532
547841	369	384	CACATTGCTTCAAGGA	eekd ₁₀ kke	42	9903	9918	1533
547842	375	390	GATGACCACATTGCTT	eekd ₁₀ kke	10	9909	9924	1534

Table 22

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	75	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	91	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	

						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
547843	384	399	CACTTATTTGATGACC	eekd ₁₀ kke	83	9918	9933	1393
547844	385	400	GCACTTATTTGATGAC	eekd ₁₀ kke	76	n/a	n/a	1394
547845	394	409	CGATGGCAAGCACTTA	eekd ₁₀ kke	64	n/a	n/a	1395
547846	395	410	TCGATGGCAAGCACTT	eekd ₁₀ kke	42	n/a	n/a	1396
547847	396	411	CTCGATGGCAAGCACT	eekd ₁₀ kke	72	n/a	n/a	1397
547848	400	415	ATGTCTCGATGGCAAG	eekd ₁₀ kke	79	12656	12671	1398
547849	401	416	AATGTCTCGATGGCAA	eekd ₁₀ kke	90	12657	12672	1399
547850	402	417	AAATGTCTCGATGGCA	eekd ₁₀ kke	80	12658	12673	1400
547851	403	418	TAAATGTCTCGATGGC	eekd ₁₀ kke	84	12659	12674	1401
547852	404	419	ATAAATGTCTCGATGG	eekd ₁₀ kke	66	12660	12675	1402
547853	405	420	TATAAATGTCTCGATG	eekd ₁₀ kke	30	12661	12676	1403
547854	416	431	ATCAACTCCTTTATAA	eekd ₁₀ kke	9	12672	12687	1404
547855	417	432	TATCAACTCCTTTATA	eekd ₁₀ kke	38	12673	12688	1405
547856	419	434	CATATCAACTCCTTTA	eekd ₁₀ kke	51	12675	12690	1406
547857	421	436	CTCATATCAACTCCTT	eekd ₁₀ kke	84	12677	12692	1535
547858	423	438	CTCTCATATCAACTCC	eekd ₁₀ kke	76	12679	12694	1407
547859	424	439	CCTCTCATATCAACTC	eekd ₁₀ kke	88	12680	12695	1408
547860	425	440	TCCTCTCATATCAACT	eekd ₁₀ kke	70	12681	12696	1409
547861	427	442	ACTCCTCTCATATCAA	eekd ₁₀ kke	57	12683	12698	1410
547862	428	443	GACTCCTCTCATATCA	eekd ₁₀ kke	88	12684	12699	1411
547863	429	444	TGACTCCTCTCATATC	eekd ₁₀ kke	77	12685	12700	1412
547864	430	445	TTGACTCCTCTCATAT	eekd ₁₀ kke	73	12686	12701	1413
547865	434	449	AAAATTGACTCCTCTC	eekd ₁₀ kke	61	12690	12705	1414
547866	436	451	TTAAAATTGACTCCTC	eekd ₁₀ kke	40	12692	12707	1415
547867	447	462	CCTTAGACACATTA	eekd ₁₀ kke	53	12703	12718	1416
547868	448	463	ACCTTAGACACATTAA	eekd ₁₀ kke	71	12704	12719	1417
547869	449	464	AACCTTAGACACATTA	eekd ₁₀ kke	77	12705	12720	1418
547870	451	466	CTAACCTTAGACACAT	eekd ₁₀ kke	83	12707	12722	1419
547871	452	467	GCTAACCTTAGACACA	eekd ₁₀ kke	77	12708	12723	1420

547872	453	468	TGCTAACCTTAGACAC	eekd ₁₀ kke	73	12709	12724	1421
547873	454	469	CTGCTAACCTTAGACA	eekd ₁₀ kke	82	12710	12725	1422
547874	455	470	ACTGCTAACCTTAGAC	eekd ₁₀ kke	60	12711	12726	1423
547875	456	471	CACTGCTAACCTTAGA	eekd ₁₀ kke	57	12712	12727	1424
547876	457	472	ACACTGCTAACCTTAG	eekd ₁₀ kke	59	12713	12728	1425
547877	458	473	AACACTGCTAACCTTA	eekd ₁₀ kke	93	12714	12729	1426
547878	459	474	CAACACTGCTAACCTT	eekd ₁₀ kke	62	12715	12730	1536
547879	460	475	TCAACACTGCTAACCT	eekd ₁₀ kke	65	12716	12731	1427
547880	461	476	TTCAACACTGCTAACC	eekd ₁₀ kke	59	12717	12732	1428
547881	465	480	ATTCTTCAACACTGCT	eekd ₁₀ kke	50	12721	12736	1429
547882	500	515	CTGGCAGCGAATGTTA	eekd ₁₀ kke	96	12756	12771	1430
547883	501	516	ACTGGCAGCGAATGTT	eekd ₁₀ kke	0	12757	12772	1431
547884	518	533	CGTGGCATATGAAAAA	eekd ₁₀ kke	49	12774	12789	1432
547885	539	554	CTCTGCCTTGTGAAAT	eekd ₁₀ kke	57	12795	12810	1433
547886	544	559	CGGTACTCTGCCTTGT	eekd ₁₀ kke	89	12800	12815	1434
547887	545	560	CCGGTACTCTGCCTTG	eekd ₁₀ kke	99	12801	12816	1537
547888	546	561	TCCGGTACTCTGCCTT	eekd ₁₀ kke	99	n/a	n/a	1538
547889	547	562	TTCCGGTACTCTGCCT	eekd ₁₀ kke	97	n/a	n/a	1435
547890	550	565	TTGTTCCGGTACTCTG	eekd ₁₀ kke	90	n/a	n/a	1436
547891	551	566	ATTGTTCCGGTACTCT	eekd ₁₀ kke	88	n/a	n/a	1437
547892	553	568	CAATTGTTCCGGTACT	eekd ₁₀ kke	28	n/a	n/a	1438
547893	554	569	GCAATTGTTCCGGTAC	eekd ₁₀ kke	80	n/a	n/a	1439
547894	555	570	GGCAATTGTTCCGGTA	eekd ₁₀ kke	91	n/a	n/a	1440
547895	556	571	AGGCAATTGTTCCGGT	eekd ₁₀ kke	94	n/a	n/a	1539
547896	557	572	TAGGCAATTGTTCCGG	eekd ₁₀ kke	95	n/a	n/a	1540
547897	558	573	ATAGGCAATTGTTCCG	eekd ₁₀ kke	82	n/a	n/a	1541
547898	563	578	CTTTAATAGGCAATTG	eekd ₁₀ kke	28	14134	14149	1441
547899	566	581	GTACTTTAATAGGCAA	eekd ₁₀ kke	68	14137	14152	1442
547900	567	582	TGTACTTTAATAGGCA	eekd ₁₀ kke	68	14138	14153	1443
547901	568	583	CTGTACTTTAATAGGC	eekd ₁₀ kke	85	14139	14154	1444
547902	569	584	ACTGTACTTTAATAGG	eekd ₁₀ kke	33	14140	14155	1445
547903	604	619	CTCAGCACCTTTATAG	eekd ₁₀ kke	6	14175	14190	1446
547904	605	620	ACTCAGCACCTTTATA	eekd ₁₀ kke	41	14176	14191	1447
547905	606	621	TACTCAGCACCTTTAT	eekd ₁₀ kke	59	14177	14192	1448
547906	607	622	TTACTCAGCACCTTTA	eekd ₁₀ kke	70	14178	14193	1449
547907	652	667	ATTTCTGAAAGGGCAC	eekd ₁₀ kke	27	14223	14238	1450
547908	654	669	CAATTTCTGAAAGGGC	eekd ₁₀ kke	71	14225	14240	1451
547909	655	670	CCAATTTCTGAAAGGG	eekd ₁₀ kke	51	14226	14241	1452
547910	656	671	ACCAATTTCTGAAAGG	eekd ₁₀ kke	34	14227	14242	1453

547911	661	676	TGGCAACCAATTTCTG	eekd ₁₀ kke	15	n/a	n/a	1454
547912	701	716	ATCCACATCTGAGAAC	eekd ₁₀ kke	53	26149	26164	1455
547913	706	721	GCAACATCCACATCTG	eekd ₁₀ kke	61	26154	26169	1456
547914	707	722	GGCAACATCCACATCT	eekd ₁₀ kke	63	26155	26170	1457
547915	708	723	TGGCAACATCCACATC	eekd ₁₀ kke	62	26156	26171	1458
547916	710	725	CCTGGCAACATCCACA	eekd ₁₀ kke	56	26158	26173	1459
547917	712	727	ACCCTGGCAACATCCA	eekd ₁₀ kke	54	26160	26175	1460
547918	713	728	AACCCTGGCAACATCC	eekd ₁₀ kke	65	26161	26176	1461
547919	714	729	GAACCCTGGCAACATC	eekd ₁₀ kke	73	26162	26177	1462

Table 23

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eekd ₁₀ keee	16	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	83	15887	15906	1267
						15945	15964	
						14746	14761	
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	

						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
547920	716	731	GAGAACCCTGGCAACA	eekd ₁₀ kke	52	26164	26179	1542
547921	717	732	TGAGAACCCTGGCAAC	eekd ₁₀ kke	43	26165	26180	1543
547922	722	737	TGGAGTGAGAACCCTG	eekd ₁₀ kke	79	26170	26185	1544
547923	725	740	ATCTGGAGTGAGAACC	eekd ₁₀ kke	68	26173	26188	1545
547924	742	757	GTCCGACACACAAAAG	eekd ₁₀ kke	53	26190	26205	1546
547925	743	758	GGTCCGACACACAAAA	eekd ₁₀ kke	16	26191	26206	1547
547927	745	760	ATGGTCCGACACACAA	eekd ₁₀ kke	79	26193	26208	1548
547928	746	761	GATGGTCCGACACACA	eekd ₁₀ kke	70	26194	26209	1549
547929	747	762	AGATGGTCCGACACAC	eekd ₁₀ kke	65	26195	26210	1550
547930	757	772	TGATAGGTGCAGATGG	eekd ₁₀ kke	48	26205	26220	1551
547931	758	773	GTGATAGGTGCAGATG	eekd ₁₀ kke	58	26206	26221	1552
547932	804	819	CGATTTTCCATACATT	eekd ₁₀ kke	33	26252	26267	1553
547933	805	820	TCGATTTTCCATACAT	eekd ₁₀ kke	44	26253	26268	1554
547934	806	821	CTCGATTTTCCATACA	eekd ₁₀ kke	38	26254	26269	1555
547935	807	822	ACTCGATTTTCCATAC	eekd ₁₀ kke	27	26255	26270	1556
547936	808	823	GACTCGATTTTCCATA	eekd ₁₀ kke	44	26256	26271	1557
547937	811	826	TGTGACTCGATTTTCC	eekd ₁₀ kke	56	26259	26274	1558
547938	812	827	TTGTGACTCGATTTTC	eekd ₁₀ kke	56	26260	26275	1559
547939	813	828	TTTGTGACTCGATTTT	eekd ₁₀ kke	70	26261	26276	1560
547940	817	832	TTTCTTTGTGACTCGA	eekd ₁₀ kke	71	n/a	n/a	1561
547941	852	867	GTGTGCCACTTTCAGA	eekd ₁₀ kke	66	27116	27131	1562
547942	853	868	GGTGTGCCACTTTCAG	eekd ₁₀ kke	85	27117	27132	1563
547943	854	869	TGGTGTGCCACTTTC	eekd ₁₀ kke	83	27118	27133	1564
547944	857	872	ACTTGGTGTGCCACTT	eekd ₁₀ kke	54	27121	27136	1565
547945	858	873	AACTTGGTGTGCCACT	eekd ₁₀ kke	62	27122	27137	1566
547946	859	874	GAACTTGGTGTGCCAC	eekd ₁₀ kke	81	27123	27138	1567
547947	860	875	GGAACCTGGTGTGCCA	eekd ₁₀ kke	80	27124	27139	1568
547948	861	876	AGGAACTTGGTGTGCC	eekd ₁₀ kke	77	27125	27140	1569
547949	880	895	GTGTTTTCTTGAGGAG	eekd ₁₀ kke	6	27144	27159	1570
547950	881	896	GGTGTTTTCTTGAGGA	eekd ₁₀ kke	49	27145	27160	1571

547951	887	902	AGATATGGTGTTCCT	eekd ₁₀ kke	25	27151	27166	1572
547952	888	903	CAGATATGGTGTTC	eekd ₁₀ kke	46	27152	27167	1573
547953	895	910	CTATATCCAGATATGG	eekd ₁₀ kke	16	27159	27174	1574
547954	902	917	TAAAAGGCTATATCCA	eekd ₁₀ kke	36	27166	27181	1575
547956	904	919	GTTAAAAGGCTATATC	eekd ₁₀ kke	13	27168	27183	1576
547957	905	920	GGTAAAAGGCTATAT	eekd ₁₀ kke	6	27169	27184	1577
547958	907	922	CAGGTAAAAGGCTAT	eekd ₁₀ kke	57	27171	27186	1578
547959	908	923	GCAGGTAAAAGGCTA	eekd ₁₀ kke	60	27172	27187	1579
547960	909	924	TGCAGGTAAAAGGCT	eekd ₁₀ kke	40	27173	27188	1580
547961	910	925	TTGCAGGTAAAAGGC	eekd ₁₀ kke	5	27174	27189	1581
547962	911	926	TTTGCAGGTAAAAGG	eekd ₁₀ kke	16	27175	27190	1582
547963	927	942	G TTCAGGTAAAGTCT	eekd ₁₀ kke	22	n/a	n/a	1583
547964	928	943	GGTTCAGGTAAAGTTC	eekd ₁₀ kke	0	n/a	n/a	1584
547965	929	944	GGGTTTCAGGTAAAGTT	eekd ₁₀ kke	29	n/a	n/a	1585
547966	930	945	AGGGTTCAGGTAAAGT	eekd ₁₀ kke	13	n/a	n/a	1586
547967	933	948	GGCAGGGTTCAGGTAA	eekd ₁₀ kke	25	n/a	n/a	1587
547968	940	955	TTAGAATGGCAGGGTT	eekd ₁₀ kke	37	27362	27377	1588
547969	953	968	TCCCGGGTAAATTTTA	eekd ₁₀ kke	0	27375	27390	1589
547970	954	969	CTCCCGGGTAAATTTT	eekd ₁₀ kke	42	27376	27391	1590
547972	958	973	TCAACTCCCGGGTAAA	eekd ₁₀ kke	49	27380	27395	1591
547973	961	976	AAGTCAACTCCCGGGT	eekd ₁₀ kke	62	27383	27398	1592
547974	962	977	AAAGTCAACTCCCGGG	eekd ₁₀ kke	52	27384	27399	1593
547975	963	978	CAAAGTCAACTCCCGG	eekd ₁₀ kke	44	27385	27400	1594
547976	964	979	CCAAAGTCAACTCCCG	eekd ₁₀ kke	49	27386	27401	1595
547977	967	982	CCTCCAAAGTCAACTC	eekd ₁₀ kke	57	27389	27404	1596
547978	1014	1029	CTTGCAAACATTCAC	eekd ₁₀ kke	71	27436	27451	1597
547979	1018	1033	GTCTCTTGCAAACAT	eekd ₁₀ kke	77	27440	27455	1598
547980	1020	1035	AAGTCTCTTGCAAAC	eekd ₁₀ kke	54	27442	27457	1599
547981	1029	1044	TCTTTGTGCAAGTCTC	eekd ₁₀ kke	76	27451	27466	1600
547982	1034	1049	AATCATCTTTGTGCAA	eekd ₁₀ kke	54	27456	27471	1601
547983	1035	1050	GAATCATCTTTGTGCA	eekd ₁₀ kke	56	27457	27472	1602
547984	1036	1051	CGAATCATCTTTGTGC	eekd ₁₀ kke	55	27458	27473	1603
547985	1037	1052	GCGAATCATCTTTGTG	eekd ₁₀ kke	63	27459	27474	1604
547986	1039	1054	CAGCGAATCATCTTTG	eekd ₁₀ kke	63	27461	27476	1605
547987	1040	1055	ACAGCGAATCATCTTT	eekd ₁₀ kke	64	27462	27477	1606
547988	1042	1057	TGACAGCGAATCATCT	eekd ₁₀ kke	56	27464	27479	1607
547989	1043	1058	CTGACAGCGAATCATC	eekd ₁₀ kke	66	27465	27480	1608
547990	1044	1059	ACTGACAGCGAATCAT	eekd ₁₀ kke	58	27466	27481	1609
547991	1077	1092	TACAGTCTTCTGGGAG	eekd ₁₀ kke	0	27499	27514	1610

547992	1080	1095	CCTTACAGTCTTCTGG	eekd ₁₀ kke	17	27502	27517	1611
547993	1113	1128	TAGATAATCTTAAGAA	eekd ₁₀ kke	26	27634	27649	1612
547994	1120	1135	CCATCCATAGATAATC	eekd ₁₀ kke	53	27641	27656	1613
547995	1149	1164	GTGTCCCATACGCAAT	eekd ₁₀ kke	64	27670	27685	1614
547996	1150	1165	TGTGTCCCATACGCAA	eekd ₁₀ kke	65	27671	27686	1615

Table 24

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	0	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	80	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	

						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
547997	1151	1166	TTGTGTCCCATACGCA	eekd ₁₀ kke	89	27672	27687	1616
547998	1152	1167	CTTGTGTCCCATACGC	eekd ₁₀ kke	82	27673	27688	1617
547999	1153	1168	CCTTGTGTCCCATACG	eekd ₁₀ kke	50	27674	27689	1618
548000	1154	1169	CCCTTGTGTCCCATAC	eekd ₁₀ kke	54	27675	27690	1619
548001	1163	1178	ACCAGAGCTCCCTTGT	eekd ₁₀ kke	64	27684	27699	1620
548002	1164	1179	AACCAGAGCTCCCTTG	eekd ₁₀ kke	56	27685	27700	1621
548003	1165	1180	TAACCAGAGCTCCCTT	eekd ₁₀ kke	66	27686	27701	1622
548004	1167	1182	AGTAACCAGAGCTCCC	eekd ₁₀ kke	80	27688	27703	1623
548005	1169	1184	AGAGTAACCAGAGCTC	eekd ₁₀ kke	77	27690	27705	1624
548006	1172	1187	CAAAGAGTAACCAGAG	eekd ₁₀ kke	54	27693	27708	1625
548007	1174	1189	CTCAAAGAGTAACCAG	eekd ₁₀ kke	70	27695	27710	1626
548008	1175	1190	TCTCAAAGAGTAACCA	eekd ₁₀ kke	71	27696	27711	1627
548009	1184	1199	GTTACACAATCTCAA	eekd ₁₀ kke	47	27705	27720	1628
548010	1187	1202	AGTGTTACACAATCTC	eekd ₁₀ kke	80	27708	27723	1629
548011	1189	1204	CCAGTGTTACACAATC	eekd ₁₀ kke	14	27710	27725	1630
548012	1192	1207	TCCCCAGTGTTACACA	eekd ₁₀ kke	3	27713	27728	1631
548013	1193	1208	GTCCCCAGTGTTACAC	eekd ₁₀ kke	37	27714	27729	1632
548014	1194	1209	TGTCCCCAGTGTTACA	eekd ₁₀ kke	31	27715	27730	1633
548015	1195	1210	TTGTCCCCAGTGTTAC	eekd ₁₀ kke	50	27716	27731	1634
548016	1248	1263	AAGAGTTTGTTCCTCC	eekd ₁₀ kke	55	27924	27939	1635
548017	1252	1267	CAAGAAGAGTTTGTTC	eekd ₁₀ kke	3	27928	27943	1636
548018	1253	1268	CCAAGAAGAGTTTGT	eekd ₁₀ kke	22	27929	27944	1637
548019	1255	1270	CCCCAAGAAGAGTTTG	eekd ₁₀ kke	24	27931	27946	1638
548020	1256	1271	TCCCCAAGAAGAGTTT	eekd ₁₀ kke	76	27932	27947	1639
548021	1261	1276	CACTCTCCCCAAGAAG	eekd ₁₀ kke	0	27937	27952	1640
548022	1262	1277	CCACTCTCCCCAAGAA	eekd ₁₀ kke	69	27938	27953	1641
548023	1290	1305	GCTTCACCTGCAGGCT	eekd ₁₀ kke	58	27966	27981	1642
548024	1297	1312	GCTGTCAGCTTCACCT	eekd ₁₀ kke	79	27973	27988	1643
548025	1300	1315	TGAGCTGTCAGCTTCA	eekd ₁₀ kke	66	27976	27991	1644
548026	1332	1347	GTCCTATGAGTGACCC	eekd ₁₀ kke	52	28008	28023	1645
548027	1334	1349	GTGTCCTATGAGTGAC	eekd ₁₀ kke	18	28010	28025	1646
548028	1335	1350	GGTGTCTATGAGTGA	eekd ₁₀ kke	38	28011	28026	1647
548029	1336	1351	TGGTGTCTATGAGTG	eekd ₁₀ kke	12	28012	28027	1648
548030	1337	1352	CTGGTGTCTATGAGT	eekd ₁₀ kke	52	28013	28028	1649
548031	1397	1412	GATGCGCCAAACATCC	eekd ₁₀ kke	73	30475	30490	1650

548032	1398	1413	AGATGCGCCAAACATC	eekd ₁₀ kke	51	30476	30491	1651
548034	1400	1415	ATAGATGCGCCAAACA	eekd ₁₀ kke	31	30478	30493	1652
548035	1404	1419	CACTATAGATGCGCCA	eekd ₁₀ kke	44	30482	30497	1653
548036	1405	1420	CCACTATAGATGCGCC	eekd ₁₀ kke	74	30483	30498	1654
548037	1427	1442	AATGTCTGACAGATTT	eekd ₁₀ kke	70	30505	30520	1655
548038	1428	1443	TAATGTCTGACAGATT	eekd ₁₀ kke	67	30506	30521	1656
548039	1445	1460	GAAAGGTGTATCTTTT	eekd ₁₀ kke	29	30523	30538	1657
548040	1449	1464	GTGAGAAAGGTGTATC	eekd ₁₀ kke	62	30527	30542	1658
548041	1450	1465	TGTGAGAAAGGTGTAT	eekd ₁₀ kke	64	30528	30543	1659
548042	1452	1467	TTTGTGAGAAAGGTGT	eekd ₁₀ kke	63	30530	30545	1660
548043	1453	1468	ATTTGTGAGAAAGGTG	eekd ₁₀ kke	76	30531	30546	1661
548044	1474	1489	TGGTGAATAATAATCT	eekd ₁₀ kke	12	30552	30567	1662
548045	1483	1498	TTATAGTTTTGGTGAA	eekd ₁₀ kke	0	30561	30576	1663
548046	1506	1521	TATCATGATTCCCTTC	eekd ₁₀ kke	84	30584	30599	1664
548047	1508	1523	GATATCATGATTCCCT	eekd ₁₀ kke	83	30586	30601	1665
548048	1509	1524	CGATATCATGATTCCC	eekd ₁₀ kke	84	30587	30602	1666
548049	1510	1525	GCGATATCATGATTCC	eekd ₁₀ kke	62	30588	30603	1667
548050	1512	1527	AGGCGATATCATGATT	eekd ₁₀ kke	37	30590	30605	1668
548051	1513	1528	AAGGCGATATCATGAT	eekd ₁₀ kke	61	30591	30606	1669
548052	1535	1550	CAAAGGAGCCTGGAGT	eekd ₁₀ kke	43	30613	30628	1670
548053	1538	1553	ATTCAAAGGAGCCTGG	eekd ₁₀ kke	36	30616	30631	1671
548054	1539	1554	AATTCAAAGGAGCCTG	eekd ₁₀ kke	45	30617	30632	1672
548055	1541	1556	GTAATTCAAAGGAGCC	eekd ₁₀ kke	78	30619	30634	1673
548056	1543	1558	GTGTAATTCAAAGGAG	eekd ₁₀ kke	40	30621	30636	1674
548057	1564	1579	CATATTGGTTTTTGGA	eekd ₁₀ kke	49	31870	31885	1675
548058	1565	1580	GCATATTGGTTTTTGG	eekd ₁₀ kke	71	31871	31886	1676
548059	1568	1583	TAGGCATATTGGTTTT	eekd ₁₀ kke	50	31874	31889	1677
548060	1588	1603	CTTGTGTCACCTTTGG	eekd ₁₀ kke	76	31894	31909	1678
548061	1589	1604	GCTTGTGTCACCTTTG	eekd ₁₀ kke	86	31895	31910	1679
548062	1598	1613	ATAAATTGTGCTTGTG	eekd ₁₀ kke	19	31904	31919	1680
548063	1600	1615	GTATAAATTGTGCTTG	eekd ₁₀ kke	35	31906	31921	1681
548064	1602	1617	TGGTATAAATTGTGCT	eekd ₁₀ kke	54	31908	31923	1682
548065	1603	1618	TTGGTATAAATTGTGC	eekd ₁₀ kke	22	31909	31924	1683
548067	1606	1621	CAGTTGGTATAAATTG	eekd ₁₀ kke	18	31912	31927	1684
548068	1609	1624	CAACAGTTGGTATAAA	eekd ₁₀ kke	0	31915	31930	1685
548069	1610	1625	CCAACAGTTGGTATAA	eekd ₁₀ kke	57	31916	31931	1686
548070	1611	1626	CCCAACAGTTGGTATA	eekd ₁₀ kke	85	31917	31932	1687
548071	1629	1644	AGAAGCCCCATCCGGT	eekd ₁₀ kke	55	31935	31950	1688
548072	1640	1655	TTTCTCCTTCGAGAAG	eekd ₁₀ kke	33	31946	31961	1689

548073	1641	1656	CTTTCTCCTTCGAGAA	eekd ₁₀ kke	24	31947	31962	1690
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Table 25

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	19	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	66	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	

548151	n/a	n/a	GGGCTTCAGCCAGACA	eekd ₁₀ kke	35	34238	34253	1691
548152	n/a	n/a	CGGGCTTCAGCCAGAC	eekd ₁₀ kke	32	34239	34254	1692
548153	2148	2163	TGCTGAAAGCGGGCTT	eekd ₁₀ kke	44	34248	34263	1693
548154	2149	2164	GTGCTGAAAGCGGGCT	eekd ₁₀ kke	7	34249	34264	1694
548155	2150	2165	CGTGCTGAAAGCGGGC	eekd ₁₀ kke	76	34250	34265	1695
548156	2167	2182	TCAGCCCCTGGTTACG	eekd ₁₀ kke	0	34267	34282	1696
548157	2171	2186	ATTGTCAGCCCCTGGT	eekd ₁₀ kke	7	34271	34286	1697
548158	2173	2188	GCATTGTCAGCCCCTG	eekd ₁₀ kke	18	34273	34288	1698
548159	2174	2189	CGCATTGTCAGCCCCT	eekd ₁₀ kke	59	34274	34289	1699
548160	2175	2190	TCGCATTGTCAGCCCC	eekd ₁₀ kke	60	34275	34290	1700
548161	2176	2191	CTCGCATTGTCAGCCC	eekd ₁₀ kke	59	34276	34291	1701
548162	2177	2192	CCTCGCATTGTCAGCC	eekd ₁₀ kke	25	34277	34292	1702
548163	2178	2193	ACCTCGCATTGTCAGC	eekd ₁₀ kke	46	34278	34293	1703
548164	2179	2194	GACCTCGCATTGTCAG	eekd ₁₀ kke	40	34279	34294	1704
548165	2180	2195	CGACCTCGCATTGTCA	eekd ₁₀ kke	53	34280	34295	1705
548166	2181	2196	GCGACCTCGCATTGTC	eekd ₁₀ kke	0	34281	34296	1706
548167	2182	2197	TGCGACCTCGCATTGT	eekd ₁₀ kke	36	34282	34297	1707
548168	2183	2198	TTGCGACCTCGCATTG	eekd ₁₀ kke	61	34283	34298	1708
548169	2184	2199	GTTGCGACCTCGCATT	eekd ₁₀ kke	7	34284	34299	1709
548170	2185	2200	AGTTGCGACCTCGCAT	eekd ₁₀ kke	68	34285	34300	1710
548171	2186	2201	CAGTTGCGACCTCGCA	eekd ₁₀ kke	47	34286	34301	1711
548172	2187	2202	TCAGTTGCGACCTCGC	eekd ₁₀ kke	0	34287	34302	1712
548173	2188	2203	CTCAGTTGCGACCTCG	eekd ₁₀ kke	51	34288	34303	1713
548174	2189	2204	TCTCAGTTGCGACCTC	eekd ₁₀ kke	68	34289	34304	1714
548175	2190	2205	ATCTCAGTTGCGACCT	eekd ₁₀ kke	0	34290	34305	1715
548176	2191	2206	GATCTCAGTTGCGACC	eekd ₁₀ kke	38	34291	34306	1716
548177	2192	2207	AGATCTCAGTTGCGAC	eekd ₁₀ kke	45	34292	34307	1717
548178	2193	2208	GAGATCTCAGTTGCGA	eekd ₁₀ kke	54	34293	34308	1718
548179	2194	2209	GGAGATCTCAGTTGCG	eekd ₁₀ kke	52	34294	34309	1719
548180	2198	2213	TCATGGAGATCTCAGT	eekd ₁₀ kke	79	34298	34313	1720
548181	2199	2214	GTCATGGAGATCTCAG	eekd ₁₀ kke	55	34299	34314	1721
548182	2200	2215	AGTCATGGAGATCTCA	eekd ₁₀ kke	55	34300	34315	1722
548183	2201	2216	CAGTCATGGAGATCTC	eekd ₁₀ kke	43	34301	34316	1723
548184	2202	2217	ACAGTCATGGAGATCT	eekd ₁₀ kke	73	34302	34317	1724
548185	2207	2222	AACACACAGTCATGGA	eekd ₁₀ kke	23	34307	34322	1725
548186	2208	2223	CAACACACAGTCATGG	eekd ₁₀ kke	0	34308	34323	1726
548187	n/a	n/a	CATCCTATCCGTGTTC	eekd ₁₀ kke	33	3279	3294	1727
548189	n/a	n/a	CATGAACATCCTATCC	eekd ₁₀ kke	24	3285	3300	1728
548190	n/a	n/a	TATTCCATGAACATCC	eekd ₁₀ kke	43	3290	3305	1729

548191	n/a	n/a	GTCAACATATTCCATG	eekd ₁₀ kke	0	3297	3312	1730
548192	n/a	n/a	CCTGTCAACATATTCC	eekd ₁₀ kke	65	3300	3315	1731
548193	n/a	n/a	TGTCCTGTCAACATAT	eekd ₁₀ kke	58	3303	3318	1732
548194	n/a	n/a	GCCAACAGTTTCAACT	eekd ₁₀ kke	61	3322	3337	1733
548195	n/a	n/a	TTCTGCCAACAGTTTC	eekd ₁₀ kke	84	3326	3341	1734
548196	n/a	n/a	CAATATTGACTTTGGG	eekd ₁₀ kke	6	3343	3358	1735
548197	n/a	n/a	TGCTTGGCTTCAATAT	eekd ₁₀ kke	68	3353	3368	1736
548198	n/a	n/a	ACTGCAGGCAATATTT	eekd ₁₀ kke	49	3369	3384	1737
548199	n/a	n/a	GCACTGCAGGCAATAT	eekd ₁₀ kke	24	3371	3386	1738
548200	n/a	n/a	CTAATGTGGCACTGCA	eekd ₁₀ kke	19	3379	3394	1739
548201	n/a	n/a	TGTTCTAATGTGGCAC	eekd ₁₀ kke	67	3383	3398	1740
548202	n/a	n/a	GCTGTTCTAATGTGGC	eekd ₁₀ kke	9	3385	3400	1741
548203	n/a	n/a	TGACTAGTGAATGGCT	eekd ₁₀ kke	73	2280	2295	1742
548204	n/a	n/a	TCTGACTAGTGAATGG	eekd ₁₀ kke	25	2282	2297	1743
548205	n/a	n/a	TCAATCTGACTAGTGA	eekd ₁₀ kke	14	2286	2301	1744
548206	n/a	n/a	GGTCAATCTGACTAGT	eekd ₁₀ kke	45	2288	2303	1745
548207	n/a	n/a	CTGGTCAATCTGACTA	eekd ₁₀ kke	60	2290	2305	1746
548208	n/a	n/a	CTCTGGTCAATCTGAC	eekd ₁₀ kke	19	2292	2307	1747
548209	n/a	n/a	CAATCTCTGGTCAATC	eekd ₁₀ kke	57	2296	2311	1748
548210	n/a	n/a	CAACAATCTCTGGTCA	eekd ₁₀ kke	55	2299	2314	1749
548211	n/a	n/a	ACCAACAATCTCTGGT	eekd ₁₀ kke	51	2301	2316	1750
548212	n/a	n/a	AGCCACCAACAATCT	eekd ₁₀ kke	44	2306	2321	1751
548213	n/a	n/a	GACAGCCCACCAACAA	eekd ₁₀ kke	70	2309	2324	1752
548214	n/a	n/a	CAGACAGCCCACCAAC	eekd ₁₀ kke	55	2311	2326	1753
548215	n/a	n/a	GCATAGACCCCAACAG	eekd ₁₀ kke	61	2324	2339	1754
548216	n/a	n/a	GTGCATAGACCCCAAC	eekd ₁₀ kke	45	2326	2341	1755
548217	n/a	n/a	CTGTGCATAGACCCCA	eekd ₁₀ kke	69	2328	2343	1756
548218	n/a	n/a	TCCTGTGCATAGACCC	eekd ₁₀ kke	59	2330	2345	1757
548219	n/a	n/a	GAAATCCTGTGCATAG	eekd ₁₀ kke	8	2334	2349	1758
548220	n/a	n/a	GCAGAAATCCTGTGCA	eekd ₁₀ kke	69	2337	2352	1759
548221	n/a	n/a	ACTCCAGCAGAAATCC	eekd ₁₀ kke	49	2343	2358	1760
548222	n/a	n/a	AATCATGCCTTGTGGG	eekd ₁₀ kke	32	4765	4780	1761
548223	n/a	n/a	TAGACCCAGAATCATG	eekd ₁₀ kke	50	4774	4789	1762
548224	n/a	n/a	CCATAGACCCAGAATC	eekd ₁₀ kke	20	4777	4792	1763
548225	n/a	n/a	AGTCACCATAGACCCA	eekd ₁₀ kke	48	4782	4797	1764
548226	n/a	n/a	TAAGTCACCATAGACC	eekd ₁₀ kke	39	4784	4799	1765
548227	n/a	n/a	GTGGCCCTCTTAAGTC	eekd ₁₀ kke	0	4794	4809	1766

Table 26

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeced ₁₀ eeeee	42	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	80	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548228	n/a	n/a	GTTGTGTGGCCCTCTT	eekd ₁₀ kke	37	4799	4814	1767
548229	n/a	n/a	CATTGTTGTGTGGCCC	eekd ₁₀ kke	31	4803	4818	1768

548230	n/a	n/a	TACTCATTGTTGTGTG	eekd ₁₀ kke	10	4807	4822	1769
548231	n/a	n/a	AATACTCATTGTTGTG	eekd ₁₀ kke	11	4809	4824	1770
548232	n/a	n/a	GCCATACATCTGAGGA	eekd ₁₀ kke	3	4831	4846	1771
548233	n/a	n/a	ATTGTAGCCATACATC	eekd ₁₀ kke	38	4837	4852	1772
548234	n/a	n/a	TTATTGTAGCCATACA	eekd ₁₀ kke	17	4839	4854	1773
548235	n/a	n/a	TCTAGATGACCTGAAG	eekd ₁₀ kke	0	18147	18162	1774
548236	n/a	n/a	TACATCTAGATGACCT	eekd ₁₀ kke	37	18151	18166	1775
548237	n/a	n/a	GTATACATCTAGATGA	eekd ₁₀ kke	22	18154	18169	1776
548238	n/a	n/a	ACTCGCCTTTGTGACT	eekd ₁₀ kke	31	26268	26283	1777
548239	n/a	n/a	TACTCGCCTTTGTGAC	eekd ₁₀ kke	18	26269	26284	1778
548240	n/a	n/a	ATACTCGCCTTTGTGA	eekd ₁₀ kke	3	26270	26285	1779
						26301	26316	
548241	n/a	n/a	CATACTCGCCTTTGTG	eekd ₁₀ kke	1	26271	26286	1780
						26302	26317	
548242	n/a	n/a	GCATACTCGCCTTTGT	eekd ₁₀ kke	25	26272	26287	1781
						26303	26318	
548243	n/a	n/a	ATGCATACTCGCCTTT	eekd ₁₀ kke	0	26274	26289	1782
						26305	26320	
548244	n/a	n/a	CATGCATACTCGCCTT	eekd ₁₀ kke	51	26275	26290	1783
						26306	26321	
548245	n/a	n/a	CCATGCATACTCGCCT	eekd ₁₀ kke	31	26276	26291	1784
						26307	26322	
548246	n/a	n/a	TTCCATGCATACTCGC	eekd ₁₀ kke	46	26278	26293	1785
548247	n/a	n/a	CGATTTTCCATGCATA	eekd ₁₀ kke	56	26283	26298	1786
548248	n/a	n/a	TGCGATTTTCCATGCA	eekd ₁₀ kke	13	26285	26300	1787
548249	n/a	n/a	TGTGATGCGATTTTCC	eekd ₁₀ kke	22	26290	26305	1788
548250	n/a	n/a	CTTTGTGATGCGATTT	eekd ₁₀ kke	0	26293	26308	1789
548251	n/a	n/a	GCCTTTGTGATGCGAT	eekd ₁₀ kke	13	26295	26310	1790
548252	n/a	n/a	ACTCGCCTTTGTGATG	eekd ₁₀ kke	33	26299	26314	1791
548253	n/a	n/a	TACTCGCCTTTGTGAT	eekd ₁₀ kke	8	26300	26315	1792
548254	n/a	n/a	CCCATGCATACTCGCC	eekd ₁₀ kke	39	26308	26323	1793
548255	n/a	n/a	CCCCATGCATACTCGC	eekd ₁₀ kke	38	26309	26324	1794
548256	n/a	n/a	GCTCCCCATGCATACT	eekd ₁₀ kke	25	26312	26327	1795
548257	n/a	n/a	AGTGCTCCCCATGCAT	eekd ₁₀ kke	2	26315	26330	1796
548258	n/a	n/a	CAAGTGCTCCCCATGC	eekd ₁₀ kke	0	26317	26332	1797
548259	n/a	n/a	GTGATGAAAGTACAGC	eekd ₁₀ kke	45	26335	26350	1798
548260	n/a	n/a	AGGAGTTTGTGAGAAC	eekd ₁₀ kke	28	3210	3225	1799
548261	n/a	n/a	TTCAGGGAGTGATGTC	eekd ₁₀ kke	36	3241	3256	1800
548262	n/a	n/a	CCTATCCGTGTTTCAGC	eekd ₁₀ kke	73	3276	3291	1801

548263	n/a	n/a	CTCTACATACTCAGGA	eekd ₁₀ kke	62	3561	3576	1802
548264	n/a	n/a	CAGTCCAAAAATCCCT	eekd ₁₀ kke	60	3701	3716	1803
548265	n/a	n/a	CCTCTTGATTTGGGCA	eekd ₁₀ kke	85	3749	3764	1804
548266	n/a	n/a	TTGGCCAACTCTGTGG	eekd ₁₀ kke	44	3816	3831	1805
548267	n/a	n/a	GACCTCCAGACTACTG	eekd ₁₀ kke	34	3848	3863	1806
548268	n/a	n/a	TGTGTCTAGGGAGTTG	eekd ₁₀ kke	52	3898	3913	1807
548269	n/a	n/a	AGCACACAATTACTGG	eekd ₁₀ kke	62	3946	3961	1808
548270	n/a	n/a	CTGCTGGTTTTAGACC	eekd ₁₀ kke	28	4029	4044	1809
548271	n/a	n/a	TTCACTTACCACAGGA	eekd ₁₀ kke	56	4122	4137	1810
548272	n/a	n/a	GGTGCCACTTGCTTGG	eekd ₁₀ kke	54	4178	4193	1811
548273	n/a	n/a	AATCTCCACCCCCGAA	eekd ₁₀ kke	5	4224	4239	1812
548274	n/a	n/a	TACCTGACAAGTGGTC	eekd ₁₀ kke	0	4287	4302	1813
548275	n/a	n/a	GTCCCAAGACATTCCT	eekd ₁₀ kke	40	4350	4365	1814
548276	n/a	n/a	CAGAGTGTCTCTGCG	eekd ₁₀ kke	49	4389	4404	1815
548277	n/a	n/a	GGATTGGACCCAGACA	eekd ₁₀ kke	57	4511	4526	1816
548278	n/a	n/a	GGTTCCCTAGCGGTCC	eekd ₁₀ kke	74	4564	4579	1817
548279	n/a	n/a	CACCTAGAACTATCCA	eekd ₁₀ kke	39	4632	4647	1818
548280	n/a	n/a	CTCCCTCTGTAATGAT	eekd ₁₀ kke	43	4736	4751	1819
548281	n/a	n/a	GGTTGAGGGACAGACA	eekd ₁₀ kke	0	4944	4959	1820
548282	n/a	n/a	GTGGGTTTGCACATGG	eekd ₁₀ kke	73	4992	5007	1821
548283	n/a	n/a	GGCTTATGCTCCTTCT	eekd ₁₀ kke	56	5017	5032	1822
548284	n/a	n/a	CCCCCTGTAGTTGGCT	eekd ₁₀ kke	35	5051	5066	1823
548285	n/a	n/a	GCTTACTTACATCCCT	eekd ₁₀ kke	52	5132	5147	1824
548286	n/a	n/a	GGGACTACATGCAATA	eekd ₁₀ kke	47	5166	5181	1825
548287	n/a	n/a	GTCAAAGAGTGTCCAC	eekd ₁₀ kke	38	5283	5298	1826
548288	n/a	n/a	GAATAGCAAGCTCCAA	eekd ₁₀ kke	64	5348	5363	1827
548289	n/a	n/a	CATGATACCACACCAC	eekd ₁₀ kke	28	5484	5499	1828
548290	n/a	n/a	GAGCACTCTTATTAGC	eekd ₁₀ kke	31	5546	5561	1829
548291	n/a	n/a	CCTGTTAGAGTTGGCC	eekd ₁₀ kke	35	5576	5591	1830
548292	n/a	n/a	AGGACACTGTTTCCAG	eekd ₁₀ kke	38	5627	5642	1831
548293	n/a	n/a	GTCACCAGAACCACAT	eekd ₁₀ kke	44	5683	5698	1832
548294	n/a	n/a	GTGTGCACTTTCTGGT	eekd ₁₀ kke	33	5716	5731	1833
548295	n/a	n/a	CTCTGATTGGGTCACC	eekd ₁₀ kke	26	5746	5761	1834
548296	n/a	n/a	ACCAACAACCTCAGGCC	eekd ₁₀ kke	34	5858	5873	1835
548297	n/a	n/a	ACTCTCAAGCTCCACG	eekd ₁₀ kke	32	5889	5904	1836
548298	n/a	n/a	GGACAATATGTCTCCT	eekd ₁₀ kke	0	5935	5950	1837
548299	n/a	n/a	CATTGTGCTCAACTGA	eekd ₁₀ kke	35	5961	5976	1838
548300	n/a	n/a	GCCCATGGTGAATCTG	eekd ₁₀ kke	53	5995	6010	1839
548301	n/a	n/a	CCTAGTACAAAGTGGC	eekd ₁₀ kke	65	6050	6065	1840

548302	n/a	n/a	GCCATTTTATCCCTGA	eekd ₁₀ kke	71	6134	6149	1841
548303	n/a	n/a	GGGCCCCCATGTCCAT	eekd ₁₀ kke	0	6336	6351	1842

Table 27

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	72	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	67	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	

						15947	15962	
548305	n/a	n/a	GTTCTTGCTTATCCTC	eekd ₁₀ kke	55	6484	6499	1843
548306	n/a	n/a	ATGTGACAGTCAGGGA	eekd ₁₀ kke	8	6559	6574	1844
548307	n/a	n/a	TTCTGCAACTGAGCCT	eekd ₁₀ kke	6	6587	6602	1845
548308	n/a	n/a	AATGGCAGGTCCTGGC	eekd ₁₀ kke	9	6616	6631	1846
548309	n/a	n/a	AGACAGTTGGTGGTTT	eekd ₁₀ kke	41	6700	6715	1847
548310	n/a	n/a	GAGGAGTTGGTTTAGT	eekd ₁₀ kke	0	6750	6765	1848
548311	n/a	n/a	TGACCACCTCTCGGGT	eekd ₁₀ kke	10	6860	6875	1849
548312	n/a	n/a	ATTTGGCCCTGAGCCC	eekd ₁₀ kke	0	6935	6950	1850
548313	n/a	n/a	GCCTTTGAGGGAGTGG	eekd ₁₀ kke	35	7024	7039	1851
548314	n/a	n/a	ACAACCTGTCCATTCC	eekd ₁₀ kke	43	7087	7102	1852
548315	n/a	n/a	GTTGTCAACTGGGACC	eekd ₁₀ kke	14	7125	7140	1853
548316	n/a	n/a	CTGTTTCAGGTAGCACA	eekd ₁₀ kke	64	7150	7165	1854
548317	n/a	n/a	CCGGGAAAGACTGTCT	eekd ₁₀ kke	42	7190	7205	1855
548318	n/a	n/a	ACTGCACCCACATAT	eekd ₁₀ kke	18	7257	7272	1856
548319	n/a	n/a	CCTCATCTCAGTATGA	eekd ₁₀ kke	26	7398	7413	1857
548320	n/a	n/a	GCACACAGACTTGCCC	eekd ₁₀ kke	0	7508	7523	1858
548321	n/a	n/a	CTGCATCTGGACTATG	eekd ₁₀ kke	38	7559	7574	1859
548322	n/a	n/a	AGGGAAATTAGAGGCA	eekd ₁₀ kke	38	7586	7601	1860
548323	n/a	n/a	CTGTTGCCTGACATGC	eekd ₁₀ kke	43	7696	7711	1861
548324	n/a	n/a	ACATAAATTCCCCACA	eekd ₁₀ kke	29	7741	7756	1862
548325	n/a	n/a	CCCCTGACTGACTAC	eekd ₁₀ kke	27	7906	7921	1863
548326	n/a	n/a	TCCTGTGACAGAACCA	eekd ₁₀ kke	27	7988	8003	1864
548327	n/a	n/a	CTACACCTTTCTGCAC	eekd ₁₀ kke	6	8221	8236	1865
548328	n/a	n/a	GGTCCTTGAACCCCGT	eekd ₁₀ kke	68	8260	8275	1866
548329	n/a	n/a	AGCAGATCTGGGTGT	eekd ₁₀ kke	59	8328	8343	1867
548330	n/a	n/a	GACTAGCTTCTACTAC	eekd ₁₀ kke	34	8404	8419	1868
548331	n/a	n/a	ACAATCCCTTAGCCCA	eekd ₁₀ kke	73	8457	8472	1869
548332	n/a	n/a	GATGAAATGTGCACCT	eekd ₁₀ kke	46	8491	8506	1870
548333	n/a	n/a	GACTGTGCTATCCGCT	eekd ₁₀ kke	58	8550	8565	1871
548334	n/a	n/a	GCTCACTATAGGCCCC	eekd ₁₀ kke	69	8656	8671	1872
548335	n/a	n/a	TAGCATCATGCCACAG	eekd ₁₀ kke	51	8684	8699	1873
548336	n/a	n/a	GCACATTAGGAGGTAG	eekd ₁₀ kke	1	9039	9054	1874
548337	n/a	n/a	TACCGCTGGGTGCGGT	eekd ₁₀ kke	10	9075	9090	1875
548338	n/a	n/a	ATGAACTGTGGCTCG	eekd ₁₀ kke	80	9131	9146	1876
548339	n/a	n/a	ACATGTGGGATCAGAG	eekd ₁₀ kke	37	9275	9290	1877
548340	n/a	n/a	GATGATCCTCACATAC	eekd ₁₀ kke	35	9316	9331	1878
548341	n/a	n/a	TAGAACCTTCCTCCAC	eekd ₁₀ kke	30	9341	9356	1879
548342	n/a	n/a	GGAAGACTTCCTCTG	eekd ₁₀ kke	0	9403	9418	1880

548343	n/a	n/a	TAGTGATAAGAGCTGG	eekd ₁₀ kke	78	9472	9487	1881
548344	n/a	n/a	GGCAACTATGTTCTCA	eekd ₁₀ kke	76	9536	9551	1882
548345	n/a	n/a	CTAACTCCATCACTGC	eekd ₁₀ kke	55	9637	9652	1883
548346	n/a	n/a	TCCCCAATACTTGCTG	eekd ₁₀ kke	35	9696	9711	1884
548347	n/a	n/a	GCTGTTCTAAGCGAGA	eekd ₁₀ kke	31	9976	9991	1885
548348	n/a	n/a	TGAGTGATGCCTTCCA	eekd ₁₀ kke	82	10024	10039	1886
548349	n/a	n/a	TCCAGAATACTGCCCC	eekd ₁₀ kke	61	10054	10069	1887
548350	n/a	n/a	GCGCTAACCTCATAAA	eekd ₁₀ kke	29	10148	10163	1888
548351	n/a	n/a	CTGGAAACGAGACACA	eekd ₁₀ kke	33	10201	10216	1889
548352	n/a	n/a	GAGAGAGATGTTCCCT	eekd ₁₀ kke	47	10240	10255	1890
548353	n/a	n/a	CTGCTGGTTGAGAATC	eekd ₁₀ kke	48	10287	10302	1891
548354	n/a	n/a	ATGTCCCCAGTGGAAG	eekd ₁₀ kke	41	10314	10329	1892
548355	n/a	n/a	GCATCCTCCCTAGTTG	eekd ₁₀ kke	47	10362	10377	1893
548356	n/a	n/a	TGTTGGTCAGCATTCA	eekd ₁₀ kke	63	10411	10426	1894
548357	n/a	n/a	GACGACTGCCCTGTGC	eekd ₁₀ kke	69	10436	10451	1895
548358	n/a	n/a	ATTTGGGCCTAGTGGT	eekd ₁₀ kke	0	10515	10530	1896
548359	n/a	n/a	CCTAGTCCTCAAGTTT	eekd ₁₀ kke	0	10580	10595	1897
548360	n/a	n/a	CAAGACATCAGTAGCT	eekd ₁₀ kke	45	10626	10641	1898
548361	n/a	n/a	CTTATCAGTCCCAGTC	eekd ₁₀ kke	52	10702	10717	1899
548362	n/a	n/a	GACAACCCATCAGTTG	eekd ₁₀ kke	33	10742	10757	1900
548363	n/a	n/a	CAGCAGGCTCAAAGTG	eekd ₁₀ kke	37	10915	10930	1901
548364	n/a	n/a	TGGCTAAGTCAGGCC	eekd ₁₀ kke	30	10982	10997	1902
548365	n/a	n/a	TGTACTCCACCTCACG	eekd ₁₀ kke	55	11017	11032	1903
548366	n/a	n/a	AGCAAGCTAAGTGAGT	eekd ₁₀ kke	5	11199	11214	1904
548367	n/a	n/a	GTTCTTGAGTGTAGAG	eekd ₁₀ kke	52	11260	11275	1905
548368	n/a	n/a	GTGTTTCATACGGAAGC	eekd ₁₀ kke	59	11299	11314	1906
548369	n/a	n/a	GTTGGGATGCGACTCT	eekd ₁₀ kke	50	11335	11350	1907
548370	n/a	n/a	ACGAAGTCTCTTTCCT	eekd ₁₀ kke	53	11385	11400	1908
548371	n/a	n/a	CGATGAGTTGGGCAGG	eekd ₁₀ kke	57	11454	11469	1909
548372	n/a	n/a	GATACCTTTCCACTCC	eekd ₁₀ kke	61	11558	11573	1910
548373	n/a	n/a	TCCCCAAGATTATGTG	eekd ₁₀ kke	16	11596	11611	1911
548374	n/a	n/a	GCACCCTTTTCATTGA	eekd ₁₀ kke	41	12074	12089	1912
548375	n/a	n/a	TCGACTTCTCCTGTCT	eekd ₁₀ kke	27	12199	12214	1913
548376	n/a	n/a	GCCTTTGACCTTTCGC	eekd ₁₀ kke	65	12261	12276	1914
548377	n/a	n/a	GTGTGCTGAGGTTTGC	eekd ₁₀ kke	80	12297	12312	1915
548378	n/a	n/a	GCAAGATGCATGCAGC	eekd ₁₀ kke	49	12393	12408	1916
548379	n/a	n/a	ATCGAACTCTGCTTGA	eekd ₁₀ kke	44	12477	12492	1917
548380	n/a	n/a	GCCCAGTTTTGGCAAC	eekd ₁₀ kke	7	12540	12555	1918
548381	n/a	n/a	CCCACTACCATTGCGG	eekd ₁₀ kke	0	12578	12593	1919

Table 28

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeced ₁₀ eeeee	46	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	64	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548459	n/a	n/a	CAACTATAACAGTATC	eekd ₁₀ kke	26	15903	15918	1920
548460	n/a	n/a	CTATACCACGGTAACT	eekd ₁₀ kke	0	16036	16051	1921

548461	n/a	n/a	CCTATATCACTGTAAC	eekd ₁₀ kke	0	16127	16142	1922
548462	n/a	n/a	ACCTATATCACTGTAA	eekd ₁₀ kke	0	16128	16143	1923
548463	n/a	n/a	TCACTGTACCTATATC	eekd ₁₀ kke	0	16135	16150	1924
548464	n/a	n/a	GTCCTATAACTATATC	eekd ₁₀ kke	0	16174	16189	1925
548465	n/a	n/a	CTGTACCTATAACTGT	eekd ₁₀ kke	0	16202	16217	1926
548466	n/a	n/a	CGTCACTGTACCTATA	eekd ₁₀ kke	71	16207	16222	1927
548467	n/a	n/a	CATCACTGTACCTATA	eekd ₁₀ kke	20	16258	16273	1928
548468	n/a	n/a	CAACATCACTGTACCT	eekd ₁₀ kke	6	16261	16276	1929
548469	n/a	n/a	TTCCCTACCCCTGGTA	eekd ₁₀ kke	0	16331	16346	1930
548470	n/a	n/a	GGTGGAATGTCATGGC	eekd ₁₀ kke	56	16404	16419	1931
548471	n/a	n/a	GCGGAAACTGGCCGT	eekd ₁₀ kke	17	16474	16489	1932
548472	n/a	n/a	CCCAATACAGGGCCAG	eekd ₁₀ kke	0	16513	16528	1933
548473	n/a	n/a	CCAACCTTCCCAATCT	eekd ₁₀ kke	0	16554	16569	1934
548474	n/a	n/a	GAAGGTGTGCTGTCGC	eekd ₁₀ kke	33	16602	16617	1935
548475	n/a	n/a	ATCGAGTCCTGCCTCC	eekd ₁₀ kke	17	16707	16722	1936
548476	n/a	n/a	GCAAATCCTTCCAGCA	eekd ₁₀ kke	27	16755	16770	1937
548477	n/a	n/a	GCACGAGCTTGCCTGT	eekd ₁₀ kke	26	16787	16802	1938
548478	n/a	n/a	GAGCCATCCAGGGTGC	eekd ₁₀ kke	53	16845	16860	1939
548479	n/a	n/a	AGGCCATTTGATCCGA	eekd ₁₀ kke	68	16913	16928	1940
548480	n/a	n/a	GCCACGCCCTTAGCAG	eekd ₁₀ kke	20	16973	16988	1941
548481	n/a	n/a	GTTCCCTGAGGAACGG	eekd ₁₀ kke	2	17010	17025	1942
548482	n/a	n/a	GGCAGTTAGGCCAGGA	eekd ₁₀ kke	53	17068	17083	1943
548483	n/a	n/a	CTACAGATCATCCCTA	eekd ₁₀ kke	5	17102	17117	1944
548484	n/a	n/a	CCCCGGAGCACCTTCA	eekd ₁₀ kke	41	17207	17222	1945
548485	n/a	n/a	GTGACCCAAGGGTCGA	eekd ₁₀ kke	17	17252	17267	1946
548486	n/a	n/a	CGTGGTTAGCCTGACA	eekd ₁₀ kke	68	17416	17431	1947
548487	n/a	n/a	TCCATGTCAGAGTTGC	eekd ₁₀ kke	71	17461	17476	1948
548488	n/a	n/a	CCTCCTTTTGGCTTGA	eekd ₁₀ kke	63	17530	17545	1949
548489	n/a	n/a	TTCCCAGAGGTGATA	eekd ₁₀ kke	16	17582	17597	1950
548490	n/a	n/a	TCTGGTTAGCCTCCGA	eekd ₁₀ kke	58	17664	17679	1951
548491	n/a	n/a	TGGCCAAGCAACCAGT	eekd ₁₀ kke	57	17715	17730	1952
548492	n/a	n/a	GCCCAATGTCCTAACC	eekd ₁₀ kke	51	17794	17809	1953
548493	n/a	n/a	CCACCGCTGCCCGCCA	eekd ₁₀ kke	37	18013	18028	1954
548494	n/a	n/a	TGTGACCCCCCACC GC	eekd ₁₀ kke	39	18022	18037	1955
548495	n/a	n/a	TTGTGACCCCCCACC G	eekd ₁₀ kke	55	18023	18038	1956
548496	n/a	n/a	ACTGAACCCCCCTTAGG	eekd ₁₀ kke	0	18571	18586	1957
548497	n/a	n/a	CCTTCATACCCCTCAC	eekd ₁₀ kke	26	18725	18740	1958
548498	n/a	n/a	CCGATAACAGACCGGC	eekd ₁₀ kke	71	18795	18810	1959
548499	n/a	n/a	ATACCCGGAGTCAGGA	eekd ₁₀ kke	56	18955	18970	1960

548500	n/a	n/a	ATTGCTCAGGCCCCCT	eekd ₁₀ kke	29	19037	19052	1961
548501	n/a	n/a	CAAGCCACTAACCCAC	eekd ₁₀ kke	33	19147	19162	1962
548502	n/a	n/a	AATTCTTGGACCAAGG	eekd ₁₀ kke	25	19234	19249	1963
548503	n/a	n/a	CCATCTACTCCCCCAT	eekd ₁₀ kke	9	19291	19306	1964
548504	n/a	n/a	GCAGCGAGCATTCCAA	eekd ₁₀ kke	28	19352	19367	1965
548505	n/a	n/a	GGACAATGCCTATGCT	eekd ₁₀ kke	21	19386	19401	1966
548506	n/a	n/a	GAAGCCATTCACTGCA	eekd ₁₀ kke	32	19436	19451	1967
548507	n/a	n/a	AAACTCCTCTCAAGGC	eekd ₁₀ kke	53	19474	19489	1968
548508	n/a	n/a	GCACCACCATGCGGTT	eekd ₁₀ kke	43	19553	19568	1969
548509	n/a	n/a	TGCAGGGCTGCGCAGT	eekd ₁₀ kke	41	19960	19975	1970
548510	n/a	n/a	TTAGCCACTCCTCTTG	eekd ₁₀ kke	30	20062	20077	1971
548511	n/a	n/a	AGCTAGCTGACCCCAA	eekd ₁₀ kke	16	20092	20107	1972
548512	n/a	n/a	TCCGCCTTTGGATACT	eekd ₁₀ kke	49	20155	20170	1973
548513	n/a	n/a	CCTGCTGATTGTGTCT	eekd ₁₀ kke	16	20240	20255	1974
548514	n/a	n/a	TCGAGGACAGCCCCCA	eekd ₁₀ kke	40	20335	20350	1975
548515	n/a	n/a	ACCCGTCAGCCTCAGC	eekd ₁₀ kke	59	20381	20396	1976
548516	n/a	n/a	CTTGCCTATTACCCCC	eekd ₁₀ kke	49	20544	20559	1977
548517	n/a	n/a	CGGACAAGCCTTACAG	eekd ₁₀ kke	43	20596	20611	1978
548518	n/a	n/a	CACACTTACCCCGCTC	eekd ₁₀ kke	12	20741	20756	1979
548519	n/a	n/a	CCTCCCCTTGTGTGTC	eekd ₁₀ kke	31	20843	20858	1980
548520	n/a	n/a	CCGCTTCCCTGACTGT	eekd ₁₀ kke	43	20919	20934	1981
548521	n/a	n/a	CAGCTCCCTTACTAGG	eekd ₁₀ kke	61	20958	20973	1982
548522	n/a	n/a	AGGTATTGACCGCCAG	eekd ₁₀ kke	55	21062	21077	1983
548523	n/a	n/a	GGTAAATCCATCCCCT	eekd ₁₀ kke	44	21157	21172	1984
548524	n/a	n/a	GCCCGATCACCTTAGA	eekd ₁₀ kke	45	21220	21235	1985
548525	n/a	n/a	GTCTAACTGGCCTGGC	eekd ₁₀ kke	2	21328	21343	1986
548526	n/a	n/a	CTAAGCTGTGTCTCAT	eekd ₁₀ kke	26	21373	21388	1987
548527	n/a	n/a	TGTTTCAAGTGCCAGA	eekd ₁₀ kke	50	21434	21449	1988
548528	n/a	n/a	TGCAGTGGTCAAGCAT	eekd ₁₀ kke	32	21478	21493	1989
548529	n/a	n/a	GCGATTCTTGCCTCT	eekd ₁₀ kke	56	21554	21569	1990
548530	n/a	n/a	ATAATAGAGGCAGCCA	eekd ₁₀ kke	50	21592	21607	1991
548531	n/a	n/a	GTCAGAAGGCCTCTTA	eekd ₁₀ kke	21	21753	21768	1992
548532	n/a	n/a	TATTTATCCGACCTCT	eekd ₁₀ kke	34	21881	21896	1993
548533	n/a	n/a	GAGGTGGTTGGAGCTA	eekd ₁₀ kke	9	21926	21941	1994
548534	n/a	n/a	CAGATCCCAATTCTTC	eekd ₁₀ kke	22	22063	22078	1995
548535	n/a	n/a	GAGTCTTTCCAATCCT	eekd ₁₀ kke	13	22142	22157	1996

Table 29

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeceed ₁₀ eeeee	46	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	64	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548536	n/a	n/a	TCTCAATCCCAACCCC	eekd ₁₀ kke	0	22168	22183	1997
548537	n/a	n/a	CCTCAATCCCAACCCA	eekd ₁₀ kke	0	22191	22206	1998

548538	n/a	n/a	TAGTGGCAAGAACCAC	eekd ₁₀ kke	0	22627	22642	1999
548539	n/a	n/a	CGCGCGAATGCCTGCC	eekd ₁₀ kke	41	22658	22673	2000
548540	n/a	n/a	GACACCTGCTTGATTA	eekd ₁₀ kke	7	22704	22719	2001
548541	n/a	n/a	GGCACTGGTCATGGAC	eekd ₁₀ kke	39	22760	22775	2002
548542	n/a	n/a	GCGCCATCCTTCAATC	eekd ₁₀ kke	7	22857	22872	2003
548543	n/a	n/a	GATCCACCCATGACCT	eekd ₁₀ kke	32	22997	23012	2004
548544	n/a	n/a	GCTGTGACTCAGATCA	eekd ₁₀ kke	62	23070	23085	2005
548545	n/a	n/a	CTCTTCGCATGGACAC	eekd ₁₀ kke	46	23100	23115	2006
548546	n/a	n/a	GCCCAAGCCTACATGC	eekd ₁₀ kke	35	23430	23445	2007
548547	n/a	n/a	GTGCGATTAAGCCCCA	eekd ₁₀ kke	86	23514	23529	2008
548548	n/a	n/a	GCTTGTAGAAGGGATT	eekd ₁₀ kke	54	23631	23646	2009
548549	n/a	n/a	TGTGCAATCAGGTGGA	eekd ₁₀ kke	56	23765	23780	2010
548550	n/a	n/a	CCGGCCTGGATACAGC	eekd ₁₀ kke	0	23831	23846	2011
548551	n/a	n/a	CGGCCAATGGGAAAGG	eekd ₁₀ kke	25	24175	24190	2012
548552	n/a	n/a	TGGAGGAGTAGGGAAT	eekd ₁₀ kke	10	24200	24215	2013
548553	n/a	n/a	CCCGAAGAGTCAAGTC	eekd ₁₀ kke	46	24255	24270	2014
548554	n/a	n/a	GTGCTGCATTGCATGA	eekd ₁₀ kke	42	24290	24305	2015
548555	n/a	n/a	ACACGCCAGGTGAAAA	eekd ₁₀ kke	2	24322	24337	2016
548556	n/a	n/a	ATGCATGCCTACCCAA	eekd ₁₀ kke	43	24526	24541	2017
548557	n/a	n/a	GTTACTCTGTGATCCA	eekd ₁₀ kke	81	24581	24596	2018
548558	n/a	n/a	AACATTGTGTAGCTGC	eekd ₁₀ kke	75	24640	24655	2019
548559	n/a	n/a	GAGACTGAAGCCCTCA	eekd ₁₀ kke	44	24676	24691	2020
548560	n/a	n/a	CACTGCCTAGAAAGGC	eekd ₁₀ kke	16	24734	24749	2021
548561	n/a	n/a	TGTAGTATCCAGAGTA	eekd ₁₀ kke	46	24930	24945	2022
548562	n/a	n/a	AGATGACCTGCAGATG	eekd ₁₀ kke	50	24983	24998	2023
548563	n/a	n/a	AAACCATGAATTAGGT	eekd ₁₀ kke	20	25100	25115	2024
548564	n/a	n/a	TTGCTACTTTACACCA	eekd ₁₀ kke	69	25208	25223	2025
548565	n/a	n/a	GGCATTAGGATAGGCA	eekd ₁₀ kke	63	25350	25365	2026
548566	n/a	n/a	CACTCAGACTGTCTGA	eekd ₁₀ kke	0	25413	25428	2027
548567	n/a	n/a	AGATCCGGAATAACCA	eekd ₁₀ kke	67	25459	25474	2028
548568	n/a	n/a	ATTGACAACCATCCTA	eekd ₁₀ kke	27	25496	25511	2029
548569	n/a	n/a	ACTCATTGGTCTACAG	eekd ₁₀ kke	41	25559	25574	2030
548570	n/a	n/a	ATGCCTTGTGCCTATT	eekd ₁₀ kke	74	25706	25721	2031
548571	n/a	n/a	ACTCTGAGGCCTTAGG	eekd ₁₀ kke	59	25794	25809	2032
548572	n/a	n/a	GCATTACTCAGCATGT	eekd ₁₀ kke	63	25836	25851	2033
548573	n/a	n/a	CCAGTCACCACCATTG	eekd ₁₀ kke	65	25862	25877	2034
548574	n/a	n/a	GGTCTAACTCTAAGGG	eekd ₁₀ kke	0	25920	25935	2035
548575	n/a	n/a	TGTCCTTTAAAGTATC	eekd ₁₀ kke	18	25971	25986	2036
548576	n/a	n/a	TCATGTGGCAACCTGT	eekd ₁₀ kke	41	26114	26129	2037

548577	n/a	n/a	AATCTGCACCTGGCAG	eekd ₁₀ kke	42	26428	26443	2038
548578	n/a	n/a	CATGGCTATTGCTTCC	eekd ₁₀ kke	73	26513	26528	2039
548579	n/a	n/a	GGGCTATATTGCCAGC	eekd ₁₀ kke	46	26614	26629	2040
548580	n/a	n/a	CCAGAGCCTTGATCAG	eekd ₁₀ kke	36	26681	26696	2041
548581	n/a	n/a	GGTGGGTATCTGAGA	eekd ₁₀ kke	13	26710	26725	2042
548582	n/a	n/a	TAGCTCCATGCTGTGT	eekd ₁₀ kke	59	26735	26750	2043
548583	n/a	n/a	GGGAATTTATGCTGCC	eekd ₁₀ kke	79	26782	26797	2044
548584	n/a	n/a	TGATGAAGTTCCACCT	eekd ₁₀ kke	47	26840	26855	2045
548585	n/a	n/a	TAGGCACAGACAACCT	eekd ₁₀ kke	33	26869	26884	2046
548586	n/a	n/a	TCCAACCTACAGGACTC	eekd ₁₀ kke	39	26943	26958	2047
548587	n/a	n/a	TTCTGGGAAACTCTCT	eekd ₁₀ kke	45	26969	26984	2048
548588	n/a	n/a	AGCTCACACCCAAAAA	eekd ₁₀ kke	10	27006	27021	2049
548589	n/a	n/a	TCTGTTACCTTGAGGA	eekd ₁₀ kke	40	27280	27295	2050
548590	n/a	n/a	TGGTCATGTCAACTGT	eekd ₁₀ kke	35	27550	27565	2051
548591	n/a	n/a	GTAAGCCTTCACAGGG	eekd ₁₀ kke	3	27583	27598	2052
548592	n/a	n/a	CTCACCAGAGTTGTCC	eekd ₁₀ kke	7	27726	27741	2053
548593	n/a	n/a	CATCCCTGACAGGTCC	eekd ₁₀ kke	61	27759	27774	2054
548594	n/a	n/a	CCCTTCTAACCAAGGA	eekd ₁₀ kke	30	27825	27840	2055
548595	n/a	n/a	GGATGAGATGCATCCA	eekd ₁₀ kke	8	28069	28084	2056
548596	n/a	n/a	ATGGCGGTGAAGCAGC	eekd ₁₀ kke	20	28127	28142	2057
548597	n/a	n/a	TGAATACCATCCCCGC	eekd ₁₀ kke	50	28171	28186	2058
548598	n/a	n/a	GCGCCATCTGCCCTGT	eekd ₁₀ kke	50	28253	28268	2059
548599	n/a	n/a	TGGGTTGGAGGAGTGG	eekd ₁₀ kke	19	28311	28326	2060
548600	n/a	n/a	TGGTGGTGGGATTGGT	eekd ₁₀ kke	53	28336	28351	2061
						28391	28406	
						28434	28449	
						28446	28461	
						28525	28540	
						28611	28626	
						28623	28638	
548601	n/a	n/a	TTGGTGGTGGGATTGG	eekd ₁₀ kke	18	28337	28352	2062
						28392	28407	
						28435	28450	
						28447	28462	
						28526	28541	
						28612	28627	
						28624	28639	
548602	n/a	n/a	GGTGGTGGGAATTGGTG	eekd ₁₀ kke	20	28347	28362	2063
548603	n/a	n/a	GAGATTGGTGGTGGGT	eekd ₁₀ kke	35	28372	28387	2064
548604	n/a	n/a	GTGGTGGGATTGGTGC	eekd ₁₀ kke	22	28432	28447	2065

548605	n/a	n/a	TGGCGGGATTGGTGGT	eekd ₁₀ kke	12	28479	28494	2066
						28558	28573	
548606	n/a	n/a	CGGTGGTGGGATTGGT	eekd ₁₀ kke	41	28501	28516	2067
						28580	28595	
548607	n/a	n/a	TCGGTGGTGGGATTGG	eekd ₁₀ kke	34	28502	28517	2068
						28581	28596	
548608	n/a	n/a	ATCGGTGGTGGGATTG	eekd ₁₀ kke	25	28503	28518	2069
						28582	28597	
548609	n/a	n/a	GATCGGTGGTGGGATT	eekd ₁₀ kke	30	28504	28519	2070
						28583	28598	
548610	n/a	n/a	GGATCGGTGGTGGGAT	eekd ₁₀ kke	2	28505	28520	2071
						28584	28599	
548611	n/a	n/a	GCGGGATCGGTGGTGG	eekd ₁₀ kke	7	28508	28523	2072
						28587	28602	
548612	n/a	n/a	GGCGGGATCGGTGGTG	eekd ₁₀ kke	20	28509	28524	2073
						28588	28603	

Table 30

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	46	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	64	14746	14761	1267
						14817	14832	

						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	
						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548382	n/a	n/a	GAGCAAATACAGTCCA	eekd ₁₀ kke	19	12620	12635	2074
548383	n/a	n/a	GTCTCGATGGCAAGCT	eekd ₁₀ kke	49	12654	12669	2075
548384	n/a	n/a	CTCACCGGTACTCTGC	eekd ₁₀ kke	49	12805	12820	2076
548385	n/a	n/a	TCCTGGAGGCACCAAT	eekd ₁₀ kke	0	12847	12862	2077
548386	n/a	n/a	AGCCCTGTTTGGTTTT	eekd ₁₀ kke	0	12903	12918	2078
548387	n/a	n/a	TGAAGGGCGAGGCGCA	eekd ₁₀ kke	22	13261	13276	2079
548388	n/a	n/a	AAGAGGATGTCAGGCT	eekd ₁₀ kke	4	13357	13372	2080
548389	n/a	n/a	TTGAGGAAAGACCTGC	eekd ₁₀ kke	11	13399	13414	2081
548390	n/a	n/a	GCTGAGTGTGACTTAA	eekd ₁₀ kke	43	13455	13470	2082
548391	n/a	n/a	GTACATGACTCCAGTG	eekd ₁₀ kke	34	13638	13653	2083
548392	n/a	n/a	GTAAGCATGGAGCGA	eekd ₁₀ kke	31	13730	13745	2084
548393	n/a	n/a	CGCTTCAGGAAAGCGA	eekd ₁₀ kke	26	13828	13843	2085
548394	n/a	n/a	GGCAGGAGACTCCGTG	eekd ₁₀ kke	25	13919	13934	2086
548395	n/a	n/a	ATCCTTCCCCTCGCAA	eekd ₁₀ kke	0	13966	13981	2087
548396	n/a	n/a	TAATGAGTGGGTTAGG	eekd ₁₀ kke	0	14007	14022	2088
548397	n/a	n/a	GGAGCAGTGCAGGTAA	eekd ₁₀ kke	1	14065	14080	2089
548398	n/a	n/a	ATAGGCAATTGTTTCCT	eekd ₁₀ kke	55	14129	14144	2090
548399	n/a	n/a	AGTCCTACAATTACCA	eekd ₁₀ kke	11	14239	14254	2091
548400	n/a	n/a	GGGCTCCTATTCCACC	eekd ₁₀ kke	13	14277	14292	2092
548401	n/a	n/a	GCCAGCTATGGGAACA	eekd ₁₀ kke	71	14333	14348	2093
548402	n/a	n/a	CCCCATCTCGAAGCCC	eekd ₁₀ kke	45	14380	14395	2094
548403	n/a	n/a	GAGTACATTGGGCCCA	eekd ₁₀ kke	25	14418	14433	2095
548404	n/a	n/a	GAGCCTTCCGCCTCTC	eekd ₁₀ kke	37	14471	14486	2096
548405	n/a	n/a	CGGACCTTCATCTTCA	eekd ₁₀ kke	35	14529	14544	2097
548406	n/a	n/a	TCTAGAGGCCGCCTGC	eekd ₁₀ kke	0	14558	14573	2098
548407	n/a	n/a	CCTATAACTGCTGCTC	eekd ₁₀ kke	24	14731	14746	2099
548408	n/a	n/a	TATCACTGTACTAGTT	eekd ₁₀ kke	47	14748	14763	1269

						14819	14834	
						14890	14905	
						14949	14964	
						15009	15024	
						15081	15096	
						15153	15168	
						15224	15239	
						15296	15311	
						15355	15370	
						15415	15430	
						15487	15502	
						15559	15574	
						15617	15632	
						15689	15704	
						15819	15834	
						15891	15906	
						15949	15964	
548409	n/a	n/a	GTATCACTGTACTAGT	eekd ₁₀ kke	81	14749	14764	2100
						14820	14835	
						14891	14906	
						14950	14965	
						15010	15025	
						15082	15097	
						15154	15169	
						15225	15240	
						15297	15312	
						15356	15371	
						15416	15431	
						15488	15503	
						15560	15575	
						15618	15633	
						15690	15705	
						15820	15835	
548410	n/a	n/a	AGTATCACTGTACTAG	eekd ₁₀ kke	85	15892	15907	2101
						15950	15965	
						14750	14765	
						14821	14836	
						14892	14907	
						14951	14966	
						15011	15026	
						15083	15098	
						15155	15170	

						15226	15241	
						15298	15313	
						15357	15372	
						15417	15432	
						15489	15504	
						15561	15576	
						15619	15634	
						15691	15706	
						15821	15836	
						15893	15908	
						15951	15966	
548411	n/a	n/a	CAGTATCACTGTACTA	eekd ₁₀ kke	72	14751	14766	2102
						14822	14837	
						14893	14908	
						14952	14967	
						15012	15027	
						15084	15099	
						15156	15171	
						15227	15242	
						15299	15314	
						15358	15373	
						15418	15433	
						15490	15505	
						15562	15577	
						15620	15635	
548412	n/a	n/a	TAACAGTATCACTGTA	eekd ₁₀ kke	17	15692	15707	2103
						15822	15837	
						15894	15909	
						15952	15967	
						14754	14769	
						14825	14840	
						14896	14911	
						14955	14970	
						15015	15030	
						15087	15102	
						15159	15174	
						15230	15245	
						15302	15317	
						15361	15376	
						15421	15436	
						15493	15508	
						15565	15580	

						15623	15638	
						15695	15710	
						15825	15840	
						15897	15912	
						15955	15970	
548413	n/a	n/a	CTAACAGTATCACTGT	eekd ₁₀ kke	55	14755	14770	2104
						14826	14841	
						14897	14912	
						15016	15031	
						15088	15103	
						15231	15246	
						15303	15318	
						15422	15437	
						15494	15509	
						15624	15639	
						15826	15841	
						15956	15971	
548414	n/a	n/a	TCTAACAGTATCACTG	eekd ₁₀ kke	20	14756	14771	2105
						14827	14842	
						14898	14913	
						15017	15032	
						15089	15104	
						15232	15247	
						15304	15319	
						15423	15438	
						15495	15510	
						15625	15640	
						15827	15842	
						15957	15972	
548415	n/a	n/a	ATAACTCTAACAGTAT	eekd ₁₀ kke	0	14761	14776	2106
						14832	14847	
						14903	14918	
						15022	15037	
						15094	15109	
						15237	15252	
						15309	15324	
						15428	15443	
						15500	15515	
						15630	15645	
						15832	15847	
						15962	15977	
548416	n/a	n/a	CTATAACTCTAACAGT	eekd ₁₀ kke	9	14763	14778	2107

						14834	14849	
						14905	14920	
						15024	15039	
						15096	15111	
						15239	15254	
						15311	15326	
						15430	15445	
						15502	15517	
						15632	15647	
						15834	15849	
						15964	15979	
548417	n/a	n/a	ACTGTCCTATAACTCT	eekd ₁₀ kke	24	14769	14784	2108
						14840	14855	
548418	n/a	n/a	TATATCACTGTCCTAT	eekd ₁₀ kke	39	14775	14790	2109
						14846	14861	
						15180	15195	
						15716	15731	
						16164	16179	
548419	n/a	n/a	CCTATATCACTGTCCT	eekd ₁₀ kke	52	14777	14792	2110
						14848	14863	
						15182	15197	
						15718	15733	
548420	n/a	n/a	TCCTATATCACTGTCC	eekd ₁₀ kke	58	14778	14793	2111
						14849	14864	
						15183	15198	
						15719	15734	
548421	n/a	n/a	CACTGTCCTATATCAC	eekd ₁₀ kke	56	14783	14798	2112
						14854	14869	
						14979	14994	
						15117	15132	
						15188	15203	
						15260	15275	
						15385	15400	
						15523	15538	
						15653	15668	
						15724	15739	
						15855	15870	
						15985	16000	
548422	n/a	n/a	GTATCACTGTCCTATA	eekd ₁₀ kke	69	14787	14802	2113
						14983	14998	
						15121	15136	
						15389	15404	

						15527	15542	
						15989	16004	
548423	n/a	n/a	AGTATCACTGTCCTAT	eekd ₁₀ kke	72	14788	14803	2114
						14984	14999	
						15050	15065	
						15122	15137	
						15390	15405	
						15456	15471	
						15528	15543	
						15990	16005	
548424	n/a	n/a	CAGTATCACTGTCCTA	eekd ₁₀ kke	90	14789	14804	2115
						14985	15000	
						15051	15066	
						15123	15138	
						15391	15406	
						15457	15472	
						15529	15544	
						15991	16006	
548425	n/a	n/a	AACAGTATCACTGTCC	eekd ₁₀ kke	90	14791	14806	2116
						14987	15002	
						15053	15068	
						15125	15140	
						15393	15408	
						15459	15474	
						15531	15546	
						15993	16008	
548426	n/a	n/a	TATAACAGTATCACTG	eekd ₁₀ kke	14	14794	14809	2117
						14990	15005	
						15056	15071	
						15128	15143	
						15161	15176	
						15363	15378	
						15396	15411	
						15462	15477	
						15534	15549	
						15567	15582	
						15697	15712	
						15899	15914	
						15996	16011	
548427	n/a	n/a	CTATAACAGTATCACT	eekd ₁₀ kke	24	14795	14810	2118
						14991	15006	
						15057	15072	

						15129	15144	
						15162	15177	
						15364	15379	
						15397	15412	
						15463	15478	
						15535	15550	
						15568	15583	
						15698	15713	
						15900	15915	
						15997	16012	
548428	n/a	n/a	TAACTATAACAGTATC	eekd ₁₀ kke	0	14798	14813	2119
						15060	15075	
						15132	15147	
						15165	15180	
						15466	15481	
						15538	15553	
						15571	15586	
						15701	15716	
						15772	15787	
						16000	16015	
548429	n/a	n/a	TATAACTATAACAGTA	eekd ₁₀ kke	0	14800	14815	2120
						15062	15077	
						15134	15149	
						15167	15182	
						15468	15483	
						15540	15555	
						15573	15588	
						15703	15718	
						15774	15789	
						16002	16017	
548430	n/a	n/a	CCTATAACTATAACAG	eekd ₁₀ kke	21	14802	14817	2121
						15064	15079	
						15169	15184	
						15470	15485	
						15542	15557	
						15575	15590	
						15705	15720	
						15776	15791	
						16004	16019	
548431	n/a	n/a	TACCTATAACTCTAAC	eekd ₁₀ kke	9	14908	14923	2122
						15027	15042	
						15099	15114	

						15242	15257	
						15314	15329	
						15433	15448	
						15505	15520	
						15635	15650	
						15837	15852	
						15967	15982	
548432	n/a	n/a	ACTGTACCTATAACTC	eekd ₁₀ kke	43	14912	14927	2123
						15031	15046	
						15246	15261	
						15318	15333	
						15437	15452	
						15509	15524	
						15639	15654	
						15841	15856	
						15971	15986	
548433	n/a	n/a	TATCACTGTACCTATA	eekd ₁₀ kke	33	14916	14931	2124
						15250	15265	
						15322	15337	
						15375	15390	
						15513	15528	
						15643	15658	
						15786	15801	
						15845	15860	
						15975	15990	
						16137	16152	
548434	n/a	n/a	ACAATATCACTGTACC	eekd ₁₀ kke	63	14920	14935	2125
						15326	15341	
						15790	15805	
						16063	16078	
						16141	16156	
548435	n/a	n/a	AACAATATCACTGTAC	eekd ₁₀ kke	19	14921	14936	2126
						15327	15342	
						15791	15806	
						16064	16079	
						16142	16157	
548436	n/a	n/a	ATATCACTGTACCTGT	eekd ₁₀ kke	8	14970	14985	2127
548437	n/a	n/a	TATATCACTGTACCTG	eekd ₁₀ kke	74	14971	14986	2128
548438	n/a	n/a	CTATATCACTGTACCT	eekd ₁₀ kke	38	14972	14987	2129
						15253	15268	
						15378	15393	
						15516	15531	

						15646	15661	
						15848	15863	
						15978	15993	
548439	n/a	n/a	CCTATATCACTGTACC	eekd ₁₀ kke	46	14973	14988	2130
						15254	15269	
						15379	15394	
						15517	15532	
						15647	15662	
						15849	15864	
						15979	15994	
548440	n/a	n/a	CCTATAACAGTATCAC	eekd ₁₀ kke	32	14992	15007	2131
						15365	15380	
						15398	15413	
548441	n/a	n/a	TCCTATAACAGTATCA	eekd ₁₀ kke	42	14993	15008	2132
						15399	15414	
548442	n/a	n/a	TTCCTATAACAGTATC	eekd ₁₀ kke	17	14994	15009	2133
						15400	15415	
548443	n/a	n/a	GTTTCCTATAACAGTA	eekd ₁₀ kke	12	14996	15011	2134
						15402	15417	
548444	n/a	n/a	CTATGTCACGTACCT	eekd ₁₀ kke	43	15038	15053	2135
						15444	15459	
548445	n/a	n/a	CCTATGTCACGTACC	eekd ₁₀ kke	62	15039	15054	2136
						15445	15460	
548446	n/a	n/a	TCCTATGTCACGTAC	eekd ₁₀ kke	16	15040	15055	2137
						15446	15461	
548447	n/a	n/a	CACTGTCCTATGTCAC	eekd ₁₀ kke	59	15045	15060	2138
						15451	15466	
548448	n/a	n/a	TCACTGTCCTATGTCA	eekd ₁₀ kke	61	15046	15061	2139
						15452	15467	
548449	n/a	n/a	ATCACTGTCCTATGTC	eekd ₁₀ kke	62	15047	15062	2140
						15453	15468	
548450	n/a	n/a	CTACCTATAACTCTAA	eekd ₁₀ kke	0	15100	15115	2141
548451	n/a	n/a	GTCCTATAACTATAAC	eekd ₁₀ kke	0	15171	15186	2142
						15577	15592	
						15707	15722	
						16006	16021	
						16077	16092	
						16102	16117	
						16155	16170	
548452	n/a	n/a	TATATCACTGTACCTA	eekd ₁₀ kke	65	15252	15267	2143
						15377	15392	
						15515	15530	

						15645	15660	
						15847	15862	
						15977	15992	
548453	n/a	n/a	TACCTATAACAGTATC	eekd ₁₀ kke	12	15367	15382	2144
548454	n/a	n/a	ACTGTACCTATAACAG	eekd ₁₀ kke	17	15371	15386	2145
548455	n/a	n/a	CACCGTACTAGTTTCC	eekd ₁₀ kke	64	15757	15772	2146
548456	n/a	n/a	TATAACAGTATCACCG	eekd ₁₀ kke	52	15768	15783	2147
548457	n/a	n/a	CTATAACAGTATCACC	eekd ₁₀ kke	13	15769	15784	2148
548458	n/a	n/a	ACCTATAACTATAACA	eekd ₁₀ kke	0	15777	15792	2149
						16249	16264	

Table 31

ISIS NO	SEQ ID NO: 1 Start Site	SEQ ID NO: 1 Stop Site	Sequence	Chemistry	% inhibition	SEQ ID NO: 10 Start Site	SEQ ID NO: 10 Stop Site	SEQ ID NO
531231	n/a	n/a	TATCACTGTACTAGTTTCCT	eeeeed ₁₀ eeee	48	14744	14763	334
						14815	14834	
						14886	14905	
						14945	14964	
						15005	15024	
						15077	15096	
						15220	15239	
						15292	15311	
						15351	15370	
						15411	15430	
						15483	15502	
						15555	15574	
						15613	15632	
						15685	15704	
						15815	15834	
						15887	15906	
						15945	15964	
547747	n/a	n/a	TCACTGTACTAGTTTC	eekd ₁₀ kke	88	14746	14761	1267
						14817	14832	
						14888	14903	
						14947	14962	
						15007	15022	
						15079	15094	
						15222	15237	
						15294	15309	

						15353	15368	
						15413	15428	
						15485	15500	
						15557	15572	
						15615	15630	
						15687	15702	
						15817	15832	
						15889	15904	
						15947	15962	
548613	n/a	n/a	TGGCGGGATCGGTGGT	eekd ₁₀ kke	39	28510	28525	2150
						28589	28604	
548614	n/a	n/a	TGGTGGCGGGATCGGT	eekd ₁₀ kke	0	28513	28528	2151
						28592	28607	
548615	n/a	n/a	TTGGTGGCGGGATCGG	eekd ₁₀ kke	10	28514	28529	2152
						28593	28608	
548616	n/a	n/a	ATTGGTGGCGGGATCG	eekd ₁₀ kke	35	28515	28530	2153
548617	n/a	n/a	GATTGGTGGCGGGATC	eekd ₁₀ kke	44	28516	28531	2154
548618	n/a	n/a	GTTGGTGGCGGGATCG	eekd ₁₀ kke	18	28594	28609	2155
548619	n/a	n/a	GGTTGGTGGCGGGATC	eekd ₁₀ kke	19	28595	28610	2156
548620	n/a	n/a	TGGTTGGTGGCGGGAT	eekd ₁₀ kke	24	28596	28611	2157
548621	n/a	n/a	GAACACATCAGGGATT	eekd ₁₀ kke	33	28638	28653	2158
548622	n/a	n/a	TTTCTATGGGCCTGAC	eekd ₁₀ kke	0	28669	28684	2159
548623	n/a	n/a	GCTGTCACTTAAGCCA	eekd ₁₀ kke	16	28862	28877	2160
548624	n/a	n/a	TCTAGGGCCACACCTC	eekd ₁₀ kke	24	28892	28907	2161
548625	n/a	n/a	GTTCTACACACAGTAC	eekd ₁₀ kke	0	29014	29029	2162
548626	n/a	n/a	GCAGTATGTTCAATCC	eekd ₁₀ kke	36	29202	29217	2163
548627	n/a	n/a	CCCACATGTACCACCG	eekd ₁₀ kke	22	29235	29250	2164
548628	n/a	n/a	GTATGGCAGAGCCCCT	eekd ₁₀ kke	9	29285	29300	2165
548629	n/a	n/a	CCCATCTTGGGACTTT	eekd ₁₀ kke	44	29341	29356	2166
548630	n/a	n/a	TGGTCCCAAATTGGAG	eekd ₁₀ kke	33	29387	29402	2167
548631	n/a	n/a	CTCACAATACTGAGCC	eekd ₁₀ kke	55	29421	29436	2168
548632	n/a	n/a	GGAGATATCAGGTGCA	eekd ₁₀ kke	45	29499	29514	2169
548633	n/a	n/a	CAAGGCATGTGTGCAC	eekd ₁₀ kke	41	29534	29549	2170
548634	n/a	n/a	GCCTTATTCTGTGCAA	eekd ₁₀ kke	0	29583	29598	2171
548635	n/a	n/a	AGGTGTGGCGCGCGCC	eekd ₁₀ kke	18	29853	29868	2172
548636	n/a	n/a	CTCTATACAGCTGGGC	eekd ₁₀ kke	5	30000	30015	2173
548637	n/a	n/a	GCTGATCTTCTAATGC	eekd ₁₀ kke	38	30063	30078	2174
548638	n/a	n/a	CCTCATTGCTCCACTA	eekd ₁₀ kke	26	30103	30118	2175
548639	n/a	n/a	TGGGAAGAACTAGCA	eekd ₁₀ kke	10	30159	30174	2176
548640	n/a	n/a	GAATGTTGCTGTCCCA	eekd ₁₀ kke	32	30194	30209	2177
548641	n/a	n/a	GCATCATGCTTACTGC	eekd ₁₀ kke	23	30225	30240	2178
548642	n/a	n/a	GCGGCAGTAGTGAATC	eekd ₁₀ kke	23	30288	30303	2179

548643	n/a	n/a	CCTACCTAATTCCTCC	eekd ₁₀ kke	0	30329	30344	2180
548644	n/a	n/a	AACTGGGCAGTCCTTC	eekd ₁₀ kke	14	30418	30433	2181
548645	n/a	n/a	CCAGCGCAATTCTGCT	eekd ₁₀ kke	8	30666	30681	2182
548646	n/a	n/a	CGTTTCCCTCAACTCC	eekd ₁₀ kke	24	30750	30765	2183
548647	n/a	n/a	CACGGCAAGTCGCGGG	eekd ₁₀ kke	39	30790	30805	2184
548648	n/a	n/a	CAGTTGTATCCCTCCC	eekd ₁₀ kke	32	30852	30867	2185
548649	n/a	n/a	GCCTCTCAGACGGCAC	eekd ₁₀ kke	0	30906	30921	2186
548650	n/a	n/a	CTGATCCCACCTTGCCC	eekd ₁₀ kke	21	30991	31006	2187
548651	n/a	n/a	AGTCTCTTTCCTACCC	eekd ₁₀ kke	61	31030	31045	2188
548652	n/a	n/a	CCACGATGCTCTGGCC	eekd ₁₀ kke	65	31068	31083	2189
548653	n/a	n/a	TCGGCTCCTGGCAGCA	eekd ₁₀ kke	46	31111	31126	2190
548654	n/a	n/a	ACCATTCCTGACCATG	eekd ₁₀ kke	34	31151	31166	2191
548655	n/a	n/a	CCCGAGGTCACATAAT	eekd ₁₀ kke	56	31416	31431	2192
548656	n/a	n/a	TTACAACAGACCCAGG	eekd ₁₀ kke	35	31497	31512	2193
548657	n/a	n/a	AGCAGGGTATCTTCAC	eekd ₁₀ kke	26	31548	31563	2194
548658	n/a	n/a	GAAGTTCCTGTGTCTT	eekd ₁₀ kke	11	31593	31608	2195
548659	n/a	n/a	CCAACCTCTAAGGCTA	eekd ₁₀ kke	17	31721	31736	2196
548660	n/a	n/a	ATGCTTACCTTTCTCC	eekd ₁₀ kke	0	31955	31970	2197
548661	n/a	n/a	ACGACCCACTCCATGT	eekd ₁₀ kke	18	32016	32031	2198
548662	n/a	n/a	TGCTTAAAAGTCTCCC	eekd ₁₀ kke	5	32155	32170	2199
548663	n/a	n/a	GCCCTAGAAGGGCCCA	eekd ₁₀ kke	20	32219	32234	2200
548664	n/a	n/a	GCGGGTGGTCTTGAC	eekd ₁₀ kke	38	32245	32260	2201
548665	n/a	n/a	GCTCCCGGCCATTAGC	eekd ₁₀ kke	8	32312	32327	2202
548666	n/a	n/a	TCTCCATAGTGAGACG	eekd ₁₀ kke	1	32342	32357	2203
548667	n/a	n/a	TGGCAAGCTACCTTCT	eekd ₁₀ kke	51	32384	32399	2204
548668	n/a	n/a	GGGAGCTTTCATGGCT	eekd ₁₀ kke	68	32506	32521	2205
548669	n/a	n/a	AATGCAGGCCAGCATC	eekd ₁₀ kke	42	32541	32556	2206
548670	n/a	n/a	GAAAAGCCCTCCGAGC	eekd ₁₀ kke	15	32590	32605	2207
548671	n/a	n/a	CAACAATCCAAAGCCT	eekd ₁₀ kke	3	32674	32689	2208
548672	n/a	n/a	CCCCCAGAAATCCCA	eekd ₁₀ kke	40	32708	32723	2209
548673	n/a	n/a	GACCTTGCTTCCATGT	eekd ₁₀ kke	40	32753	32768	2210
548674	n/a	n/a	GAGAGACGGCACCTTG	eekd ₁₀ kke	4	32829	32844	2211
548675	n/a	n/a	GGGAAGGTAGTGTTAC	eekd ₁₀ kke	8	32898	32913	2212
548676	n/a	n/a	GTGAATCAGAGCAGTG	eekd ₁₀ kke	63	32963	32978	2213
548677	n/a	n/a	TCACCTGTGAGTAACC	eekd ₁₀ kke	40	33089	33104	2214
548678	n/a	n/a	GAGTTACCTTACAAGC	eekd ₁₀ kke	22	33232	33247	2215
548679	n/a	n/a	TCTCAAGCAGCCTATT	eekd ₁₀ kke	0	33267	33282	2216
548680	n/a	n/a	GCCCCTCTTAAATAGC	eekd ₁₀ kke	9	33446	33461	2217
548681	n/a	n/a	GATATCATCATCCCAA	eekd ₁₀ kke	22	33513	33528	2218
548682	n/a	n/a	GTATCCCCTTTTCTAT	eekd ₁₀ kke	0	33556	33571	2219
548683	n/a	n/a	AGTATCTCATGTGCCT	eekd ₁₀ kke	46	33581	33596	2220
548684	n/a	n/a	CAAGACCTTGCTTGCC	eekd ₁₀ kke	24	33658	33673	2221

548685	n/a	n/a	TAGTCCACTACACAGC	eekd ₁₀ kke	24	33802	33817	2222
548686	n/a	n/a	ACGACAATGGGATTCA	eekd ₁₀ kke	0	33844	33859	2223
548687	n/a	n/a	GAATCTCCCTGAGTCA	eekd ₁₀ kke	20	33888	33903	2224
548688	n/a	n/a	TAGAGGGATCCCAGGA	eekd ₁₀ kke	0	34416	34431	2225
548689	n/a	n/a	CCAGGTGCAGCACGGA	eekd ₁₀ kke	12	34483	34498	2226

Example 4: Dose-dependent antisense inhibition of human PKK in HepaRG™ cells

Gapmers from the studies described above exhibiting significant *in vitro* inhibition of PKK mRNA were selected and tested at various doses in HepaRG™ cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.12 μ M, 0.37 μ M, 1.11 μ M, 3.33 μ M, and 10.00 μ M concentrations of antisense oligonucleotide. After a treatment period of approximately 16 hours, RNA was isolated from the cells and PKK mRNA levels were measured by quantitative real-time PCR. Human PKK primer probe set RTS3454 was used to measure mRNA levels. PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. The antisense 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. Results are presented as percent inhibition of PKK, relative to untreated control cells.

The half maximal inhibitory concentration (IC₅₀) of each oligonucleotide is also presented. PKK mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 32

ISIS No	0.12 μ M	0.37 μ M	1.11 μ M	3.33 μ M	10.00 μ M	IC ₅₀ (μ M)
486847	0	34	48	71	87	1.1
530933	15	13	42	67	66	1.7
530959	12	27	53	80	94	0.9
530965	8	5	63	83	91	0.8
530967	30	36	48	82	91	0.7
530970	1	0	66	76	84	1.0
530971	12	40	52	66	70	1.3
530988	0	25	54	86	78	0.9
530992	0	50	63	83	80	0.7
531002	6	28	58	82	86	0.9
531004	0	14	25	71	84	2.1
531005	14	28	61	73	77	0.9
531022	0	0	32	62	77	2.2
531078	10	27	54	69	92	1.1
531231	23	30	76	89	94	0.6

Table 33

ISIS No	0.12 μM	0.37 μM	1.11 μM	3.33 μM	10.00 μM	IC ₅₀ (μM)
531026	23	26	49	75	85	1.0
531055	3	28	64	76	81	0.9
531069	19	39	48	76	83	0.9
531071	23	37	56	83	83	0.7
531110	14	29	49	76	85	1.1
531121	0	13	47	69	79	1.5
531123	14	43	51	71	64	0.9
531172	0	16	37	60	60	2.1
531198	0	35	62	76	60	0.8
531231	18	0	36	76	84	2.0
531232	15	26	40	62	76	1.7
531233	17	27	50	77	84	1.0
531234	24	21	47	72	82	1.4
531235	27	55	62	84	95	0.4
531236	4	28	59	85	93	0.8

Example 5: Dose-dependent antisense inhibition of human PKK in HepaRG™ cells

Gapmers from the studies described above exhibiting significant *in vitro* inhibition of PKK mRNA were selected and tested at various doses in HepaRG™ cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.19 μM, 0.56 μM, 1.67 μM, and 5.00 μM concentrations of antisense oligonucleotide. After a treatment period of approximately 16 hours, RNA was isolated from the cells and PKK mRNA levels were measured by quantitative real-time PCR. Human PKK primer probe set RTS3454 was used to measure mRNA levels. PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. The antisense 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. Results are presented as percent inhibition of PKK, relative to untreated control cells. 'n/a' indicates that there was no measurement done for that particular antisense oligonucleotide for that particular dose.

The half maximal inhibitory concentration (IC₅₀) of each oligonucleotide is also presented. PKK mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 34

ISIS No	0.19 μ M	0.56 μ M	1.67 μ M	5.00 μ M	IC ₅₀ (μ M)
531231	32	30	73	89	0.5
546158	5	45	79	83	0.7
546188	36	55	81	83	0.4
546253	1	13	46	81	1.7
546254	51	66	80	91	0.2
546343	28	64	87	87	0.4
546825	46	73	86	88	0.2
546827	32	70	84	90	0.3
546828	39	58	87	93	0.3
546829	3	30	73	88	1.0
546846	36	45	71	82	0.5
547413	0	0	41	83	2.2
547423	37	50	92	90	0.4
547445	41	75	82	88	0.2
547456	12	67	66	80	1.0
547464	21	52	67	97	0.6
547564	51	48	82	90	0.2
547587	20	62	84	86	0.5
548758	41	47	82	94	0.4

Table 35

ISIS No	0.19 μ M	0.56 μ M	1.67 μ M	5.00 μ M	IC ₅₀ (μ M)
531231	25	34	84	92	0.7
546190	33	65	86	n/a	0.4
546208	16	45	79	91	0.7
546216	62	69	88	88	0.1
546255	32	35	78	87	0.5
546268	56	50	82	93	0.1
546301	25	50	53	87	0.8
546849	23	35	83	91	0.7
546852	19	40	78	85	0.8
546889	23	54	78	91	0.6
546916	43	71	79	89	0.2
546967	20	39	76	71	0.7
547273	44	69	87	87	0.2
547276	35	44	71	77	0.6
547335	8	52	85	92	0.7

547340	46	79	88	n/a	0.2
547602	18	53	92	87	0.5
547647	1	70	72	n/a	0.8
547694	0	29	67	90	1.2

Table 36

ISIS No	0.19 μM	0.56 μM	1.67 μM	5.00 μM	IC ₅₀ (μM)
531231	58	64	77	98	0.1
546247	0	29	71	88	1.1
546251	31	60	99	89	0.5
546753	28	47	83	96	0.5
546826	17	40	87	97	0.7
546833	8	33	74	94	0.9
546854	23	39	83	94	0.6
546894	15	47	50	93	0.9
546897	40	56	71	95	0.4
546903	15	37	74	98	0.8
546986	31	49	77	89	0.5
547293	53	57	80	86	0.2
547298	32	61	74	90	0.4
547364	38	47	54	89	0.6
547373	20	7	49	86	1.1
547426	19	50	84	93	0.6
547454	19	40	58	92	0.9
547617	52	66	77	93	0.2
548770	26	54	77	91	0.5

Table 37

ISIS No	0.19 μM	0.56 μM	1.67 μM	5.00 μM	IC ₅₀ (μM)
531231	34	47	72	n/a	0.5
546214	0	0	68	85	1.3
546304	0	6	51	71	2.1
546739	35	55	57	79	0.6
546832	19	38	70	95	0.8
546847	39	57	75	89	0.4
546855	18	7	30	82	2.2
546877	0	19	75	80	1.3
546939	1	66	86	90	0.6
547349	0	8	66	76	1.6

547360	8	27	76	76	0.8
547368	0	0	31	80	2.5
547483	0	9	49	71	2.1
547575	0	34	82	93	1.1
547618	0	0	73	98	1.3
547622	0	47	79	90	0.9
547637	10	21	36	82	1.8
547731	0	0	17	56	5.0
548752	0	0	51	90	1.9

Table 38

ISIS No	0.19 μ M	0.56 μ M	1.67 μ M	5.00 μ M	IC ₅₀ (μ M)
531231	21	45	67	96	0.7
546195	34	51	79	92	0.5
546198	7	3	45	92	1.3
546287	0	15	39	89	1.7
546358	0	19	71	80	1.3
546403	0	20	37	41	>5.0
546410	13	43	52	75	1.2
546412	0	1	61	62	2.3
546429	6	10	44	69	2.3
546834	1	0	30	83	2.3
547006	0	0	54	77	1.5
547294	28	59	87	86	0.4
547337	23	41	55	79	1.0
547514	18	8	51	80	1.9
547584	26	34	76	86	0.7
547585	42	57	70	95	0.4
547615	20	26	41	84	1.4
547636	0	24	79	94	1.1
548744	14	35	63	83	1.0

Table 39

ISIS No	0.19 μ M	0.56 μ M	1.67 μ M	5.00 μ M	IC ₅₀ (μ M)
531231	21	39	90	97	0.6
546232	49	50	94	97	0.2
546248	25	66	87	93	0.4
546835	9	35	68	93	0.9
546848	0	18	91	97	1.0

546853	47	64	84	n/a	0.2
546870	35	42	80	95	0.5
546872	32	33	82	94	0.4
546876	0	50	85	95	0.8
547275	34	66	82	95	0.3
547341	36	58	91	95	0.3
547366	0	45	68	91	1.2
547453	25	40	54	92	0.8
547457	41	65	80	85	0.3
547616	26	50	72	89	0.6
547632	44	47	81	97	0.6
547633	12	46	78	n/a	0.7
547718	36	12	69	74	1.6
548757	18	49	82	93	0.6

Table 40

ISIS No	0.19 μM	0.56 μM	1.67 μM	5.00 μM	IC ₅₀ (μM)
531231	6	38	74	95	0.8
546291	22	32	34	72	2.0
546310	0	36	56	80	1.3
546896	0	45	82	97	0.8
546980	0	18	29	80	2.2
547009	0	9	21	63	3.6
547019	0	6	54	86	1.6
547277	2	32	34	62	2.8
547288	0	0	0	38	>5.0
547374	0	15	24	44	>5.0
547493	0	26	64	77	1.3
547520	0	25	66	64	1.1
547712	0	5	21	62	3.8
547722	0	15	32	73	2.4
547728	0	2	16	61	4.4
547780	0	10	36	55	3.9
548743	25	57	73	88	0.5
548753	0	23	49	84	1.5
548756	0	4	16	86	>5.0

Table 41

ISIS No	0.19 μM	0.56 μM	1.67 μM	5.00 μM	IC ₅₀ (μM)
531231	25	55	89	97	0.5
546188	27	69	88	97	0.4
546216	23	78	95	98	<0.2
546254	40	63	84	95	0.3
546268	0	71	92	92	0.5
546343	37	32	83	95	0.4
546825	38	82	n/a	99	0.2
546827	23	74	98	96	0.4
546828	0	64	89	97	0.2
546846	26	49	85	n/a	0.5
546967	22	45	74	92	0.7
547273	0	60	82	83	0.6
547340	34	84	96	n/a	0.3
547423	78	92	n/a	n/a	<0.2
547445	80	87	98	91	<0.2
547564	46	66	90	97	0.2
547587	38	64	91	97	0.3
547602	1	9	52	93	1.4
548758	0	72	79	n/a	0.6

Table 42

ISIS No	0.19 μM	0.56 μM	1.67 μM	5.00 μM	IC ₅₀ (μM)
531231	7	39	56	97	1.0
546190	21	34	76	98	0.7
546208	5	33	70	97	0.9
546251	19	45	91	97	0.6
546255	5	39	82	96	0.8
546739	4	62	84	86	0.6
546753	17	31	70	91	0.9
546849	13	45	84	98	0.7
546889	25	9	73	92	1.4
546897	16	17	69	97	0.8
546916	0	27	73	97	1.0
546986	7	28	69	86	1.1
547276	6	3	53	68	2.2
547293	0	45	65	70	1.3
547298	0	12	67	87	1.7

547335	0	13	73	95	1.3
547426	18	35	80	95	0.7
547617	17	37	79	98	0.7
548770	9	0	61	92	1.7

Table 43

ISIS No	0.19 μM	0.56 μM	1.67 μM	5.00 μM	IC ₅₀ (μM)
531231	6	56	68	97	0.8
546195	0	27	91	94	0.9
546232	0	74	95	96	0.2
546248	0	59	73	89	0.8
546832	36	49	85	97	0.4
546847	14	44	83	95	0.7
546853	4	49	74	92	0.8
546870	36	34	61	91	1.0
546872	42	13	59	99	1.4
546896	35	60	83	n/a	0.4
546939	16	71	96	95	0.4
547275	56	16	80	86	1.2
547294	4	70	84	91	0.6
547341	45	44	81	95	0.6
547457	33	42	70	83	0.6
547584	0	21	64	92	1.3
547585	0	46	89	93	0.8
547632	0	0	63	91	1.6
548743	22	47	74	96	0.6

Example 6: Dose-dependent antisense inhibition of human PKK in HepaRG™ cells

5 Gapmers from the studies described above exhibiting significant *in vitro* inhibition of PKK mRNA were selected and tested at various doses in HepaRG™ cells. Cells were plated at a density of 20,000 cells per well and transfected using electroporation with 0.11 μM, 0.33 μM, 1.00 μM, and 3.00 μM concentrations of antisense oligonucleotide. After a treatment period of approximately 16 hours, RNA was isolated from the cells and PKK mRNA levels were measured by quantitative real-time PCR. Human PKK primer probe

10 set RTS3454 was used to measure mRNA levels. PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN®. The antisense 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. Results are presented as percent inhibition of PKK, relative to untreated control cells.

‘n/a’ indicates that there was no measurement done for that particular antisense oligonucleotide for that particular dose.

The half maximal inhibitory concentration (IC₅₀) of each oligonucleotide is also presented. PKK mRNA levels were significantly reduced in a dose-dependent manner in antisense oligonucleotide treated cells.

Table 44

ISIS No	0.11 μM	0.33 μM	1.00 μM	3.00 μM	IC ₅₀ (μM)
547747	24	29	81	89	0.4
547769	12	17	80	96	0.6
547824	45	73	78	n/a	0.1
547835	44	27	53	79	0.9
547843	0	52	80	91	0.4
547857	36	66	77	93	0.2
547870	0	44	80	97	0.6
547943	33	70	87	90	0.2
547946	0	47	74	n/a	0.5
547947	24	58	81	93	0.3
547998	55	73	91	91	0.1
548004	24	47	80	92	0.3
548010	0	11	49	64	1.4
548047	50	62	76	95	0.1
548147	59	94	80	n/a	0.0
548338	41	58	79	95	0.2
548348	19	46	67	91	0.4
548409	21	60	90	93	0.3
548557	5	47	82	95	0.4

Table 45

ISIS No	0.11 μM	0.33 μM	1.00 μM	3.00 μM	IC ₅₀ (μM)
547747	8	61	90	92	0.3
547807	26	71	61	94	0.4
547922	67	75	81	92	0.0
547927	56	64	92	88	0.1
547948	60	80	88	97	0.0
547979	56	58	94	97	0.1
548005	53	49	71	95	0.4
548024	28	57	84	82	0.3

548043	14	60	90	92	0.3
548055	43	57	50	88	0.3
548106	53	54	82	94	0.1
548109	50	92	79	85	0.1
548155	49	50	70	81	0.3
548180	11	59	71	88	0.4
548278	3	59	78	93	0.4
548343	61	67	88	92	0.0
548558	53	61	78	95	0.1
548570	20	40	70	94	0.4
548583	43	46	93	88	0.2

Table 46

ISIS No	0.11 μ M	0.33 μ M	1.00 μ M	3.00 μ M	IC ₅₀ (μ M)
547747	3	44	72	90	0.5
547849	36	52	67	n/a	0.3
547851	16	46	83	n/a	0.4
547859	29	56	83	78	0.3
547862	26	71	69	n/a	0.3
547877	29	66	83	n/a	0.2
547942	25	51	91	n/a	0.3
547997	39	68	n/a	82	0.2
548046	7	35	64	77	0.7
548048	49	66	86	92	0.1
548061	26	61	59	n/a	0.4
548070	26	35	48	63	1.1
548125	33	50	81	73	0.3
548195	5	23	61	76	0.8
548265	47	69	78	67	0.1
548410	31	58	85	82	0.2
548424	17	67	86	72	0.3
548425	41	57	68	80	0.2
548547	30	41	76	90	0.4

Table 47

ISIS No	0.11 μ M	0.33 μ M	1.00 μ M	3.00 μ M	IC ₅₀ (μ M)
547747	16	59	85	96	0.3
547808	19	22	48	71	1.1
547861	7	40	75	84	0.5

548069	6	0	27	66	1.9
548128	14	29	49	66	1.1
548170	0	8	26	65	2.0
548174	20	18	29	62	2.0
548197	33	37	51	75	0.8
548201	0	7	70	85	0.8
548217	22	24	54	71	0.9
548220	0	0	0	6	>3
548247	16	50	62	82	0.5
548422	0	32	71	93	0.7
548479	2	52	82	97	0.4
548486	20	48	77	92	0.4
548521	21	0	3	1	>3
548655	0	0	8	33	>3
548667	0	37	73	86	0.7
548668	10	30	61	84	0.7

Example 7: Efficacy of antisense oligonucleotides targeting human PKK in transgenic mice

Transgenic mice containing a 37,390 base pair fragment of the human KLKB1 gene sequence (chromosome 4: position 187148672-187179625, accession no: NC_000004.11) were treated with ISIS antisense oligonucleotides selected from studies described above, which were evaluated for efficacy in this model.

Treatment

Groups of transgenic mice were injected subcutaneously twice a week for 3 weeks with 2.5 mg/kg/week, 5.0 mg/kg/week, 10 mg/kg/week or 20 mg/kg/week of ISIS 546232, ISIS 546251, ISIS 546254, ISIS 546343, ISIS 546828, ISIS 547455, ISIS 547457, ISIS 547927, and ISIS 548048. One group of transgenic mice was injected subcutaneously twice a week for 3 weeks with PBS. Mice were euthanized 48 hours after the last dose, and organs and plasma were harvested for further analysis.

RNA analysis

To evaluate the effect of ISIS oligonucleotides on target reduction, RNA was extracted from liver tissue for real-time PCR analysis of human PKK. Results are presented as percent inhibition of PKK mRNA, relative to PBS control. As shown in Table 48, treatment with ISIS antisense oligonucleotides resulted in significant reduction of PKK mRNA in comparison to the PBS control.

Table 48

Percent Inhibition of PKK mRNA in the transgenic mice liver relative to the PBS control

ISIS No	Dose	% inhibition
547927	20	71
	10	93
	5	52
	2.5	35
547455	20	62
	10	45
	5	69
	2.5	0
546232	20	84
	10	30
	5	53
	2.5	57
546254	20	83
	10	84
	5	55
	2.5	31
546343	20	86
	10	66
	5	n/a
	2.5	46
548048	20	80
	10	72
	5	77
	2.5	7
546828	20	83
	10	32
	5	62
	2.5	77
546251	20	79
	10	66
	5	51
	2.5	13
547457	20	62
	10	45
	5	69
	2.5	0

Protein analysis

- 5 Plasma PKK protein levels were evaluated in all groups. Results are presented as percent inhibition of PKK protein, relative to PBS control. As shown in Table 49, treatment with ISIS antisense oligonucleotides resulted in significant reduction of PKK protein levels in comparison to the PBS control.

Table 49

Percent reduction of PKK protein levels in the transgenic mice relative to the PBS control

ISIS No	Dose	% inhibition
547927	20	80
	10	n/a
	5	21
	2.5	25
547455	20	78
	10	32
	5	0
	2.5	0
546232	20	79
	10	33
	5	6
	2.5	0
546254	20	76
	10	51
	5	36
	2.5	0
546343	20	79
	10	38
	5	n/a
	2.5	0
548048	20	98
	10	89
	5	70
	2.5	23
546828	20	93
	10	36
	5	25
	2.5	0
546251	20	69
	10	52
	5	30
	2.5	22
547457	20	60
	10	31
	5	4
	2.5	0

Example 8: Effect of ISIS antisense oligonucleotides targeting human PKK in cynomolgus monkeys

5 Cynomolgus monkeys were treated with ISIS antisense oligonucleotides selected from studies described above. Antisense oligonucleotide efficacy and tolerability were evaluated. The human antisense oligonucleotides tested are cross-reactive with the rhesus genomic sequence (GENBANK Accession No.

NW_001118167.1 truncated from nucleotides 2358000 to 2391000 and designated herein as SEQ ID NO: 18). The target start site of each oligonucleotide to SEQ ID NO: 18 is presented in Table 50. 'Mismatch' indicates that the number of nucleotides by which the oligonucleotide is mismatched to the rhesus sequence. The greater the complementarity between the human oligonucleotide and the rhesus monkey sequence, the more likely the human oligonucleotide can cross-react with the rhesus monkey sequence. 'n/a' indicates that the oligonucleotide is has more than 3 mismatches with the rhesus gene sequence.

Table 50

Antisense oligonucleotides complementary to SEQ ID NO: 18

ISIS No	Target Start Site	Mismatches	Sequence	Chemistry	SEQ ID NO.
547927	22059	1	ATGGTCCGACACACAA	Deoxy, MOE and cEt	1548
546232	n/a	n/a	AGGAACTTGGTGTGCCACTT	5-10-5 MOE	526
547455	27391	0	ATATCATGATTCCCTTCTGA	5-10-5 MOE	657
546254	23858	1	TGCAAGTCTCTTGGCAAACA	5-10-5 MOE	570
546343	30532	0	CCCCCTTCTTTATAGCCAGC	5-10-5 MOE	705
548048	27397	0	CGATATCATGATTCCC	Deoxy, MOE and cEt	1666
546828	13632	1	ACAGTATCACTGTACTAGTT	5-10-5 MOE	904
546251	23846	0	GGCAAACATTCACTCCTTTA	5-10-5 MOE	566
547457	27397	0	AAGGCGATATCATGATTCCC	5-10-5 MOE	660

10 Treatment

Prior to the study, the monkeys were kept in quarantine for a 30-day period, during which the animals were observed daily for general health. The monkeys were 2-4 years old and weighed between 2 and 4 kg. Ten groups of four randomly assigned male cynomolgus monkeys each were injected subcutaneously with ISIS oligonucleotide or PBS. PBS solution or ISIS oligonucleotides at a dose of 40 mg/kg were administered initially with a loading regimen consisting of four doses on the first week of the study (days 1, 3, 5, and 7), followed by a maintenance regimen consisting of once weekly administration starting on Day 14 (weeks 2 to 13). Subcutaneous injections were performed in clock-wise rotations at 4 sites on the back; one site per dose. The injection sites were delineated by tattoo, while sedated using ketamine, and were separated by a minimum of 3 cm.

During the study period, the monkeys were observed a minimum of once daily for signs of illness or distress. Any animal experiencing more than momentary or slight pain or distress due to the treatment, injury or illness was promptly reported to the responsible veterinarian and the Study Director. Any animal in poor health or in a possible moribund condition was identified for further monitoring and possible euthanasia. For example, two monkeys treated with ISIS 547445 were euthanized due to subdued behavior, lateral position,

lack of response to stimuli and decreased respiration. The protocols described in the Example were approved by the Institutional Animal Care and Use Committee (IACUC).

Target Reduction

RNA analysis

5 On day 87 or 88, 48 hours after the final dose, RNA was extracted from liver tissue for real-time PCR analysis of PKK using primer probe set RTS3455 (forward sequence CCTGTGTGGAGGGTCACTCA, designated herein as SEQ ID NO: 23; reverse sequence CCACTATAGATGCGCCAAACATC, designated herein as SEQ ID NO: 24; probe sequence CCCACTGCTTTGATGGGCTTCCC, designated herein as SEQ ID NO: 25). The results were normalized to the housekeeping gene, Cyclophilin. Results are presented as
10 percent inhibition of PKK mRNA, relative to PBS control. As shown in Table 51, treatment with ISIS antisense oligonucleotides resulted in significant reduction of PKK mRNA in comparison to the PBS control.

Table 51

Percent Inhibition of PKK mRNA in the cynomolgus monkey liver relative to the PBS control

ISIS No	% inhibition
546232	88
546251	90
546254	88
546343	74
546828	45
547455	90
547457	89
547927	54
548048	95

15 *Protein analysis*

Approximately 0.9 mL of blood was collected each time from all available animals at pre-dose, day 17, day 31, day 45, day 59, and day 73, and placed in tubes containing 3.2% sodium citrate. The tubes were centrifuged (3000 rpm for 10 min at room temperature) to obtain plasma. PKK protein levels were measured in the plasma by ELISA. The results are presented in Table 52, expressed as percentage inhibition compared
20 to the PBS control levels. The results indicate that ISIS oligonucleotides significantly reduced PKK protein levels.

Table 52

PKK protein level reduction (%) in the cynomolgus monkey plasma relative to control levels

	Day 17	Day 31	Day 45	Day 59	Day 73
ISIS 546232	53	58	72	75	70
ISIS 546251	71	75	75	81	77
ISIS 546254	38	51	63	74	73
ISIS 546343	56	74	69	70	70
ISIS 546828	0	8	23	39	39
ISIS 547455	26	33	43	58	58
ISIS 547457	68	75	79	76	80
ISIS 547927	8	0	15	10	18
ISIS 548048	90	93	95	95	95

Tolerability studies

Liver function

- 5 To evaluate the effect of ISIS oligonucleotides on hepatic function, the monkeys were fasted overnight. Approximately, 1.5 mL of blood samples were collected from all the study groups. Blood was collected in tubes without anticoagulant for serum separation. The tubes were kept at room temperature for a minimum of 90 min and then centrifuged at 3,000 rpm for 10 min. Levels of various liver function markers were measured using a Toshiba 120FR NEO chemistry analyzer (Toshiba Co., Japan). The results are presented in Table 53 and indicate that antisense oligonucleotides had no effect on liver function outside the expected range for antisense oligonucleotides.

Table 53

Liver function markers in cynomolgus monkey plasma

	Albumin (g/dL)	AST (IU/L)	ALT (IU/L)
PBS	4.2	48	60
ISIS 546232	4.1	63	140
ISIS 546251	3.7	51	58
ISIS 546254	3.8	68	54
ISIS 546343	4.3	49	76
ISIS 546828	3.7	75	67
ISIS 547455	3.8	56	61
ISIS 547457	4.0	54	52
ISIS 547927	4.2	59	61
ISIS 548048	4.2	44	47

To evaluate any effect of ISIS oligonucleotides in cynomolgus monkeys on hematologic parameters, blood samples of approximately 1.2 mL of blood was collected pre-dose and on day 87 or day 88 from each of the available study animals in tubes containing K₂-EDTA. Samples were analyzed for red blood cell (RBC) count, white blood cells (WBC) count, platelet count, hemoglobin content and hematocrit, using an ADVIA2120i hematology analyzer (SIEMENS, USA). The data is presented in Table 54.

The data indicate treatment with most of the oligonucleotides did not cause any changes in hematologic parameters outside the expected range for antisense oligonucleotides at this dose.

Table 54
Hematological parameters in cynomolgus monkeys

	RBC (x 10 ⁶ /μL)	Platelets (x 10 ³ /μL)	WBC (x 10 ³ /μL)	Hemoglobin (g/dL)	HCT (%)
PBS	5.4	458	13	13.1	43
ISIS 546232	5.4	391	11	12.9	42
ISIS 546251	5.7	419	8	12.9	43
ISIS 546254	5.3	436	11	12.4	41
ISIS 546343	5.5	373	14	12.6	42
ISIS 546828	6.0	408	11	12.9	43
ISIS 547455	4.5	448	13	10.2	34
ISIS 547457	6.4	367	10	13.8	45
ISIS 547927	5.2	461	45	12.5	41
ISIS 548048	5.9	393	11	13.4	44

Kidney function

To evaluate the effect of ISIS oligonucleotides on kidney function, the monkeys were fasted overnight. Approximately, 1.5 mL of blood samples were collected from all the study groups. Blood was collected in tubes without anticoagulant for serum separation. The tubes were kept at room temperature for a minimum of 90 min and then centrifuged at 3,000 rpm for 10 min. Levels of BUN and creatinine were measured using a Toshiba 120FR NEO chemistry analyzer (Toshiba Co., Japan). Results are presented in Table 55, expressed in mg/dL. The plasma chemistry data indicate that most of the ISIS oligonucleotides did not have any effect on the kidney function outside the expected range for antisense oligonucleotides. Specifically, treatment with ISIS 546254 was well tolerated in terms of the kidney function of the monkeys.

Kidney function was also assessed by urinalysis. Fresh urine from all animals was collected using a clean cage pan on wet ice. Food was removed overnight the day before fresh urine collection was done but water was supplied. The total protein and creatinine levels were measured using a Toshiba 120FR NEO

automated chemistry analyzer (Toshiba Co., Japan) and the protein to creatinine ratio was calculated. The results are presented in Table 56.

Table 55
Plasma BUN and creatinine levels (mg/dL) in cynomolgus monkeys

	BUN	Creatinine
PBS	22.8	0.9
ISIS 546232	22.7	1.0
ISIS 546251	25.4	1.1
ISIS 546254	25.7	0.9
ISIS 546343	26.2	1.0
ISIS 546828	24.7	0.9
ISIS 547455	29.4	0.9
ISIS 547457	24.3	1.0
ISIS 547927	22.3	1.0
ISIS 548048	21.9	0.9

5

Table 56
Urine protein/creatinine ratio in cynomolgus monkeys

	Ratio
ISIS 546232	0.03
ISIS 546251	0.12
ISIS 546254	0.04
ISIS 546343	0.01
ISIS 546828	0.03
ISIS 547455	0.70
ISIS 547457	0.03
ISIS 547927	0.04
ISIS 548048	0.03
PBS	0.06

C-reactive protein level analysis

10 To evaluate any inflammatory effect of ISIS oligonucleotides in cynomolgus monkeys, the monkeys were fasted overnight. Approximately, 1.5 mL of blood samples were collected from all the study groups. Blood was collected in tubes without anticoagulant for serum separation. The tubes were kept at room temperature for a minimum of 90 min and then centrifuged at 3,000 rpm for 10 min. C-reactive protein (CRP), which is synthesized in the liver and which serves as a marker of inflammation, was measured using a

Toshiba 120FR NEO chemistry analyzer (Toshiba Co., Japan). Complement C3 was also measured similarly, and the data is presented as a percentage of baseline values. The results are presented in Table 57 and indicate that treatment with ISIS oligonucleotides did not cause any inflammation in monkeys.

Table 57

C-reactive protein and C3 levels in cynomolgus monkey plasma

	CRP (mg/dL)	C3 (% of baseline)
PBS	0.2	73
ISIS 546232	0.5	50
ISIS 546251	0.7	62
ISIS 546254	0.8	61
ISIS 546343	0.2	60
ISIS 546828	0.6	56
ISIS 547455	1.9	64
ISIS 547457	0.3	53
ISIS 547927	0.2	73
ISIS 548048	0.2	69

Example 9: Antisense inhibition of murine PKK mRNA in mouse primary hepatocytes

Antisense oligonucleotides targeting a murine PKK nucleic acid were designed and tested for their effects on PKK mRNA *in vitro*. Cultured mouse primary hepatocytes at a density of 10,000 cells per well were transfected using Cytofectin reagent with 12.5 nM, 25.0 nM, 50.0 nM, 100.0 nM, and 200.0 nM of antisense oligonucleotide. After a treatment period of approximately 24 hours, RNA was isolated from the cells and mouse PKK mRNA levels were measured by quantitative real-time PCR using the murine primer probe set RTS3313 (forward sequence TGCCTGCTGTTCAGCTTTCTC, designated herein as SEQ ID NO: 2228; reverse sequence TGGCAAAGTCCCTGTAATGCT, designated herein as SEQ ID NO: 2229; probe sequence CGTGACTCCACCCAAAGAGACAAATAAACG, designated herein as SEQ ID NO: 2230). PKK mRNA levels were adjusted according to total RNA content, as measured by RIBOGREEN.

The chimeric antisense oligonucleotides were designed as 5-10-5 MOE gapmers. The gapmers are 20 nucleotides in length, wherein the central gap segment is comprised of ten 2'-deoxynucleosides and is flanked on both sides (in the 5' and 3' directions) by wings comprising 5 nucleosides each. Each nucleoside in the 5' wing segment and each nucleoside in the 3' wing segment has a 2'-O-methoxyethyl modification. The internucleoside linkages throughout each gapmer are phosphorothioate linkages. All cytosine residues

throughout each gapmer are 5-methylcytosines. Results demonstrate that PKK mRNA levels were significantly reduced in a dose dependent manner.

In one specific example, ISIS 482584 (GGCATATTGGTTTTTGAAT; SEQ ID NO: 2244) reduced PKK mRNA in a dose dependent manner yielding a half maximal inhibitory concentration (IC₅₀) of 84 nM (see Table 58). ISIS 482584 is targeted to SEQ ID NO: 11 (GENBANK Accession No. NM_008455.2) and has a target start site of 1586 and a target stop site of 1605. "Target start site" indicates the 5'-most nucleotide to which the gapmer is targeted. "Target stop site" indicates the 3'-most nucleotide to which the gapmer is targeted.

Table 58
Dose-dependent inhibition of mouse PKK mRNA levels by ISIS 482584

Dose	% inhibition
12.5 nM	0
25.0 nM	47
50.0 nM	27
100.0 nM	60
200.0 nM	82

Example 10: Antisense inhibition of PKK mRNA in BALB/c mice

ISIS 482584 was tested for its effect on murine PKK mRNA *in vivo*.

Treatment

Six groups of male BALB/c mice each were treated with 2.5 mg/kg, 5.0 mg/kg, 10.0 mg/kg, 20.0 mg/kg, 40.0 mg/kg, or 80.0mg/kg of ISIS 482584, administered subcutaneously twice a week for 3 weeks (weekly doses of 5.0 mg/kg, 10.0 mg/kg, 20.0 mg/kg, 40.0 mg/kg, 80.0 mg/kg, or 160.0 mg/kg). A control group of BALB/c mice was treated with PBS, administered subcutaneously twice a week for 3 weeks. Two days after the last dose of antisense oligonucleotide or PBS, mice from all groups were anesthetized with 150 mg/kg ketamine mixed with 10 mg/kg xylazine, administered by intraperitoneal injection. Liver was collected for RNA analysis.

RNA Analysis

RNA was extracted from liver tissue for real-time PCR analysis of PKK. PKK mRNA levels were measured using the murine primer probe set (forward sequence ACAAGTGCATTTTACAGACCAGAGTAC, designated herein as SEQ ID NO: 2231; reverse sequence GGTGTGTCGCTGACTTTATGCT, designated herein as SEQ ID NO: 2232; probe sequence AAGCACAGTGCAAGCGGAACACCC, designated herein as SEQ ID NO: 2233). Results are presented as

percent inhibition of PKK, relative to PBS control. As shown in Table 59, treatment with ISIS 482584 resulted in significant dose-dependent reduction of PKK mRNA in comparison to the PBS control.

Table 59
Dose-dependent reduction of PKK mRNA in BALB/c mice liver

Dose (mg/kg/wk)	% inhibition
5	3
10	42
20	68
40	85
80	91
160	94

Protein Analysis

Plasma was collected in tubes containing sodium citrate as an anticoagulant. The samples were run on a 4-12% gradient SDS-polyacrylamide gel (Invitrogen), followed by immunoblotting with murine PKK antibody (R&D Systems). Blots were incubated with secondary fluorophore-labeled antibodies (LI-COR) and imaged in an Odyssey Imager (LI-COR). Results are presented as percent inhibition of PKK, relative to PBS control. As shown in Table 60, treatment with ISIS 482584 resulted in significant dose-dependent reduction of PKK plasma protein in comparison to the PBS control.

Table 60
Dose-dependent reduction of PKK protein in BALB/c mice plasma

Dose (mg/kg/wk)	% inhibition
5	5
10	24
20	47
40	76
80	81
160	n.d.

n.d. = no data

Example 11: *In vivo* effect of antisense inhibition of murine PKK in an angioedema mouse model

Hereditary angioedema (HAE) is characterized by local swelling and increase in vascular permeability in subcutaneous tissues (Morgan, B.P. N. Engl. J. Med. 363: 581-83, 2010). It is caused by a deficiency of the C1 inhibitor, a protein of the complement system. Two mouse models were used in this study including an established mouse model of C1-INH deficiency and a captopril-induced edema model,

both of which cause vascular permeability, a hallmark of HAE. Reversal of vascular permeability is accompanied by increased plasma levels of high molecular weight kininogen (HMWK).

In the first model, angioedema was induced by treatment with Captopril, a known antihypertensive agent, which increases vascular permeability in mice and replicates the pathology of hereditary angioedema.

5 In the second model, angioedema was induced by treatment with ISIS 461756, an antisense oligonucleotide which targets murine C1 inhibitor mRNA, which increases vascular permeability in mice and replicates the pathology of hereditary angioedema. ISIS 461756 (SEQ ID NO: 2245; AAAGTGGTTGATACCCTGGG) is a 5-10-5 MOE gapmer targeting nucleosides 1730-1749 of NM_009776.3 (SEQ ID NO: 2243).

10 The effect of HOE-140 and ISIS 482584, an antisense oligonucleotide inhibitor of PKK, were evaluated in the Captopril and ISIS 461756-induced mouse models of vascular permeability. Some of the murine groups were treated with HOE-140, a selective antagonist of the bradykinin B2 receptor, which blocks vasodilation and vascular permeability (Cruden and Newby, Expert Opin. Pharmacol. 9: 2383-90, 2008). Other mice were treated with ISIS 482584, which inhibits PKK mRNA expression. The effect of
15 treatment with HOE-140 was compared with the effect of treatment with ISIS 482584.

Treatment

The various treatment groups for this assay are presented in Table 61.

Group 1 consisted of 4 C57BL/6J-Tyrc-2J mice treated with PBS administered subcutaneously twice a week for 4 weeks. No other treatment was administered to Group 1 which served as a control group to
20 measure the basal level of vascular permeability.

Group 2 consisted of 8 C57BL/6J-Tyrc-2J mice treated with PBS administered subcutaneously twice a week for 4 weeks. At the end of the treatment, the mice were intraperitoneally administered 20 µg of captopril. Group 2 served as a PBS control group for captopril-induced vascular permeability.

Group 3 consisted of 8 C57BL/6J-Tyrc-2J mice treated with PBS administered subcutaneously twice
25 a week for 4 weeks. On day 14, the mice were treated with 50 mg/kg of the antisense oligonucleotide targeting C1 inhibitor, ISIS 461756, administered subcutaneously twice a week for 2 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 3 served as a PBS control group for captopril and ISIS 461756-induced vascular permeability.

Group 4 consisted of 8 C57BL/6J-Tyrc-2J mice treated with PBS administered subcutaneously twice
30 a week for 4 weeks. On day 14, the mice were treated with 50 mg/kg of the antisense oligonucleotide targeting C1 inhibitor, ISIS 461756, administered subcutaneously twice a week for 2 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. The mice were then

also intraperitoneally administered 30 µg of HOE-140. Group 4 served as a positive control for inhibition of vascular permeability with HOE-140.

Group 5 consisted of 8 C57BL/6J-Tyrc-2J mice treated with 40 mg/kg of control oligonucleotide ISIS 141923, a 5-10-5 MOE gapmer with no known murine target, (CCTTCCCTGAAGGTTTCCTCC; SEQ ID NO: 2246) administered subcutaneously twice a week for 4 weeks. On day 14, the mice were treated with 50 mg/kg of the antisense oligonucleotide targeting C1 inhibitor, ISIS 461756, administered subcutaneously twice a week for 2 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 5 served as a control group for captopril and ISIS 461756-induced vascular permeability.

Group 6 consisted of 8 C57BL/6J-Tyrc-2J mice and was treated with 40 mg/kg of ISIS 482584 administered subcutaneously twice a week for 4 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 6 served as the experimental treatment group for examining the effect of PKK ASO on captopril-induced vascular permeability.

Group 7 consisted of 8 C57BL/6J-Tyrc-2J mice treated with 40 mg/kg of ISIS 482584 administered subcutaneously twice a week for 4 weeks. On day 14, the mice were treated with 50 mg/kg of the antisense oligonucleotide targeting C1 inhibitor, ISIS 461756, administered subcutaneously twice a week for 2 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 7 served as the experimental treatment group for examining the effect of PKK ASO on captopril and ISIS 461756-induced vascular permeability.

All the groups were then injected with 30 mg/kg of Evans Blue solution into the tail vein. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, ears, and intestines were harvested. Blood samples were taken through cardiac puncture.

Table 61
Treatment groups

Group No.	Treatment	Captopril	ISIS 461756	HOE-140
1. (N=4)	PBS	No	No	No
2. (N=8)	PBS	Yes	No	No
3. (N=8)	PBS	Yes	Yes	No
4. (N=8)	PBS	Yes	Yes	Yes
5. (N=8)	ISIS 141923	Yes	Yes	No
6. (N=8)	ISIS 482584	Yes	No	No
7. (N=8)	ISIS 482584	Yes	Yes	No

Quantification of vascular permeability

The harvested tissues from the feet, colon, ears, and intestines were placed separately in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing ear and feet tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}, and is presented in Table 62. Mice displaying any manifestation of angioedema take up more dye and, therefore, demonstrate high OD values.

As presented in Table 62, treatment with ISIS 482584 prevents vascular permeability in mice treated with captopril (Group 6) and in mice treated with captopril and ISIS 461756 (Group 7) compared to the respective PBS control groups (Groups 2 and 3). Measures of vascular permeability in mice of Groups 6 and 7 were also reduced in most of the tissues in comparison to the mice treated with the control oligonucleotide, ISIS 141923 (Group 5), where vascular permeability was induced with captopril and ISIS 461756. Measures of vascular permeability in the colon and feet tissues of both the treatment groups (Groups 6 and 7) were comparable to basal levels, as observed in mice treated with only PBS (Group 1). Reduction in vascular permeability in mice treated with ISIS 482584 was comparable to that seen in mice treated with the bradykinin 2 receptor antagonist, HOE140, which served as a positive control in this assay.

Therefore, antisense inhibition of PKK mRNA may be beneficial for the treatment and prevention of vascular permeability, which is symptomatic of HAE.

Table 62
OD_{600nm} of Evans Blue dye to measure vascular permeability

Group No.	Treatment	Captopril	ISIS 461756	HOE-140	Colons	Intestines	Feet	Ears
1	PBS	No	No	No	0.26	0.16	0.11	0.02
2	PBS	Yes	No	No	0.49	0.29	0.12	0.07
3	PBS	Yes	Yes	No	0.49	0.34	0.11	0.12
4	PBS	Yes	Yes	Yes	0.14	0.18	0.07	0.09
5	ISIS 141923	Yes	Yes	No	0.44	0.29	0.14	0.08
6	ISIS 482584	Yes	No	No	0.27	0.30	0.07	0.14
7	ISIS 482584	Yes	Yes	No	0.21	0.34	0.07	0.06

Quantification of High Molecular Weight Kininogen (HMWK)

Western blot quantification of HMWK from blood samples are presented in Figure 1.

As shown in Figure 1, samples from Groups 1 and 2 have low levels of HMWK as compared to Groups 6 and 7 indicating that vascular permeability is reversed in Groups 6 and 7. Also as shown in Figure 1, samples from Groups 1 and 2 have increased HMWK cleavage product as compared to Groups 6 and 7.

Thus, lack of HMWK is caused by PKK cleavage of HMWK into cleavage products (including bradykinin and HKa).

Example 12: *In vivo* effect of antisense inhibition of murine PKK on basal permeability and captopril-induced permeability in mice

Basal permeability is the level of vascular permeability occurring in the tissues of naïve, untreated mice. The effect of ISIS 482584 in the prevention of vascular permeability, either basal or captopril-induced, was evaluated.

Treatment

The various treatment groups for this assay are presented in Table 63.

Group 1 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 4 weeks. No other treatment was administered to Group 1 which served as a control group to measure the basal levels of vascular permeability.

Group 2 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 4 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 2 served as the negative control group for captopril-induced vascular permeability.

Group 3 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 4 weeks. At the end of the treatment period, the mice were intraperitoneally administered 30 µg of HOE-140. Group 3 served as a positive control for inhibition of basal vascular permeability.

Group 4 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 4 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. The mice were also intraperitoneally administered 30 µg of HOE-140. Group 4 served as a positive control for inhibition of captopril-induced vascular permeability.

Group 5 consisted of 8 mice and was treated with 40 mg/kg of ISIS 482584 administered subcutaneously twice a week for 4 weeks. Group 5 served as an experimental treatment group for examining the effect of ISIS 482584 on basal vascular permeability.

Group 6 consisted of 8 mice and was treated with 40 mg/kg of ISIS 482584 administered subcutaneously twice a week for 4 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 6 served as an experimental treatment group for examining the effect of ISIS 482584 on captopril-induced vascular permeability.

All the groups were then injected with 30 mg/kg of Evans Blue solution. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, ears, and intestines were harvested.

Table 63
Treatment groups

Group No.	Treatment	Captopril	HOE-140
1. (N=8)	PBS	No	No
2. (N=8)	PBS	Yes	No
3. (N=8)	PBS	No	Yes
4. (N=8)	PBS	Yes	Yes
5. (N=8)	ISIS 482584	No	No
6. (N=8)	ISIS 482584	Yes	No

Quantification of vascular permeability

The harvested tissues from the feet, colon, intestine, and ears were placed separately in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing feet and ear tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}, and is presented in Table 64. Mice displaying any manifestation of angioedema take up more dye and, therefore, demonstrate high OD values.

As presented in Table 64, mice treated with ISIS 482584 demonstrated reduced basal vascular permeability compared to the PBS control (Group 5 vs. Group 1). The reduction in basal vascular permeability by treatment with ISIS 482584 was comparable to that caused by treatment with HOE-140 (Group 3, which served as the positive control). Mice treated with ISIS 482584 also demonstrated reduced captopril-induced vascular permeability in most tissues compared to the PBS control (Group 6 vs. Group 2). The reduction in captopril-induced vascular permeability by treatment with ISIS 482584 was comparable to that caused by treatment with HOE-140 (Group 4, which served as the positive control).

Table 64
OD_{600nm} of Evans Blue dye to measure vascular permeability

Group No.	Treatment	Captopril	HOE-140	Colon	Feet	Intestine	Ears
1	PBS	No	No	0.27	0.08	0.23	0.06
2	PBS	Yes	No	0.61	0.08	0.24	0.01
3	PBS	No	Yes	0.18	0.06	0.21	0.03
4	PBS	Yes	Yes	0.29	0.03	0.14	0.00
5	ISIS 482584	No	No	0.19	0.07	0.22	0.04
6	ISIS 482584	Yes	No	0.37	0.05	0.22	0.00

Example 13: Dose-dependent effect of antisense inhibition of murine PKK on captopril-induced vascular permeability

The effect of varying doses on ISIS 482584 on captopril-induced vascular permeability was evaluated.

5 Treatment

The various treatment groups for this assay are presented in Table 65.

Group 1 consisted of 4 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. No other treatment was administered to Group 1 which served as a control group to measure the basal levels of vascular permeability.

10 Group 2 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 2 served as the control group for captopril-induced vascular permeability.

Group 3 consisted of 4 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril.

15 The mice were also intraperitoneally administered 30 µg of Icatibant (HOE-140). Group 4 served as a positive control for inhibition of captopril-induced vascular permeability.

Groups 4, 5, 6, 7, 8, and 9 consisted of 8 mice each and were treated with 2.5 mg/kg, 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, or 80 mg/kg (corresponding to 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, 80 mg/kg, or 160 mg/kg per week), respectively of ISIS 482584 administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice of all the groups were intraperitoneally administered 20 µg of captopril. Groups 4-9 served as the experimental treatment groups for examining the effect of varying doses of ISIS 482584 on captopril-induced vascular permeability.

All the groups were then injected with 30 mg/kg of Evans Blue solution in the tail vein. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, ears, and intestines were harvested. Blood samples were taken through cardiac puncture.

Table 65
Treatment groups

Group No.	Treatment	Dose (mg/kg/wk)	Captopril	HOE-140
1. (N=4)	PBS	-	No	No
2. (N=8)	PBS	-	Yes	No
3. (N=4)	PBS	-	Yes	Yes

4. (N=8)	ISIS 482584	160	Yes	No
5. (N=8)	ISIS 482584	80	Yes	No
6. (N=8)	ISIS 482584	40	Yes	No
7. (N=8)	ISIS 482584	20	Yes	No
8. (N=8)	ISIS 482584	10	Yes	No
9. (N=8)	ISIS 482584	5	Yes	No

Quantification of vascular permeability

The harvested tissues were placed in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing feet and ear tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}, and is presented in Table 66. Mice displaying any manifestation of angioedema take up more dye and, therefore, demonstrate high OD values.

As presented in Table 66, mice treated with higher doses of ISIS 482584 (Groups 4, 5, and 6) had reduced levels of captopril-induced vascular permeability compared to the corresponding PBS control group (Group 2). The reduction in vascular permeability in mice of these treatment groups (Groups 4 and 5) was comparable to the levels of basal vascular permeability (as shown in Group 1) as well as in mice treated with HOE-140 (Group 3).

Table 66
OD_{600nm} of Evans Blue dye to measure vascular permeability

Group No.	Treatment	Dose (mg/kg)	Captopril	HOE-140	Colon	Feet	Intestine	Ears
1	PBS	-	No	No	0.16	0.07	0.13	0.01
2	PBS	-	Yes	No	0.39	0.12	0.18	0.07
3	PBS	-	Yes	Yes	0.15	0.03	0.10	0.04
4	ISIS 482584	160	Yes	No	0.26	0.10	0.15	0.05
5	ISIS 482584	80	Yes	No	0.21	0.04	0.17	0.03
6	ISIS 482584	40	Yes	No	0.36	0.10	0.20	0.05
7	ISIS 482584	20	Yes	No	0.40	0.11	0.20	0.07
8	ISIS 482584	10	Yes	No	0.41	0.10	0.19	0.05
9	ISIS 482584	5	Yes	No	0.41	0.10	0.17	0.05

Quantification of vascular leakage

The blood drawn through cardiac puncture was immediately mixed with 3 times the volume of ice-cold ethanol. The solution was centrifuged at 15,000 g for 20 minutes at 4°C to remove cell debris and

precipitated plasma proteins. The ethanol extracts were further purified by ultra-filtration through a 10 kDa MWCO filter. The color intensity of the ethanol extracted plasma solution was then measured at OD_{620nm}. The results are presented in Table 67 as percentage increase or decrease of the OD values of the Group 1 PBS control. It was expected that tissues from mice displaying manifestation of angioedema would leak more dye from the plasma and, therefore, demonstrate low OD values, whereas treatment groups may display higher OD values due to reduced vascular leakage. Mice treated with 160 mg/kg/week and 80 mg/kg/week of ISIS 482584 (Groups 4 and 5) demonstrated less vascular leakage compared to the PBS negative control treated with captopril (Group 2). The results from Groups 4 and 5 were comparable to the positive control treated with HOE-140 (Group 3).

Table 67

Percentage of OD_{620nm} of Evans Blue dye compared to the PBS basal control to measure vascular leakage

Group No.	Treatment	Dose (mg/kg)	Captopril	HOE-140	Plasma
2	PBS	-	Yes	No	-43
3	PBS	-	Yes	Yes	5
4	ISIS 482584	160	Yes	No	91
5	ISIS 482584	80	Yes	No	40
6	ISIS 482584	40	Yes	No	-31
7	ISIS 482584	20	Yes	No	-26
8	ISIS 482584	10	Yes	No	-20
9	ISIS 482584	5	Yes	No	-23

Example 14: Dose-dependent effect of antisense inhibition of murine PKK on basal permeability in mice

The effect of varying doses on ISIS 482584 on basal vascular permeability was evaluated.

Treatment

The various treatment groups for this assay are presented in Table 68.

Group 1 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. No other treatment was administered to Group 1 which served as a control group to measure the basal levels of vascular permeability.

Group 2 consisted of 4 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice were intraperitoneally administered 30 µg of HOE-140. Group 2 served as a positive control for inhibition of basal vascular permeability.

Groups 3, 4, 5, 6, 7, and 8 consisted of 8 mice each and were treated with 2.5 mg/kg, 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, or 80 mg/kg (corresponding to 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, 80 mg/kg, or 160 mg/kg per week), respectively of ISIS 482584 administered subcutaneously twice a week for 3 weeks. Groups 4-9 served as the experimental treatment groups for examining the effect of varying doses of ISIS 482584 on basal vascular permeability.

All the groups were then injected with 30 mg/kg of Evans Blue solution in the tail vein. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, and ears were harvested and examined for permeability defects. Blood samples were taken through cardiac puncture.

Table 68
Treatment groups

Group No.	Treatment	Dose (mg/kg/week)	HOE-140
1. (N=8)	PBS	-	No
2. (N=4)	PBS	-	Yes
3. (N=8)	ISIS 482584	160	No
4. (N=8)	ISIS 482584	80	No
5. (N=8)	ISIS 482584	40	No
6. (N=8)	ISIS 482584	20	No
7. (N=8)	ISIS 482584	10	No
8. (N=8)	ISIS 482584	5	No

Quantification of vascular permeability

The harvested tissues from the feet, colon, and ears were placed in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing feet and ear tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}, and is presented in Table 69. Higher OD values are associated with higher levels of permeability.

As presented in Table 10, most of the tissues of mice treated with ISIS 482584 at all doses (Groups 3-8) demonstrated reduced basal vascular permeability compared to the PBS control (Group 1). The reduction in basal vascular permeability of the ISIS oligonucleotide-treated groups was comparable to the same demonstrated in the positive control group treated with HOE-140 (Group 2).

Table 69
OD_{600nm} of Evans Blue dye to measure vascular permeability

Group No.	Treatment	Dose (mg/kg/week)	HOE-140	Colon	Feet	Ears
1	PBS	-	No	0.27	0.17	0.013
2	PBS	-	Yes	0.24	0.09	0.047
3	ISIS 482584	160	No	0.25	0.11	0.019
4	ISIS 482584	80	No	0.24	0.09	0.014
5	ISIS 482584	40	No	0.27	0.11	0.011
6	ISIS 482584	20	No	0.26	0.11	0.009
7	ISIS 482584	10	No	0.31	0.10	0.015
8	ISIS 482584	5	No	0.32	0.11	0.009

Quantification of vascular leakage

- 5 The blood drawn through cardiac puncture was immediately mixed with 3 times the volume of ice-cold ethanol. The solution was centrifuged at 15,000 g for 20 minutes at 4°C to remove cell debris and precipitated plasma proteins. The ethanol extracts were further purified by ultra-filtration through a 10 kDa MWCO filter. The color intensity of the ethanol extracted plasma solution was then measured at OD_{620nm}. The results are presented in Table 70 as percentage increase or decrease of the OD values of the Group 1 PBS control. It was expected that treatment groups may display higher OD values due to reduced vascular leakage. All the mice in the ISIS oligonucleotide-treated groups demonstrated significantly reduced vascular leakage compared to the PBS negative control.

Table 70
Percentage of OD_{620nm} of Evans Blue dye compared to the PBS basal control to measure vascular leakage

Group No.	Treatment	Dose (mg/kg/week)	HOE-140	Plasma
2. (N=8)	ISIS 482584	160	No	95
3. (N=8)	ISIS 482584	80	No	93
4. (N=8)	ISIS 482584	40	No	83
5. (N=8)	ISIS 482584	20	No	56
6. (N=8)	ISIS 482584	10	No	36

Quantification of High Molecular Weight Kininogen (HMWK)

Western blot quantification of HMWK from blood samples are presented in Figure 2 and Tables 71 and 72.

As shown in Table 71, Groups treated with 482584 have higher levels of HMWK as compared to PBS control, increasing in a dose-dependent manner. Treatment with PKK antisense oligonucleotide results in stabilization of HMWK. Thus, vascular permeability is reduced in ISIS 482584-treated groups in a dose-dependent manner. As shown in Table 72, Groups treated with ISIS 482584 have lower HMWK cleavage product as compared to PBS control, decreasing in a dose-dependent manner. Thus, reduced HMWK is caused by PKK cleavage of HMWK into cleavage products (including bradykinin and HKa). Data are presented in Intensity Units as measured by densitometer.

Table 71

Quantification of HMWK by densitometer

Group No	Treatment	Dose (mg/kg/week)	Intensity Units
1	PBS	-	89
3	ISIS 482584	160	21358
4	ISIS 482584	80	7279
5	ISIS 482584	40	873
6	ISIS 482584	20	608
7	ISIS 482584	10	507

Table 72

Quantification of HMWK cleavage product by densitometer

Group No	Treatment	Dose (mg/kg/week)	Intensity Units
1	PBS	-	401738
3	ISIS 482584	160	19936
4	ISIS 482584	80	204482
5	ISIS 482584	40	388135
6	ISIS 482584	20	403360
7	ISIS 482584	10	414774

15 **Example 15: Combination therapy of antisense oligonucleotides targeting PKK and Factor 12 on captopril-induced vascular permeability in mice**

Mice were treated varying doses of ISIS 410944, a 5-10-5 MOE gapmer targeting Factor 12 (GCATGGGACAGAGATGGTGC; SEQ ID NO: 2247), and ISIS 482584 in a captopril-induced vascular permeability model.

Treatment

The various treatment groups for this assay are presented in Table 73.

Group 1 consisted of 4 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. No other treatment was administered to Group 1 which served as a control group to measure the basal levels of vascular permeability.

Group 2 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. Group 2 served as the control group for captopril-induced vascular permeability.

Group 3 consisted of 4 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice were intraperitoneally administered 20 µg of captopril. The mice were also intraperitoneally administered 30 µg of HOE-140. Group 3 served as a positive control for inhibition of captopril-induced vascular permeability.

Groups 4, 5, 6, 7, and 8 consisted of 8 mice each and were treated with 2.5 mg/kg, 5 mg/kg, 10 mg/kg, 20 mg/kg, or 40 mg/kg (corresponding to 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, or 80 mg/kg per week), respectively of ISIS 482584 and ISIS 410944 each administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice of all the groups were intraperitoneally administered 20 µg of captopril. Groups 4-8 served as the experimental treatment groups for examining the effect of ISIS 410944 and ISIS 482584 on captopril-induced vascular permeability.

All the groups were then injected with 30 mg/kg of Evans Blue solution in the tail vein. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, ears, and intestines were harvested.

Table 73
Treatment groups

Group No.	Treatment	Dose (mg/kg/wk) of each ASO	Captopril	HOE-140
1. (N=4)	PBS	-	No	No
2. (N=8)	PBS	-	Yes	No
3. (N=4)	PBS	-	Yes	Yes
4. (N=8)	ISIS 482584+ISIS 410944	80	Yes	No
5. (N=8)	ISIS 482584+ISIS 410944	40	Yes	No

6. (N=8)	ISIS 482584+ISIS 410944	20	Yes	No
7. (N=8)	ISIS 482584+ISIS 410944	10	Yes	No
8. (N=8)	ISIS 482584+ISIS 410944	5	Yes	No

Quantification of vascular permeability

The harvested tissues from the feet, colon, and ears were placed in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing feet and ear tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}, and is presented in Table 74. Higher OD values are associated with higher levels of permeability.

As presented in Table 74, most of the tissues of mice treated with a combination of ISIS 482584 and ISIS 410944 at all doses (Groups 3-8) demonstrated reduced vascular permeability compared to the PBS control (Group 1). The reduction in vascular permeability of the ISIS oligonucleotide-treated groups was comparable to the same demonstrated in the basal PBS control (Group 1), as well as the positive control group treated with HOE140 (Group 2). Combination of PKK and Factor 12 antisense oligonucleotides results in synergistic decrease in permeability. As expected, a corresponding synergistic decrease in vascular leakage was also observed.

Table 74
OD_{600nm} of Evans Blue dye to measure vascular permeability

Group No.	Treatment	Dose (mg/kg/wk) of each ASO	Captopril	HOE-140	Colon	Feet	Intestines	Ears
1	PBS	-	No	No	0.24	0.11	0.13	0.01
2	PBS	-	Yes	No	0.38	0.15	0.11	0.05
3	PBS	-	Yes	Yes	0.23	0.06	0.15	0.04
4	ISIS 482584+ISIS 410944	80	Yes	No	0.19	0.07	0.11	0.04
5	ISIS 482584+ISIS 410944	40	Yes	No	0.19	0.07	0.12	0.03
6	ISIS 482584+ISIS 410944	20	Yes	No	0.22	0.08	0.12	0.04
7	ISIS 482584+ISIS 410944	10	Yes	No	0.38	0.13	0.13	0.05

8	ISIS 482584+ISIS 410944	5	Yes	No	0.53	0.12	0.13	0.03
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Example 16: Combination therapy of antisense oligonucleotides targeting PKK and Factor 12 on basal vascular permeability in mice

Mice were treated with varying doses of ISIS 410944, an antisense oligonucleotide targeting Factor 12, and ISIS 482584 in a basal vascular permeability model.

Treatment

The various treatment groups for this assay are presented in Table 75.

Group 1 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. No other treatment was administered to Group 1 which served as a control group to measure the basal levels of vascular permeability.

Group 2 consisted of 4 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. At the end of the treatment period, the mice were intraperitoneally administered 30 µg of HOE-140. Group 2 served as a positive control for inhibition of basal vascular permeability.

Groups 3, 4, 5, 6, and 7 consisted of 8 mice each and were treated with 2.5 mg/kg, 5 mg/kg, 10 mg/kg, 20 mg/kg, or 40 mg/kg (corresponding to 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, or 80 mg/kg per week), respectively of ISIS 482584 and ISIS 410944 each administered subcutaneously twice a week for 3 weeks. Groups 3-7 served as the experimental treatment groups for examining the effect of ISIS 410944 and ISIS 482584 on basal vascular permeability.

All the groups were then injected with 30 mg/kg of Evans Blue solution in the tail vein. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, ears, and intestines were harvested.

Table 75
Treatment groups

Group No.	Treatment	Dose (mg/kg/wk)	HOE-140
1. (N=8)	PBS	-	No
2. (N=4)	PBS	-	Yes
3. (N=8)	ISIS 482584+ISIS 410944	80	No

4. (N=8)	ISIS 482584+ISIS 410944	40	No
5. (N=8)	ISIS 482584+ISIS 410944	20	No
6. (N=8)	ISIS 482584+ISIS 410944	10	No
7. (N=8)	ISIS 482584+ISIS 410944	5	No

Quantification of vascular permeability

The harvested tissues from the feet, colon, intestines, and ears were placed in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing feet and ear tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}, and is presented in Table 76. Higher OD values are associated with higher levels of permeability.

As presented in Table 76, most of the tissues of mice treated with a combination of ISIS 482584 and ISIS 410944 at all doses (Groups 2-7) demonstrated reduced vascular permeability compared to the PBS control (Group 1). The reduction in vascular permeability of the ISIS oligonucleotide-treated groups was comparable to the same demonstrated in positive control group treated with HOE140 (Group 2). Combination of PKK and Factor 12 antisense oligonucleotides results in synergistic decrease in permeability. As expected, a corresponding synergistic decrease in vascular leakage was also observed.

Table 76
OD_{600nm} of Evans Blue dye to measure vascular permeability

Group No.	Treatment	Dose (mg/kg/wk)	HOE-140	Colon	Feet	Intestines	Ears
1	PBS	-	No	0.19	0.08	0.10	0.004
2	PBS	-	Yes	0.14	0.04	0.08	0.008
3	ISIS 482584+ISIS 410944	80	No	0.14	0.04	0.09	0.01
4	ISIS 482584+ISIS 410944	40	No	0.15	0.05	0.10	0.006
5	ISIS 482584+ISIS 410944	20	No	0.15	0.04	0.10	0.007
6	ISIS 482584+ISIS 410944	10	No	0.15	0.06	0.10	0.004

7	ISIS 482584+ISIS 410944	5	No	0.14	0.05	0.13	0.002
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Example 17: Inhibition of Factor 12 protein activation by ISIS 482584

The effect of antisense inhibition of PKK mRNA on Factor 12 protein activation was evaluated.

Treatment

5 The various treatment groups for this assay are presented in Table 77.

Group 1 consisted of 8 mice and was treated with PBS administered subcutaneously twice a week for 3 weeks. No other treatment was administered to Group 1 which served as a control group to measure Factor 12 activation.

10 Groups 2, 3, 4, 5, and 6 consisted of 8 mice each and were treated with 2.5 mg/kg, 5 mg/kg, 10 mg/kg, 20 mg/kg, or 40 mg/kg (corresponding to 5 mg/kg, 10 mg/kg, 20 mg/kg, 40 mg/kg, or 80 mg/kg per week), respectively of ISIS 482584 administered subcutaneously twice a week for 3 weeks. Groups 2-6 served as the treatment groups for measuring the effect of ISIS 482584 on Factor 12 activation.

At the end of the treatment period, plasma was harvested from the mice for the Spectrozyme® Factor 12a based amidolytic assay for Factor 12 in plasma.

15

Table 77
Treatment groups

Group No.	Treatment	Dose (mg/kg/wk)
1. (N=8)	PBS	-
2. (N=8)	ISIS 482584	80
3. (N=8)	ISIS 482584	40
4. (N=8)	ISIS 482584	20
5. (N=8)	ISIS 482584	10
6. (N=8)	ISIS 482584	5

Assay for Factor 12 activation in plasma

20 Plasma (5 µL) was added to 85 µL of PBS with 1 µg/ml dextran sulfate (500kDa) in a 96 well polypropylene microplate and the solution was incubated for 5 minutes at room temperature. Spectrozyme® FXIIa (10 µL of a 2 mM solution) and 0.2 mM KALLISTOP™ solution was added and the absorbance kinetic was measured at 405 nm. Factor 12 activation was measured in the linear phase of absorbance

accumulation. The results are presented in Table 78 as a percentage of Factor 12 activation measured in the PBS control sample. As observed in Table 78, inhibition of PKK by ISIS 482584 results in decreased activation of Factor 12 by its substrate, implying the that PKK is required for proper factor 12 activation.

5

Table 78
Percentage Factor 12 activation compared to the PBS control

Dose (mg/kg/wk)	% F12 activation
80	14
40	24
20	47
10	63
5	82

Example 18: *In vivo* effect of antisense inhibition of murine PKK on C1-INH antisense oligonucleotide-induced vascular permeability

10 Vascular permeability induced by ISIS 461756, an antisense oligonucleotide which targets murine C1 inhibitor mRNA, increases vascular permeability in mice and replicates the pathology of hereditary angioedema. The effect of ISIS 482584 on this model was evaluated.

Treatment

15 One group of 8 mice was treated with 40 mg/kg ISIS 482584 administered subcutaneously twice a week for 3 weeks (weekly dose of 80 mg/kg). A second group of 8 mice was treated with 40 mg/kg of the control oligonucleotide, ISIS 141923, administered subcutaneously twice a week for 3 weeks (weekly dose of 80 mg/kg). A third group of 8 mice was treated with PBS administered subcutaneously twice a week for 3 weeks. On day 14, all the groups were treated with 12.5 mg/kg ISIS 461756 administered subcutaneously twice a week for 3 weeks (weekly dose of 25 mg/kg). A control group of mice was treated with PBS
20 administered subcutaneously twice a week for 3 weeks but was not administered ISIS 461756.

At the end of the treatment period, all the groups were injected with 30 mg/kg of Evans Blue solution into the tail vein. The mice were sacrificed 30 min after the Evans Blue solution administration and colons, feet, ears, and intestines were harvested. The liver was also harvested for RNA analysis.

RNA analysis

25 RNA was isolated from the liver for RT-PCR analysis of C1-INH and PKK mRNAs. The primer probe set for C1-INH is RTS3218 (forward sequence GAGTCCCCCAGAGCCTACAGT, designated herein as SEQ ID NO: 2234; reverse sequence TGTCATTTGTTATTGTGATGGCTACA, designated herein as

SEQ ID NO: 2235; probe sequence CTGCCCTCTACCTGGCCAACAACCA, designated herein as SEQ ID NO: 2236). The primer probe set for PKK is RTS3287 (forward sequence ACAAGTGCATTTTACAGACCAGAGTAC, designated herein as SEQ ID NO: 2237; reverse sequence GGTGTGTCGCTGACTTTATGCT, designated herein as SEQ ID NO: 2238; probe sequence AAGCACAGTGCAAGCGGAACACCC, designated herein as SEQ ID NO: 2239). The results are presented in Table 79 as percent inhibition compared to the PBS control not treated with ISIS 461756. The data indicates that ISIS 461756 significantly reduced C1-INH mRNA expression and that treatment with ISIS 482584 significantly reduced PKK expression.

Table 79

Percent inhibition of mRNA expression in mice treated with ISIS 461756 compared to the untreated PBS control

Treatment	C1-INH mRNA	PKK mRNA
PBS	76	0
ISIS 141923	79	0
ISIS 482584	77	78

Quantification of vascular permeability

The harvested tissues from the feet, colon, and intestines were placed in formamide solution overnight to leach out the Evans Blue dye. The formamide solution containing feet tissue was heated to 55°C and left overnight. The color intensity of the dye-infused formamide solution was then measured at OD_{600nm}. The data is presented in Table 80 as percent increase or reduction compared to the PBS control not treated with ISIS 461756. The data indicates that treatment with ISIS 482584 prevented vascular permeability induced by ISIS 461756.

Table 80

Percent change in vascular permeability in mice treated with ISIS 461756 compared to the untreated PBS control

Treatment	Colon	Feet	Intestines
PBS	13	70	27
ISIS 141923	2	80	14
ISIS 482584	-23	2	-25

Example 19: *In vivo* effect of antisense inhibition of murine PKK in the FeCl₃-induced inferior vena cava thrombosis model

ISIS 482584, which demonstrated significant *in vitro* and *in vivo* inhibition of PKK, was evaluated in the FeCl₃-induced inferior vena cava thrombosis mouse model.

5 Treatment

Three groups of 8 male BALB/c mice were treated with 10 mg/kg, 20 mg/kg, or 40 mg/kg of ISIS 482584, administered subcutaneously twice a week for 3 weeks (weekly doses of 20 mg/kg, 40 mg/kg, or 80 mg/kg). Two control groups of 12 BALB/c mice each were treated with PBS, administered subcutaneously twice a week for 3 weeks. Two days after the last dose of antisense oligonucleotide or PBS, mice from all groups were anesthetized with 150 mg/kg ketamine mixed with 10 mg/kg xylazine, administered by intraperitoneal injection. Thrombus formation was induced with FeCl₃ in all groups of anesthetized mice except the first control group.

In mice undergoing FeCl₃ treatment, thrombus formation was induced by applying a piece of filter paper (2 x 4 mm) pre-saturated with 10 % FeCl₃ solution directly on the vena cava. After 3 minutes of exposure, the filter paper was removed. Thirty minutes after the filter paper application, a fixed length of the vein containing the thrombus was dissected out for platelet analysis. Liver was collected for RNA analysis.

Quantification of Platelet Composition

Real-time PCR quantification of platelet factor-4 (PF-4) was used to quantify platelets in the vena cava as a measure of thrombus formation. PF-4 mRNA levels were measured using the murine primer probe set mPF4_LTS_00086 (forward sequence AGACCCATTCCTCAAGGTAGAACT, designated herein as SEQ ID NO: 2240; reverse sequence CGCAGCGACGCTCATG, designated herein as SEQ ID NO: 2241; probe sequence TCTTTGGGTCCAGTGGCACCTCTT, designated herein as SEQ ID NO: 2242). Results are presented as a percentage of PF-4 in ISIS oligonucleotide-treated mice, as compared to the two PBS-treated control groups. As shown in Table 81, treatment with ISIS 482584 resulted in a significant reduction of PF-4 in comparison to the PBS control. Therefore, reduction of PKK by the compound provided herein is useful for inhibiting thrombus formation.

Table 81

Analysis of thrombus formation by real-time PCR quantification of PF-4 in the FeCl₃ induced venous thrombosis model

	Dose in mg/kg/wk	PF-4
PBS-FeCl ₃	-	0
PBS+FeCl ₃	-	100
ISIS 482584	20	62

	40	34
	80	25

Example 20: *In vivo* effect of antisense inhibition of murine PKK in a tail bleeding assay

Tail-bleeding was measured to observe whether treatment with ISIS 482584 causes excess bleeding or hemorrhage in mice.

5 *Treatment*

Groups of 10 male BALB/c mice were treated with 10 mg/kg, 20 mg/kg, or 40 mg/kg of ISIS 482584, administered subcutaneously twice a week for 3 weeks (weekly doses of 20 mg/kg, 40 mg/kg, or 80 mg/kg). A control group of 8 BALB/c mice was treated with PBS, administered subcutaneously twice a week for 3 weeks.

10 *Tail-bleeding Assay*

Two days after the final treatment of ISIS oligonucleotides or PBS, mice were placed in a tail bleeding chamber. Mice were anesthetized in the chamber with isoflurane. Then, a small piece of tail (approximately 4 mm from the tip) was cut with sterile scissors. The cut tail was immediately placed in a 15 mL Falcon tube filled with approximately 10 mL of 0.9 % NaCl buffer solution warmed to 37°C. The blood
15 was collected over the course of 40 minutes. The saline filled tubes were weighed both before and after bleeding. The results are provided in Table 82.

Treatment with ISIS 482584 did not significantly affect bleeding. These data suggest that the hemorrhagic potential of the compounds provided herein is low. These data taken with the results provided in Example 19 suggest inhibition of PKK with the compounds described herein are useful for providing
20 antithrombotic activity without associated bleeding risk.

Table 82
Tail bleeding assay after treatment with ISIS 482584

	Dose (mg/kg/wk)	Bleeding (mL)
PBS	-	0.03
ISIS 482584	20	0.03
	40	0.14
	80	0.07

Example 21: *In vivo* effect of antisense inhibition of murine PKK in the FeCl₃ induced mesenteric thrombosis model

ISIS 482584 was evaluated in the FeCl₃ induced mesenteric thrombosis mouse model.

Treatment

A group of 6-8 Swiss-Webster mice was treated with 40 mg/kg of ISIS 482584, administered subcutaneously twice a week for 3 weeks (weekly dose of 80 mg/kg). A control group of 6 Swiss-Webster mice was treated with PBS, administered subcutaneously twice a week for 3 weeks. Two days after the last dose of antisense oligonucleotide or PBS, mice from all groups were anesthetized with 75 mg/kg ketamine mixed with 25 mg/kg xylazine, administered by subcutaneous injection.

Rhodamine 6G dye at a dosage of 5 mg/kg was injected subcutaneously to stain platelets. Alexa-647-labeled anti-fibrinogen antibody at a dosage of 1 mg/kg was injected via tail vein injection to stain fibrin. The abdomen was opened by a middle incision. The visceral mesentery was spread on a glass coverslip and the mesenteric arterioles (70-120 μ m) were located by observation under a microscope. Thrombus formation was induced by applying of cotton threads (2 x 0.3 mm) pre-saturated with 6% FeCl₃ solution directly on the target vessel. After three minutes of exposure, the thread was removed and the color intensities of both the dyes were recorded by fluorescent microscopy (Olympus FluoView 1000 confocal laser scanning microscope) with appropriate filters for 70 min.

The results for platelet aggregation in the control and treatment groups are presented in Table 83, expressed in arbitrary units (a.u.). Platelet aggregation was reduced in mice treated with ISIS 482584 at a dose of 80 mg/kg/week as compared to mice treated with PBS. The results for fibrin formation in the control and treatment groups are presented in Table 84, also expressed in arbitrary units (a.u.). Fibrin formation was reduced in mice treated with ISIS 482584 at a dose of 80 mg/kg/week as compared to mice treated with PBS. Therefore, these results suggest that ISIS 482584 inhibits thrombus formation.

Table 83

Analysis of platelet aggregation by real-time measurement of fluorescent intensity (a.u.) in a FeCl₃ induced mesenteric thrombus model

Time (sec)	PBS	80 mg/kg/wk
752	54	74
1018	315	11
1284	485	7
1550	654	0
1815	1079	0
2081	1164	0
2347	1452	0

2613	1440	38
2879	1689	148
3144	1716	129
3410	1845	169
3676	1865	131
3944	2055	87

Table 84

Analysis of fibrin formation by real-time measurement of fluorescent intensity (a.u.) in a FeCl₃ induced mesenteric thrombus model

Time (sec)	PBS	80 mg/kg/wk
752	9	54
1018	86	7
1284	203	1
1550	319	10
1815	521	16
2081	598	15
2347	831	61
2613	959	88
2879	1157	141
3144	1236	150
3410	1374	173
3676	1629	160
3944	1822	128

5

Example 22: *In vivo* effect of antisense inhibition of murine PKK in the stenosis-induced inferior vena cava thrombosis model

ISIS 482584 was evaluated in the stenosis-induced inferior vena cava (IVC) thrombosis model. Reduced blood flow and endothelial damage are hallmarks of this model, also known as the St. Tomas model.

10 *Treatment*

Four groups of 6-8 BALB/c mice were treated with 5 mg/kg, 10 mg/kg, 20 mg/kg, or 40 mg/kg of ISIS 482584, administered subcutaneously twice a week for 3 weeks (weekly doses of 10 mg/kg, 20 mg/kg, 40 mg/kg, or 80 mg/kg). A control group of 8 BALB/c mice was treated with PBS, administered subcutaneously twice a week for 3 weeks. Two days after the last dose of antisense oligonucleotide or PBS was administered, mice from all groups were anesthetized with 2.5% inhalant isoflurane. The IVC of the mice was exposed via a midline abdominal incision below the left renal vein, and was separated from the abdominal aorta by blunt dissection. A 6-0 silk tie (Ethicon, UK) was placed behind the blood vessel just below the left renal vein and a metal 4-0 suture (Ethicon, UK) was placed longitudinally over the IVC to tie

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the silk tie on top. The metal suture was then removed. Two neurovascular surgical clips (Braun Medical Inc, PA) were placed at two seaparate positions below the ligation for 20 seconds each, after which they were removed. The abdominal cavity contents were then replaced and the abdomen was closed. After 24 hrs, the IVC was exposed and checked for thrombi formation. All thrombi formed were collected and fixed in 10% formalin for 24 hrs.

The thrombi were weighed and the results are presented in Table 85, expressed in miligrams. As demonstrated by the results, treatment with increasing doses of ISIS 482584 resulted in corresponding decrease in thrombus weight. The results indicate that antisense inhibition of PKK is useful for inhibiting thrombus formation.

Table 85

Thrombi weights in the stenosis-induced IVC thrombosis model

	Dose in mg/kg/wk	Weight (mg)
PBS	-	10
ISIS 482584	10	8
	20	6
	40	5
	80	3

WHAT IS CLAIMED:

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: 30-2226.
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 the nucleobase sequence of SEQ ID NO: 570.
3. 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 the nucleobase sequence of SEQ ID NO: 705.
4. 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, or at least 16 consecutive nucleobases of the nucleobase sequence of SEQ ID NO: 1666.
5. A compound, comprising a modified oligonucleotide consisting of 20 linked nucleosides and having the nucleobase sequence of SEQ ID NO: 570.
6. A compound, comprising a modified oligonucleotide consisting of 20 linked nucleosides and having the nucleobase sequence of SEQ ID NO: 705.
7. A compound, comprising a modified oligonucleotide consisting of 16 linked nucleosides and having the nucleobase sequence of SEQ ID NO: 1666.
8. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 62, 72, 103, 213, 312, 334-339, 344, 345, 346, 348, 349, 351, 369, 373, 381, 382, 383, 385, 387-391, 399, 411, 412, 414, 416, 444, 446-449, 452, 453, 454, 459, 460, 462-472, 473, 476, 477, 479, 480, 481, 484, 489-495, 497, 500, 504, 506, 522, 526, 535, 558, 559, 560, 564, 566, 568-571, 573, 576, 577, 578, 587, 595, 597-604, 607, 608, 610, 613, 615, 618, 619, 622, 623, 624, 633, 635, 636, 638, 639, 640, 642, 643, 645, 652, 655-658, 660, 661, 670, 674-679, 684, 685, 698, 704, 705, 707,

708, 713, 716, 717, 728, 734, 736, 767, 768, 776, 797, 798, 800, 802, 810, 815, 876, 880, 882, 883, 886, 891, 901-905, 908-911, 922, 923, 924, 931, 942, 950-957, 972, 974, 978, 979, 980, 987-991, 1005, 1017-1021, 1025, 1026, 1029, 1030, 1032, 1034, 1035, 1037, 1040, 1041, 1045, 1046, 1051, 1054, 1059, 1060, 1061, 1064, 1065, 1066, 1075, 1076, 1087, 1089, 1111, 1114, 1116, 1117, 1125, 1133, 1153, 1169, 1177, 1181, 1182, 1187, 1196, 1200, 1214, 1222, 1267, 1276, 1277, 1285, 1286, 1289, 1290, 1291, 1303, 1367, 1389, 1393, 1398-1401, 1406, 1407, 1408, 1411, 1419-1422, 1426, 1430, 1431, 1432, 1434-1437, 1439, 1440, 1443, 1444, 1451, 1452, 1471, 1516, 1527, 1535, 1537, 1538, 1539, 1540, 1541, 1563, 1564, 1567, 1568, 1616, 1617, 1623, 1629, 1664, 1665, 1666, 1679, 1687, 1734, 1804, 1876, 1886, 1915, 2008, 2018, 2100, 2101, 2115, and 2116.

9. The compound of claim 8, wherein the modified oligonucleotide achieves at least 80% mRNA inhibition of PKK.

10. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 62, 72, 103, 213, 334-339, 344, 346, 348, 349, 351, 381, 382, 383, 385, 389, 390, 391, 446, 448, 452, 453, 454, 466-473, 476, 481, 484, 491, 492, 494, 495, 497, 504, 526, 558, 559, 566, 568-571, 576, 578, 587, 595, 597, 598, 600-604, 607, 610, 613, 618, 619, 624, 635, 638, 639, 645, 652, 656, 657, 658, 660, 674, 675, 676, 684, 698, 704, 705, 707, 713, 716, 768, 876, 880, 901-905, 908-911, 922, 923, 924, 931, 942, 951, 954-957, 972, 974, 978, 979, 987, 988, 990, 1005, 1019, 1020, 1021, 1025, 1032, 1037, 1040, 1041, 1045, 1054, 1059, 1060, 1061, 1064, 1065, 1066, 1075, 1111, 1116, 1117, 1125, 1133, 1153, 1169, 1177, 1200, 1222, 1267, 1285, 1290, 1291, 1303, 1367, 1398, 1399, 1401, 1406, 1408, 1411, 1419, 1420, 1421, 1426, 1430, 1431, 1432, 1434-1437, 1440, 1443, 1444, 1451, 1537-1540, 1563, 1616, 1679, 1687, 1804, 2008, 2101, 2115, and 2116.

11. The compound of claim 10, wherein the modified oligonucleotide achieves at least 85% mRNA inhibition of PKK.

12. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 346, 351, 382, 390, 391, 446, 448, 452, 453, 468, 469, 470, 471, 472, 476, 481, 491, 495, 504, 558, 566, 568, 570, 571, 578, 587, 597, 598, 600, 604, 613, 635, 638, 645, 656, 658, 660, 674, 675, 684, 704, 705, 880, 901-905, 909, 922, 931, 951, 954, 956, 990, 1005, 1020, 1032, 1037, 1040, 1041, 1045, 1054, 1075, 1111, 1125, 1133, 1153, 1200, 1267, 1291, 1303, 1398, 1399, 1401, 1406, 1420, 1426, 1430, 1431, 1434, 1435, 1436, 1440, 1443, 1451, 1537-1540, 2115, and 2116.

13. The compound of claim 12, wherein the modified oligonucleotide achieves at least 90% mRNA inhibition of PKK.

14. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 391, 448, 468, 469, 568, 570, 598, 635, 658, 674, 684, 705, 901, 903, 904, 922, 990, 1267, 1291, 1420, 1430, 1431, 1434, 1435, 1436, 1537, 1538, and 1540.

15. The compound of claim 14, wherein the modified oligonucleotide achieves at least 95% mRNA inhibition of PKK.

16. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 338, 346, 349, 382, 383, 390, 448, 452, 453, 454, 495, 526, 559, 570, 587, 598, 635, 660, 705, 901, 903, 904, 908, 923, 931, 955, 974, 988, 990, 1020, 1039, 1040, 1111, 1117, 1267, 1291, 1349, 1352, 1367, 1389, 1393, 1399, 1401, 1408, 1411, 1426, 1499, 1516, 1535, 1544, 1548, 1563, 1564, 1568, 1569, 1598, 1616, 1617, 1623, 1624, 1643, 1661, 1665, 1666, 1673, 1679, 1695, 1720, 1804, 1817, 1876, 1881, 1886, 1940, 1947, 2008, 2018, 2019, 2031, 2044, 2100, 2101, 2115, and 2116.

17. The compound of claim 16, wherein the modified oligonucleotide achieves an IC_{50} (μ M) of 0.4 or less.

18. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 346, 349, 382, 453, 454, 495, 526, 570, 587, 598, 635, 660, 901, 903, 904, 931, 955, 990, 1020, 1111, 1267, 1349, 1352, 1367, 1389, 1399, 1408, 1411, 1426, 1516, 1535, 1544, 1548, 1563, 1564, 1568, 1569, 1598, 1616, 1617, 1623, 1643, 1661, 1665, 1666, 1673, 1695, 1804, 1876, 1881, 2019, 2044, 2100, 2101, 2115, and 2116.

19. The compound of claim 18, wherein the modified oligonucleotide achieves an IC_{50} (μ M) of 0.3 or less.

20. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 346, 382, 453, 495, 526, 570, 587, 598, 635, 901, 904, 931, 955, 1020,

1111, 1349, 1352, 1389, 1426, 1516, 1535, 1544, 1548, 1564, 1569, 1598, 1616, 1617, 1665, 1666, 1804, 1876, 1881, 2019, 2044, 2101, and 2116.

21. The compound of claim 20, wherein the modified oligonucleotide achieves an IC_{50} (μM) of 0.2 or less.

22. 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, or at least 16 consecutive nucleobases of any of the nucleobase sequences of SEQ ID NOs: 334, 495, 587, 598, 635, 1349, 1352, 1389, 1516, 1544, 1548, 1569, 1598, 1617, 1665, 1666, 1804, 1881, and 2019.

23. The compound of claim 22, wherein the modified oligonucleotide achieves an IC_{50} (μM) of less than 0.2.

24. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 27427-27466 of SEQ ID NO: 10.

25. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 33183-33242 of SEQ ID NO: 10.

26. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 30570-30610 of SEQ ID NO: 10.

27. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 27427-27521 of SEQ ID NO: 10.

28. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 33085-33248 of SEQ ID NO: 10.

29. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 30475-30639 of SEQ ID NO: 10.

30. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 27362-27525 of SEQ ID NO: 10.

31. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 33101-33241 of SEQ ID NO: 10.

32. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of nucleobases 30463-30639 of SEQ ID NO: 10.

33. A compound, comprising a modified oligonucleotide consisting of 12 to 30 linked nucleosides and comprising 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 complementary to an equal length portion of exon 9, exon 12, or exon 14 of a PKK nucleic acid.

34. The compound of claims 24-33, 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: 10.

35. The compound of any preceding claim, consisting of a single-stranded modified oligonucleotide.

36. The compound of any preceding claim, wherein at least one internucleoside linkage is a modified internucleoside linkage.

37. The compound of claim 36, wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

38. The compound of claim 37, wherein each internucleoside linkage is a phosphorothioate linkage.

39. The compound of any preceding claim, wherein at least one nucleoside comprises a modified nucleobase.

40. The compound of claim 39, wherein the modified nucleobase is a 5-methylcytosine.

41. The compound of any preceding claim, wherein the modified oligonucleotide comprises at least one modified sugar.

42. The compound of claim 41, wherein the modified sugar is a 2' modified sugar, a BNA, or a THP.

43. The compound of claim 42, wherein the modified sugar is any of a 2'-O-methoxyethyl, 2'-O-methyl, a constrained ethyl, a LNA, or a 3'-fluoro-HNA.

44. The compound of any preceding claim, comprising at least one 2'-O-methoxyethyl nucleoside, 2'-O-methyl nucleoside, constrained ethyl nucleoside, LNA nucleoside, or 3'-fluoro-HNA nucleoside.

45. The compound of any preceding claim, 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.

46. The compound of any preceding claim, wherein the modified oligonucleotide consists of 20 linked nucleosides.

47. The compound of any preceding claim, wherein the modified oligonucleotide consists of 19 linked nucleosides.

48. The compound of any preceding claim, wherein the modified oligonucleotide consists of 18 linked nucleosides.

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

A = an adenine,
mC = a 5'-methylcytosine
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethyl modified nucleoside,
d = a 2'-deoxynucleoside, and
s = a phosphorothioate internucleoside linkage.

50. A compound consisting of a modified oligonucleotide according to the following formula: mCes mCes mCes mCes mCes Tds Tds mCds Tds Tds Tds Ads Tds Ads Gds mCes mCes Aes Ges mCe; wherein,

A = an adenine,
mC = a 5'-methylcytosine;
G = a guanine,
T = a thymine,
e = a 2'-O-methoxyethyl modified nucleoside,
d = a 2'-deoxynucleoside, and
s = a phosphorothioate internucleoside linkage.

51. A compound consisting of a modified oligonucleotide according to the following formula: mCes Ges Aks Tds Ads Tds mCds Ads Tds Gds Ads Tds Tds mCks mCks mCe; wherein,

A = an adenine,
 mC = a 5'-methylcytosine;
 G = a guanine,
 T = a thymine,
 e = a 2'-O-methoxyethyl modified nucleoside,
 k = a cEt modified nucleoside,
 d = a 2'-deoxynucleoside, and
 s = a phosphorothioate internucleoside linkage.

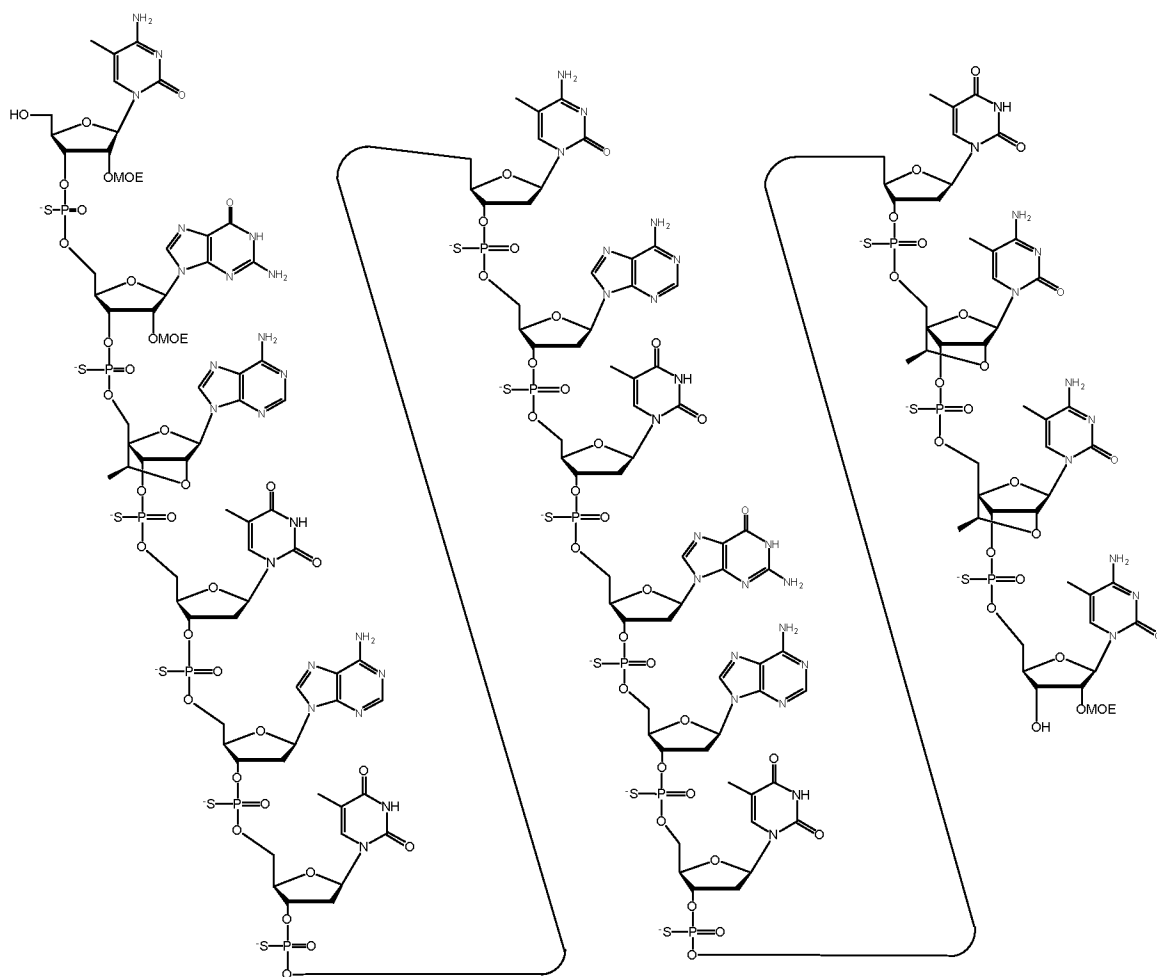
52. A compound consisting of a modified oligonucleotide according to the following formula:



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



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



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

56. A method comprising administering to an animal the compound or composition of any preceding claim.

57. The method of claim 56, wherein the animal is a human.

58. The method of claim 57, wherein administering the compound prevents, treats, or ameliorates a PKK associated disease, disorder or condition.

59. The method of claim 57, wherein the PKK associated disease, disorder or condition is a hereditary angioedema (HAE), edema, angioedema, swelling, angioedema of the lids, ocular edema,

macular edema, cerebral edema, thrombosis, embolism, thromboembolism, deep vein thrombosis, pulmonary embolism, myocardial infarction, stroke, or infarct.

60. Use of the compound or composition of any preceding claim for the manufacture of a medicament for treating an inflammatory disease or a thromboembolic disease.

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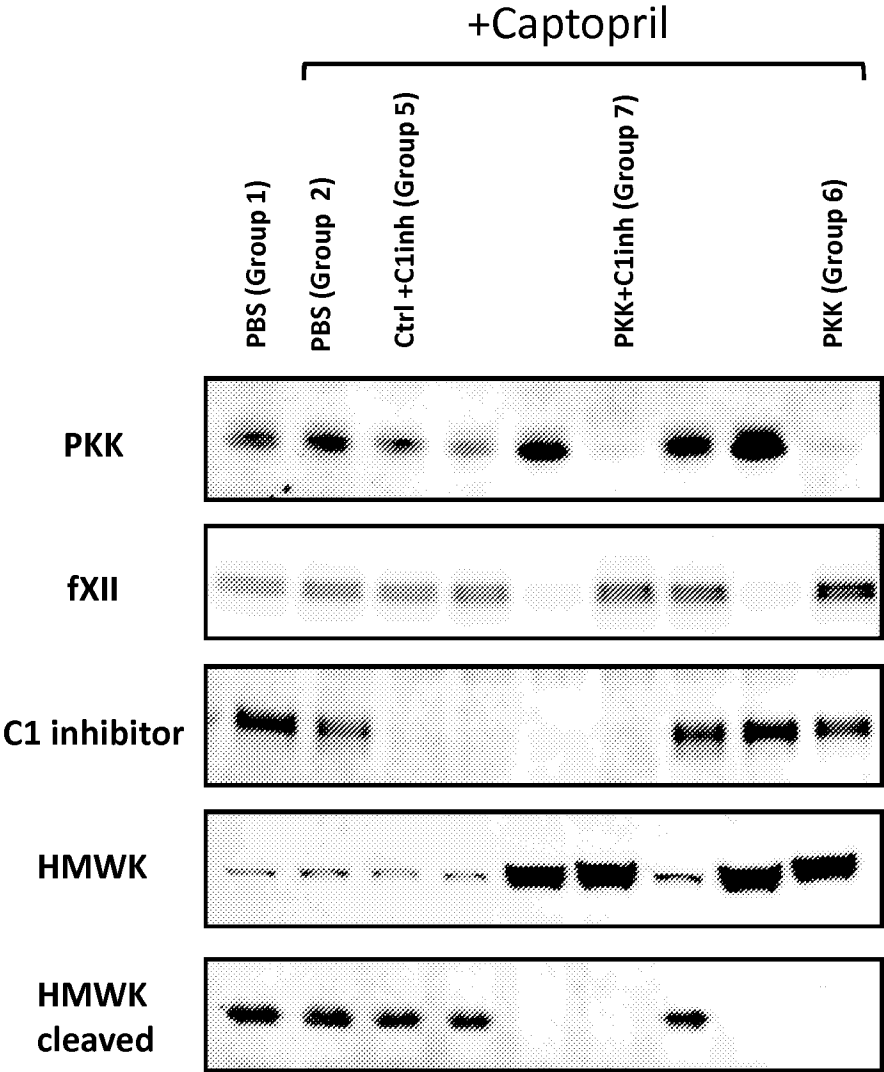


Figure 1

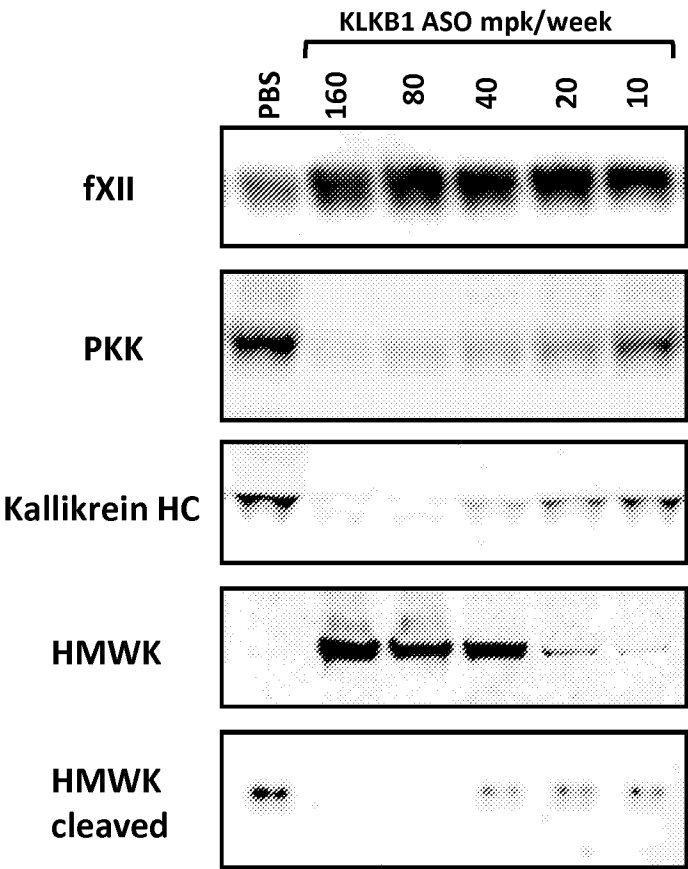


Figure 2